

From: Riggins, Patrick S.
Sent: Monday, February 07, 2005 8:35 AM
To: STIC-Biotech/ChemLib
Subject: seq search

This is in regard to case #10006265

Please search SEQ ID NOs, 2, 4, and 17(protein) against the commercial nucleotide databases in both a standard search and a standard oligomer search. The following information may be helpful in the search. I previously requested an alignment of these sequences. The results were as follows: SEQ ID NOs 2 and 17 are identical from 1-642. SEQ ID NO 2 and 17 are identical with SEQ ID NO 4 from 1-238. If this is in any way unclear, please call and I'll be happy to clarify.

The claims of interest are appended below. If you identify any other necessary searches based on these claims I would appreciate they be performed also. I'm fairly confident I have requested all that is necessary though. Incidentally, SEQ ID NOs 1, 3, and 16 encode SEQ ID NOs 2, 4, and 17, respectively.

1. An isolated nucleic acid of any one of (a) to (d) below:

(a) a nucleic acid encoding a protein comprising the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17,

(b) a nucleic acid comprising a coding region in the nucleotide sequence of any one of SEQ ID NOs:1, 3 or 16,

(c) a nucleic acid encoding a protein that comprises the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17, in which one or more amino acids are replaced, deleted, inserted and/or added and that is functionally equivalent to the protein comprising the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17, and

(d) a nucleic acid that hybridizes under stringent conditions with the nucleic acid comprising the nucleotide sequence of any one of SEQ ID NOs:1, 3 or 16, and that encodes a protein functionally equivalent to the protein comprising the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17.

2. An isolated nucleic acid encoding the amino acid sequence of any one of SEQ ID NOs:2, 4 or 17 or a fragment thereof.

Thank you,
Pat Riggins

Patrick Riggins
Examiner
Art Unit 1636
REM 3A64
571-272-6102

RECEIVED
FEB - 7 2005
STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: 2-7-05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
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FEATURES

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US-10-006-265-2 (1-652) x BD091864 (1-2969)

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DEFINITION Novel hemopoietin receptor protein, NR10.
ACCESSION BD091877
VERSION BD091877.1 GI:22637488
KEYWORDS WO 0075314-A/14.
SOURCE Homo sapiens (human)
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REFERENCE 1 (bases 1 to 2119)
AUTHORS Maeda,M. and Yaguchi,N.
TITLE Novel hemopoietin receptor protein, NR10
JOURNAL Patent: WO 0075314-A 14 14-DEC-2000;
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU
MADA, NORIKO YAGUCHI
COMMENT OS Homo sapiens (human)
PN WO 0075314-A/14
PD 14-DEC-2000
PF 01-JUN-2000 WO 2000JP003556
PR 02-JUN-1999 JP 99P 155797,30-JUL-1999 JP 99P 217797 PI
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RESULT 3
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DEFINITION Sequence 53 from Patent WO0200721.
ACCESSION AX365201
VERSION AX365201.1 GI:18696955
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuiper, J.L.
AUTHORS and Maurer, M.F.
TITLE Cytokine receptor zcytor17
JOURNAL Patent: WO 0200721-A 53 03-JAN-2002;
Zymogenetics, Inc. (US)
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Alignment Scores:
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Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.05% Indels: 1
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Qy	401	Leu	Val	Pro	Phe	Thr	Pro	Trp	Cys	Trp	Val	Asn	Ile	Ser	Val	Trp	Met	Leu	His	Asp	Val	420	
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Qy	481	Phe	Ser	Trp	Thr	Val	Asn	Ser	Ile	Leu	Gln	Trp	Gly	Leu	Glu	Ser	Leu	Val	Arg	Val	500		
Db	1937	TTCTCCAA	GACAGT	CAATTTCCAG	CACTTCCAGT	ACGCGCTGAGATCTCCTGA	AAAGAAAG	1996															
Qy	501	Thr	Ser	Trp	Ile	Val	Gln	Val	Met	Ala	Asn	Thr	Ser	Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	520	
Db	1997	ACCTCTT	CACTAT	TTGTTCA	GCTCATG	CCACGACACAGT	GCTGGGGAAACCAACGAC	2056															
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Db	2057	ATAAATT	CAAGAC	ATCTGTCA	TTCAGT	GTCTTTGAGTTATTCCTCAT	TAATCTTCTGATT	2116															
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Db	2117	GGTGAG	GCCTCTT	TAATCTCAT	TATCTCGAC	AGGAGCATGTGGCTCA	AAAAAAACCCAA	2176															
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Db	2177	AAATTGA	CTCATCTG	TGTGTGG	CCACCCGTTCC	CAACCTGCTGAA	AGATGATMACCA	2236															
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Db	2237	TGGCAT	TGAGATG	ATTTCA	AGATAA	CGTAAACCTGAAGAGT	CTGATGATCTGTGAAC	2296															
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RESULT 4
1499342

LOCUS	AV499342	2903 bp	mRNA	linear	PRI 10-JUN-2004
DEFINITION	Homo sapiens interleukin 31RA splice variant x4 (IL31RA) mRNA.				
ACCESSION	AY499342				
VERSION	AY499342.1	GI:46276462			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J., 1 (bases 1 to 2903) 2 (bases 1 to 2903) Dillon,S.R., Sprecher,C., Hammond,A., Bilsborough,J., Prensell,S.R., Haugen,H., Bilsborough,J., Maurer,M., Harder,B., Johanson,J., Bort,S., Mudri,S., Kuljper,J., Bukowski,T., Shea,P., Dong,D., Daovich,M., Lockwood,L., Levin,S., Leckel,C., Waggle,K., Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and Gross,J.A.				
TITLE	Interleukin 31, a cytokine produced by activated T cells, induces dermatitis in mice				
JOURNAL	Nat. Immunol. 5 (7), 752-760 (2004)				
PUBMED	15184896				
REFERENCE	2 (bases 1 to 2903)				
AUTHORS	Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M., Prensell,S.R., Haugen,H., Bilsborough,J., Maurer,M., Harder,B., Johanson,J., Bort,S., Mudri,S., Kuljper,J., Bukowski,T., Shea,P., Dong,D., Daovich,M., Lockwood,L., Levin,S., Leckel,C., Waggle,K., Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and Gross,J.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA				
FEATURES	Location/Qualifiers				
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gene					
CDS					
ORIGIN					
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RESULT 5
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 DEFINITION Sequence 45 from Patent WO0200721.
 ACCESSION AX365193
 VERSION AX365193.1 GI:18696949
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 ORGANISM Homo sapiens
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuiper, J.L.
 and Maurer, M.F.

TITLE Cytokine receptor zcytor17
JOURNAL Patent: WO 0200721-A 45 03-JAN-2002;
ZymoGenetics, Inc. (US)
FEATURES
SOURCE Location/Qualifiers
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CDS

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Alignment Scores:
Pred. No.: 2,126-239 Length: 2529
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Best Local Similarity: 99.69% Mismatches: 1
Query Match: 98.77% Indels: 1
DB: 6 Gaps: 0
US-10-006-265-2 (1-652) x AX365193 (1-2529)

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DEFINITION complete cds, alternatively spliced.
ACCESSION AY499339
VERSION AY499339.1 GI:46276456
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1. (bases 1 to 2529)
Dillon,S.R., Sprecher,C., Hammond,A., Bilisporough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J., Bukowski,T.,
Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., Leckel,C., Maggile,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
Interleukin 31, a cytokine produced by activated T cells, induces
dermatitis in mice
Nat. Immunol. 5 (7), 752-760 (2004)
JOURNAL
PUBMED 15184896
REFERENCE
2. (bases 1 to 2529)
Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M.,
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Dong,D., Dasovich,M., Lockwood,L., Levin,S., Leckel,C., Maggile,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
Direct Submission
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA
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Percent Similarity:	99.85%	Conservative:	1
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 REFERENCE 1 (bases 1 to 4315)
 AUTHORS Maeda,M., Yaguchi,N. and Hasegawa,M.
 TITLE NR10 splicing variants
 JOURNAL Patent: WO 02077230-A 1 03-OCT-2002;
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 MASAKAZU HASEGAWA
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 PN WO 02077230-A/1
 PD 03-OCT-2002
 PF 22-MAR-2002 WO 2002JP002769
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 PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE 1
 Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.
 Hematopoietic receptors hprt1 and hprt2
 JOURNAL Patent: WO 0229060-A 5 11-APR-2002;
 ImmuneX Corporation (US)
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 ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS

TITLE	Interleukin 31, a cytokine produced by activated T cells, induces dermatitis in mice
JOURNAL	Nat. Immunol.
PUBMED	5 (7), 752-760 (2004)
REFERENCE	15184896
AUTHORS	2 (bases 1 to 2393) Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M., Kraemer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and Gross,J.A. Rosenfeld-Franklin,M., Flechner,S.R., Haugen,A.S., Maier,W., Harder,B., Johnston,J., Bott,S., Muddi,S., Knipfer,J.L., Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J., Lockwood,L., Levyn,S.D., Leticl,C., Maggie,K., Day,H., Topouzis,S., Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and Gross,J.A.

TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA
FEATURES	Location/Qualifiers
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CDS	/gene="IL31RA" 66. .2360

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US-10-006-265-2 (1-652) x AY499341 (1-2393)

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QY	143	ValLysProValLeuGlyILeLysArgMetILeGlnILeGluTrpILeLysProGluLeu	162
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AK365149	ACCESSION	AX365149	
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
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Speicher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuiper,J.L.			
and Maurel,M.F.			
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ORIGIN

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US-10-006-265-2 (1-652) x AX365149 (1-2402)

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 Qy 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
 Db 1998 GTGAACCTTGGAAATGTTTGCAGAGAAATTTTTCACAGATGAAGCCGAAACGGGTCA 2056
 Qy 643 LysGlnPheArgArgGlyLysGluTrp 651
 Db 2057 AAACATTTAGAGGCGGAAAGAAATGG 2083
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 AX467333 2480 bp DNA linear PART 16-JUL-2002
 LOCUS AX467333
 DEFINITION Sequence 3 from Patent WO0229060.
 ACCESSION AX467333
 VERSION AX467333.1 GI:21900584
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 1 Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.
 Hematopoietic receptors hprt1 and hprt2
 Patent: WO 0229060-A 3 11-APR-2002;
 Immunex Corporation (US)
 FEATURES
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 Pred. No.: 7,15e-299 Length: 2480
 Score: 3435.00 Matches: 647
 Percent Similarity: 99.69% Conservative: 2
 Best Local Similarity: 99.39% Mismatches: 2
 Query Match: 98.59% Indels: 1
 DB: 6 Gaps: 0
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 Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
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 Qy 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
 Db 192 TGAATGCTCCCTTCACTCGCAAAATTCAGCTCGGACAGCTCTCCAGCTAAGCCTGAGA 251
 Qy 41 IleSerCysValTyrTyrTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 Db 252 ATTTCTGTGTACTACTATAGAAAAATTTAACTGACTTGAGATGACAGAAAAAGGA 311
 Qy 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn 80
 Db 312 ACCAGTTATACCAAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAAATGATAT 371
 Qy 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 Db 372 TGTAAACCAATATAGTTCTCAAGTGAATAATCGTGTCTGTGCTCTTTTCTCTCAAGA 431
 Qy 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 Db 432 ATTAACGATCCAGATATATATACATTGAGTGGAAAGCTGAAAGATGAGATGTATAT 491

QY 121 LysSerHisMetThrTyrTrpArgLeuGluIleAlaValThrGluProProValIle 140
 DB 492 AAATCTCATATGACTACTGAGATTTAAGAACATAGGAAACCACTTAAGATT 551
 QY 141 PheArgValIleProValLeuGlyIleIleValArgMetIleGlnIleGluTrpIleValPro 160
 DB 552 TTCCGTGTGAACACAGTTTGGGCATCAACGAATGATTCAATTTGAATGATTAAGCT 611
 QY 161 GluLeuAlaProValSerSerAspLeuValTyrThrLeuArgPheArgThrValAsnSer 180
 DB 612 GAGTTGGGCGCTGTTCATCTGATTAAATATACACATCTCGATTGAGACAGTCAACGT 671
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 QY 261 ArgLeuLeuTrpIleValIleArgGlyValAlaProValLeuGluIleValThrLeuGlyTyrAsn 280
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 QY 301 GlnLeuGluLeuValIleGluGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320
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 QY 321 LeuGlyIleValSerProValAlaThrLeuArgIleProAlaIleGlnIleValSerPheGln 340
 DB 1092 CTTGGGAAGTCTCCAGTGGCCACCTGAGATTCAGCTATTCAGAAATAATCATTTTCAG 1151
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 DB 1272 ACCACCTTCTCTGGAACTGTGTCTAGGCCCAAGACTGACGATCCAGCAAGATTA 1331
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 QY 461 GluArgIleGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyValGly 480
 DB 1512 GAGAGAAAGGCTATCATCTGCACTACACCATCTTTTACCAAGCTGAAGGTGAGAAAGGA 1571

QY 481 PheSerIleThrValAsnSerIleLeuGlnIleValGluLeuSerLeuValArgVal 500
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 QY 501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyIleValThrAsnGlyThrSer 520
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 QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
 DB 1812 AAATTGACTCATCTGTGTGGCCACCGTCCCAACCTGCTGAAGATATAGCCACA 1871
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 QY 601 ThrGluAspArgIleLeuValProCysSerThrProSerAspValLeuValIleAspVal 620
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 QY 621 LeuValValAsnPheGlyAsnValLeuGlnIleValPheThrAspGluAlaArgThrGly 640
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RESULT 12
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 DEFINITION NR10 splicing variants.
 ACCESSION BD178872
 VERSION BD178872.1 GI:30016139
 KEYWORDS WO 02077230-A/3
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 2952)
 Maeda, M., Yaguchi, N. and Hasegawa, M.
 NR10 splicing variants
 Patent: WO 02077230-A 3 03-OCT-2002.
 CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,
 MASAKAZU HASEGAWA
 OS Homo sapiens (human)
 PN WO 02077230-A/3
 PD 03-OCT-2002
 PF 22-MAR-2002 WO 2002JP002769
 PI 26-MAR-2001 JP 01P 087298
 PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
 C12N5/12, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC
 C12N5/10
 PC C12P21/02, G01N33/15, G01N33/50, G01N33/53
 CC NR10 splicing variants
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ORIGIN
 Alignment Scores:

Pred. No.: 9,08e-299 Length: 2952
 Score: 3435.00 Matches: 647
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 98.69% Mismatches: 1
 Query Match: 98.59% Indels: 1
 DB: 6 Gaps: 0

US-10-006-265-2 (1-652) x BD178872 (1-2952)

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 DB |||||
 QY 130 CTCCTCCACTCTCGAAATTCACCTGGGAGCTCTCCAGCTTAAGCTGGAACATTTCC 189
 QY 43 CysValIysTrpTrpAlaGlyAsnLeuThrCysThrTrpSerProGlyIysGluTrpSer 62
 DB |||||
 QY 190 TGTGTACTACTATAGAAAAATTTAACTGCACTTGAGTCCAGGAAAGCAACAGT 249
 QY 63 TyrThrGlnTyrThrValIysArgThrTyrAlaPheGlyGluIysHisAspAsnCysThr 82
 DB |||||
 QY 250 TATACCCAGTACACAGTTAAAGAACTTACGCTTTGGAGAAAAAATGATTAATGTACA 309
 QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProAlaIleThr 102
 DB |||||
 QY 310 ACCAATAGTTCTACAGTGAATTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 369
 QY 103 IleProAspAsnTrpThrIleGluValGluValGluAsnGlyAspGlyValIleIysSer 122
 DB |||||
 QY 370 ATCCCAATATATATACCATTTGAGTGAAGCTGAAATGAGATGTGTAATTAATCT 429
 QY 123 HisMetThrTrpTrpArgLeuGluAsnIleAlaIysThrGluProProIysIlePheArg 142
 DB |||||
 QY 430 CATATACATACCTGAGATTTAGAAACATAGCAAAAACTGAACACCTTAAGATTTCCGT 489
 QY 143 ValIysProValLeuGlyIleIysArgMetIleGlnIleGluTrpIleIysProGluLeu 162
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 QY 490 GTGAAACCAAGTTTGGGCAATCAACCAATGATTTCAATGAAATGCAATTAAGCTGAGTTC 549
 QY 163 AlaProValSerSerAspLeuIysTrpThrLeuArgPheArgThrValAsnSerThrSer 182
 DB |||||
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 QY 243 LeuGlnLeuTrpArgValLeuIysProAlaGluAlaAspGlyArgArgProValArgLeu 262
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 DB |||||
 QY 850 TTATGGAAGAGGCAAGAGAGCCCAAGTCTTGAAGAAAACTTGGCTTCAACATATGG 909
 QY 283 TyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnIleu 302
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 QY 910 TACTATTCAGAAAGCAACTAATCTCAAGAAACATGAACATTAACCAAGCAGCTT 969
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 QY 970 GAACGTATCTGGAGGCGAGAGCTTTGGGTGTATATGTTCTTAATATCTCTTGGG 1029

QY 323 IysSerProValAlaIleThrLeuArgIleProAlaIleGlnIulysSerPheGlnCysIle 342
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 QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
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 QY 1330 TATTCATCAGGCTTATGCCAAAGAGCGCTTCATCAGAAAGTCTTGAACCAAGTGTG 1389
 QY 443 GluAsnIleGlyValIysThrValThrIleThrTrpIysGluIleProIysSerGluArg 462
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 QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuIysArgIysThrSer 502
 DB |||||
 QY 1510 AAGACATGATATTCAGCATCTTGCAGTACGCGCTGAGATCCCTGAACGAAGACTCT 1569
 QY 503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyIysThrAsnGlyThrSerIleAsn 522
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 QY 583 GlyAspAspPheIysAspIysLeuAsnLeuIysGluSerAspAspSerValAsnTrpGlu 602
 DB |||||
 QY 1810 GGAAGATGATTTCAAGGATTAAGCTTAACCTGAAGGAGTCTGAAGACTGTGAAACAGAA 1869
 QY 603 AspArgIleLeuIysProCysSerThrProSerAspIysLeuValIleAspIysLeuVal 622
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 QY 1870 GACAGGATCTTAAACCATGTTCCACCCCAAGTACAAATGTGTGATTAACAAGTTGGTG 1929
 QY 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnIu 642
 DB |||||
 QY 1930 GTGAACCTTTGGGAAGTGTCTGCAAGAAATTTTCAAGATGAAAGCCAGAACGGGTACGA 1988
 QY 643 IysGlnPheArgArgGlyIysGluTrp 651
 DB |||||
 QY 1989 AAACAATTTAGAGGCGAAAGAAATGG 2015

RESULT 13
 BD178871
 LOCUS BD178871 5271 bp DNA linear PAT 16-APR-2003
 DEFINITION NR10 splicing variants.
 ACCESSION BD178871

VERSION BD178871.1 GI:30016138
KEYWORDS MO 02077230-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 5271)
AUTHORS Maeda, M., Yaguchi, N. and Hasegawa, M.
TITLE NR10 splicing variants
JOURNAL Patent: WO 02077230-A 2 03-OCT-2002;
CHUGAI PHARMACEUTICAL CO LTD, MASATSU MAEDA, NORIKO YAGUCHI,
MASAKAZU HASEGAWA
COMMENT OS Homo sapiens (human)
PN MO 02077230-A/2
PD 03-OCT-2002
PF 22-MAR-2002 WO 2002JP002769
PI 26-MAR-2001 JP 01P 087298
PI MASATSU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
C12N15/12, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, G01N33/15, G01N33/50, G01N33/53
CC NR10 splicing variants
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity: 98.69% Mismatches: 1
Query Match: 99.59% Indels: 1
DB: 6 Gaps: 0
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QY 23 LeuProSerLeuCybLysPheSerLeuAlaAlaLeuProAlaLysProGlnAsnLLeSer 42
DB 130 CTCCCTCCTCCTCGCAAAATTCAGCCTGGCAGCTGCGCAGCTGAAGCTGAGAACATTTCC 189
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
DB 190 TGTGTCTACTACTATAGGAAAAATTTAACTGCACCTTGAGTCCAGAAAGGAAACCACT 249
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysLysAspAsnCybThr 82
DB 250 TATACCCAGTACACAGTTAAGAACTTACCGCTTTGGAGAAAAACATGATTAATTGTACA 309
QY 83 ThrAsnSerSerThrSerGluAsnArgLAserCysSerPhePheLeuProArgLLeThr 102
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QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
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DB 1450 AAGGATATCATCTGCAATCAACATCTTTTACCAACCTGAAGGTGAAGAAAGATTCCTC 1509
QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer 502
DB 1510 AAGACATCAATTCACACATCTTGCACTAGCGCTGAGAGTCCCGAAGCAAAACACTCT 1529
QY 503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
DB 1570 TACATTTGTCAGGTCATGGCCAGACCAAGTGTGGGGAACCAACGGGAGCAAGATTAAT 1629
QY 523 PheLysThrLeuSerPheSerValPheGluLLeLLeuLLeThrSerLeuLLeGlyGly 542

Db	1530	TTCAAGACATTGTCATTCAAGTGTCTTGAAGATTATCCCAACATCTTCTGAATTGGTGA	1689
Qy	543	GlyLeuLeuLeuLeuLeuLeuThrValAlaTyrGlyLeuValProAluLeu	562
Db	1690	GGCCTTCATTATTCATTATTCCTACAGTGCATATGCTCCAAAAAACCACAAATTGG	1749
Qy	563	ThrHisLeuCySTPPProThrValProAsnProAlaGluSerSerIleAlaThrTyrHis	582
Db	1750	ACTCATCTGTGTGGCCACCCTGCCACCTGCTGAAAGTAGTATGCCACATGGCAT	1809
Qy	583	GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu	602
Db	1810	GGAGATGATTTCAAGATTAACCTAAACCTGAAGAAGTGTGATGACTCTGTGAACACAGAA	1869
Qy	603	AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal	622
Db	1870	GACAGGATCTTAAACCAATGTTCCACCCCACTGACCAAGTGGTATGACCAAGTGGTG	1929
Qy	623	ValAsnPheGlyAsnValIleGluGlnLysPheThrAspGluAlaArgThrGlyGlnGlu	642
Db	1930	GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTTCACAGTGAAGCCAGAAAGGCTCAGGA	1988
Qy	643	LysGlnPheArgArgGlyLysGluTyr	651
Db	1989	AAACATTTTAGAGAGGGAAGAAATGG	2015

RESULT	14				
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DEFINITION	NR10 splicing variants.				
ACCESSION	BD178873				
VERSION	BD178873.1	GI:30016140			
KEYWORDS	WO 02077230-A/4.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Maeda,M., Yasuchi,N. and Hasegawa,M.				
TITLE	NR10 splicing variants				
JOURNAL	Patent: WO 02077230-A 03-OCT-2002;				

COMMENT

OS Homo sapiens (human)
PN WO 02077230-A/4

PD 03-OCT-2002

PF 22-MAR-2002 WO 2002JP002769

PI 26-MAR-2001 JP 01P 087298

PR MASATOSHI MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA
PC C12N15/12, C07K14/775, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC

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FH	Key
FT	Location/Qualifiers
CDS	(7) . . (1887) .

FEATURES	Location/Qualifiers
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	/mol_type="genomic DNA"
	/db_xref="taxon:9606"

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Percent Similarity:	94.05%	Conservative:	1
Best Local Similarity:	93.90%	Mismatches:	1
Query Match:	97.73%	Indels:	41
DB:	6	Gaps:	1

US-10-006-265-2 (1-652) x BD178873 (1-3072)

QY	3	LeuSerProGlnIProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet	22
Db	70	CTCTCTCCCAAGCCTTCATGTGTAACTCGGGATGATGTGGACCTGGCACTGGATG	129
QY	23	LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnLysSer	42
Db	130	CTCCCTCACTGTGCAAAATTCAGCCTGGCAGCTCTGGCAGCTAAAGCTGAAACATTTC	189
QY	43	CysValIlyTrpTrpZaArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer	62
Db	190	TGTCTCTACTACTTATAGAAAAAATTTAACTGCACTTGGAGTCCAGGAAAGAAACAGT	249
QY	63	TyrThrGlnTrpThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr	82
Db	250	TATACCAAGTACACAGTTAAAGAACTTAGCCTTTTGAGAAAAAACATGATATGTACA	309
QY	83	ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgLysThr	102
Db	310	ACCAATAGTTCTACAAATGAAATTCGGTCTCGTCTTTTTCCTTCCAGAAATACG	369
QY	103	LleProAspAsnTrpThrLleGluValGluAlaGluAsnGlyAspGlyValLleLysSer	122
Db	370	ATCCCAATATATTATACATTGAGGTGGAAGCTGAAATAGCAAGATGTGTAATTAATCT	429
QY	123	HisMetThrTrpTrpArgLeuGluAsnLleAlaLysThrGluProPheLysLlePheArg	142
Db	430	CATATGTGACATCTGGAGATTAGAGAAATATGCGGAAACTGAAACCACTAAGATTTCGT	489
QY	143	ValLysProValLleGluGlyLleLysArgMetLleGlnLleGluTrpLleLysProGluLeu	162
Db	490	GTGAAACCAAGTTTGGGCACTCAACGAAATGATTTCAATTGAATGATTAAGCCTGATTG	549
QY	163	AlaProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSerThrSer	182
Db	550	GCGCTGTTCATCTGATTTAAATACACACTTGATTGACAGACGCAACAGTACAGC	609
QY	183	TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr	202
Db	610	TGGATGGAAAGCACTTCGCTTAAGAACCGTAAGGATTAATAACCAAGGTCAACCTCAGC	669
QY	203	GlyLeuGlnProPheThrArgLysTrpValLleAlaLeuArgCysAlaValLysGluSerLys	222
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QY	223	PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlnGluAlaProCysGly	242
Db	730	TTCTGGAGTGACTGGACCAAGAAAAAATAGGAATGACTGAGGAAGAAGCTCCATGTGC	789
QY	243	LeuGluLeuTrpArgValLleLysPheProAlaGluAlaAspGlyArgArgProValArgLeu	262
Db	790	CTGGAACCTGTGAGAGCTCTGAAACCAAGCTGAGGCGGATGGAAGAAAGCCAGTCCGATTG	849
QY	263	LeuTrpLysLysAlaArgGlyAlaProValLeuGlnLysThrLeuGlyTyrAsnLleTrp	282
Db	850	TTATGAGAAAGGAGAAAGAGGCCCTCAAGCTCTTAAGAGAAACCTTGCTCAACATATGG	909
QY	283	TyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGlnLeu	302
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QY	303	GluLeuHisLleGluGlyGlyLysPheTrpValSerMetLleSerTyrAsnSerLeuGly	322
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QY	423	TySerIleGlnAlaTyrAlaIysGlnGlyValProSerGlnGlyProGluThrLysVal	442
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QY	443	GluAenIleGlyValLysThrValThrIleThrTPrLysGlnIleProLysSerGlnArg	462
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Db	1450	AAGGTATCATCTGCACATCCATCCATCTTTTACCAAGCTGAAGGTGAAAAAGGATTCTCC	1509
QY	483	LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer	502
Db	1510	AAGACATGCAATTCAGACATCTTGACAGTACGGCTGTGAGTCCCTGAAACGAAAGCCTC	1569
QY	503	TyrIleValGlnValMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSerIleAsn	522
Db	1570	TACATGTGTTCAGGTGATGATGGCCAGCACAGTGTGGGGAGAACAGGACCATTAAT	1629
QY	523	PheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerLeuIleGlyIle	542
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QY	543	GlyLeuLeuIleIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu	562
Db	1690	GGCCTCTTATTTCTCATATTACTGACAGTGGATATGGTCTCAAAAAACCAACAAATTG	1749
QY	563	ThrIleIleCybTPrProThrValProAsnProAlaGlnSerSerIleAlaThrTrpHis	582
Db	1750	ACTATCTGTGTGGCCACCGTTCCCAACCTGTGTAAGTATAGTACCAATGCGAT	1809
QY	583	GlyAspAspPheLys-----	587
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QY	588	-----	602
Db	1930	ACTTCTGATTTTTCGATTAACCTTAACCTGGAAGATGTGATGACTCTGTAAACACAGAA	1989
QY	603	AspArgIleLeuLysProCybSerThrProSerAspIysLeuValIleAspLysLeuVal	622
Db	1990	GACAGGATCTTAAAAACATGTTTCCACCCCAAGTGACAAAGTTGGATTTGACAAAGTTGGTG	2049
QY	623	ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGlnAlaArgThrGlyGlnGlu	642
Db	2050	GTTGAACCTTTGGAAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAACGGGTACAGA-	2108
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RESULT 15

AF486620

LOCUS Homo sapiens gp130-like monocyte receptor mRNA, complete cds.

ACCESSION AF486620.1 GI:20563276

VERSION

2199 bp

mRNA

linear

PRI 14-MAY-2002

KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 2199) Ghilardi N., Li J., Hongo, J.A., Yi S., Gurney A. and de Savage, F.J. A novel type I cytokine receptor is expressed on monocytes, signals proliferation, and activates STAT-3 and STAT-5
TITLE	2 (bases 1 to 2199) Ghilardi, N., Li, J., Hongo, J.-A., Yi, S., Gurney, A. and de Savage, F. J. Direct Submission
JOURNAL	Submitted (21-FEB-2002) Molecular Oncology, Genentech, 1 DNA Way, J. Biol. Chem. 277 (19), 16831-16836 (2002)
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ORIGIN	
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Best Local Similarity: 99.69% Mismatch: 1	
Query Match: 96.87% Indels: 1	
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 05:20:17 ; Search time 963.011 Seconds

(without alignments)
4007.918 Million cell updates/sec

Title: US-10-006-265-2

Perfect score: 3484

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Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3451	99.1	2119	4 AAC92350	AAC92350 Human hae
3	3451	99.1	2903	6 ABA93808	ABA93808 Human zcy
4	3451	99.1	10	ADL68146	ADL68146 Human zcy
5	3451	99.1	2903	11 ADL26569	ADL26569 Human cyt

6	3441	98.8	2529	6 ABA93803	ABA93803 Human zcy
7	3441	98.8	2529	11 ADL26671	ADL26671 Human cyt
8	3441	98.8	4315	8 ABO83363	ABO83363 Human NR1
9	3435	98.6	2386	6 ABA93767	ABA93767 Human zcy
10	3435	98.6	2402	11 ADL26673	ADL26673 Human cyt
11	3435	98.6	2480	6 AAD38772	AAD38772 Human hae
12	3435	98.6	2481	10 ACF36434	ACF36434 Human tlp
13	3435	98.6	2952	8 ABO83365	ABO83365 Human NR1
14	3435	98.6	5271	8 ABO83364	ABO83364 Human NR1
15	3435	97.7	3072	8 ABO83366	ABO83366 Human NR1
16	3245.5	93.2	2858	8 ABO83368	ABO83368 Human NR1
17	3232.5	92.8	2870	8 ABO83367	ABO83367 Human NR1
18	3065.5	88.0	2776	8 ABO83369	ABO83369 Human NR1
19	3049	87.5	2108	10 ADL21969	ADL21969 Novel hum
20	2850	81.8	2295	6 ABA93821	ABA93821 Human zcy
21	2850	81.8	2295	10 ADL68179	ADL68179 Human zcy
22	2850	81.8	2295	11 ADL26602	ADL26602 Human zcy
23	2810	80.7	1986	6 ABA93809	ABA93809 Human zcy
24	2810	80.7	1986	11 ADL26685	ADL26685 Human cyt
25	2779	79.8	1557	10 ADD68201	ADD68201 Human zcy
26	2779	79.8	1557	11 ADL26633	ADL26633 Human cyt
27	2758	79.2	1947	6 ABA93804	ABA93804 Human zcy
28	2758	79.2	1947	11 ADL26684	ADL26684 Human cyt
29	2758	79.2	2196	6 ABA93768	ABA93768 Human zcy
30	2758	79.2	2196	11 ADL26683	ADL26683 Human cyt
31	2606	74.8	2445	6 ABL83581	ABL83581 Human PRO
32	2606	74.8	2445	6 ABL88257	ABL88257 Human PRO
33	2606	74.8	2445	6 ABL95746	ABL95746 Human ang
34	2606	74.8	2445	9 ACA68542	ACA68542 Novel hum
35	2606	74.8	2445	9 ABL44271	ABL44271 Human PRO
36	2606	74.8	2445	9 ABL44554	ABL44554 Human PRO
37	2606	74.8	2445	9 ACD82221	ACD82221 Human sec
38	2606	74.8	2445	9 ABL43927	ABL43927 Human mem
39	2606	74.8	2445	9 ADB83581	ADB83581 Novel hum
40	2606	74.8	2445	9 ADB80687	ADB80687 Novel hum
41	2606	74.8	2445	9 ADB73228	ADB73228 Novel hum
42	2606	74.8	2445	9 ADB78310	ADB78310 Novel hum
43	2606	74.8	2445	10 ADB84958	ADB84958 Human PRO
44	2606	74.8	2445	10 ADB78064	ADB78064 Novel hum
45	2606	74.8	2445	10 ADB87130	ADB87130 Human PRO

ALIGNMENTS

RESULT 1
AAC92337
ID AAC92337 standard; cDNA; 2969 BP.
XX
AC AAC92337;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human haemopoietin receptor protein NR10.1 encoding cDNA seq ID NO:1.
XX
KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KW immunoregulation; haematopoietic cell regulation; transmembrane;
KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW metal allergy; pollen allergy; ss.
XX
OS Homo sapiens.
XX
PM WO200075314-A1.
XX
PD 14-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-JP003556.
XX
PR 02-JUN-1999; 99JP-00155797.
XX
PR 30-JUL-1999; 99JP-00217797.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
XX Maeda M, Yaguchi N.
PI

XX WPI; 2001-061720/07.
DR P-PSDB; AAB51242.
XX Hematopoietin receptor protein NR10 for screening potential ligands for
PT treatment of immune and hematopoietic disorders such as autoimmune
PT diseases and allergies.
XX Claim 1; Fig 3-5; 127bp; Japanese.
XX
CC The present sequence encodes a human haemopoietin receptor protein
CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC which participates in immunoregulation and haematopoietic cell regulation
CC in vivo, and is useful in searching for haematopoietic factors capable of
CC binding to the receptor. NR10 can be used for the identification of
CC substances for the treatment and prevention of immune and haematopoietic
CC disorders including autoimmune diseases and allergies such as metal and
CC pollen allergy
XX
SQ Sequence 2969 BP; 939 A; 618 C; 662 G; 750 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2969
Score: 3484.00 Matches: 652
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-006-265-2 (1-652) x AAC92337 (1-2969)
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyWcMetTrpThrTrpAlaLeu 20
Db 523 ATAAAGCTCTCTCCCAAGCCTTATGTTTAACTGGGAGTGAATGGAGCTGGCACTG 582
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db 583 TGGATCGTCCCTCAGCTGCAATTCAGCCTGGAGCTCTGCAGCTAAGCTGAGAAC 642
QY 41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db 643 ATTTCTGTGTCTACCTAATAGAAAATTTTAACTGCACCTTGAGTCCAGAAAGGAA 702
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysIleAspAsn 80
Db 703 ACCAGTTATACCCAGTACACAGTAAAGAACTTACGCTTCCGAGAAAACATGATAT 762
QY 81 CysThrThraAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 763 TGTACAACCAATAGTTCTACAGATGAAATCGTTCGTTCCTTTTCTTCCAAAG 822
QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyLysArgValIle 120
Db 823 ATTAACATCCCAATATATATACCATTTGAGTGAAGCTGAAAATGAGATGCTGTAAT 882
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
Db 883 AAATTCATATGACATCTGAGATTAAGACATTAACCAAACTGAAACCACTTAAGATT 942
QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
Db 943 TTCGATGGAAACAGTTTGGGCAATCAACGATGATTCAAATTTGATGATTAAGCCT 1002
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
Db 1003 GAGTTGGCGCTTTTCATCTGATTTAAATACACACTTCGATTCGAGAACAGTCAACGT 1062
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db 1063 ACCAGCTGGAGTGAAGTCAACTTCGCTAAGAACCCGTAAGATTAACCAAGATTCACAC 1122
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220

Db 1123 CTCACGGGGCTCAGCTTTTACAGAAATATGTCATAGCTCTCGATGTCGGTCAAGAG 1182
QY 221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetGlyWcMetThrGluGluAlaPro 240
Db 1183 TCAAAGTTTGGAGTGAAGTCTGGAGCCAGAAAGAAATGGAAATATCTGAGAAAGAGTCCA 1242
QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
Db 1243 TGTGGCTGGAACTGTGGAGATCTCTGAAACAGCTGAGGCCGATGGAAGAGGCCAGTG 1302
QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
Db 1303 CGATTGTTATGAGAGAGCAAGAGAGCCCAAGTCTTAAGAAAAACACTTGGCTTACAAC 1362
QY 281 IleTrpTyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
Db 1363 ATATGGTACTATCCAGAAAGCAACTAATCTCAAGAAACATTAAGAACTACTAACCAG 1422
QY 301 GlnLeuGluLeuHisLeuGlyLysGlyLysSerPheTrpValSerMetIleSerTyrAsnSer 320
Db 1423 CAGCTTGAATCGATCTGGAGAGCGAGAGCTTTGGGTGTCTATGATTTCTTATATATCT 1482
QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlyLysSerPheGln 340
Db 1483 CTTGGGAATCTCCAGTGGCCACCTGAGGATTCACAGCTATTCAGAAAAATCATTTTCAG 1542
QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSer 360
Db 1543 TGCATTGAGTCAATGAGGCGCTGCTGTGAGAACCAAGTATGTGTGAATGGCAAGC 1602
QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db 1603 TCTGCTCTAGAGTGAACCTTGGATGATTTGATGATTTCCGAGATGGCACTCAAGGCC 1662
QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
Db 1663 ACCACCTTTCTGGGAATCTGTGTCTCAGGCGACAGAACCTGACAGATCCAGCAAGTAA 1722
QY 401 LeuLysProPheTrpCysThrTrpAsnIleSerValTyrProMetLeuHisAspLysValGly 420
Db 1723 TTAAACCTTTCTGGGTCTATTAACATCTGTGTATCAATGTTCATACAAAGTTGGC 1782
QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
Db 1783 GAGCATATTCATCCAGCTTATGCAAGAAAGGCTTCATCAGAAAGTCCCTGAGACC 1842
QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
Db 1843 AAGGTGAGAAACATTTGGCTGAAAGCGTCAAGATCAATGAAAGAGATTCACCAAGAT 1902
QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
Db 1903 GAGAGAAAGGATATCTGCAACTACACATCTTTTACAAAGCTGAAAGTGAAGAAAGCA 1962
QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
Db 1963 TTCTCCAAAGACGTCAATTCAGCAATCTTGCAATCGGCTGGAAGTCCCTGAAACGAAAG 2022
QY 501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520
Db 2023 ACCTCTTACATTTGTTCAAGTCAATGCGCAACACAGAGCTGGGGGAAACCAACGGACCA 2082
QY 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db 2083 ATTAATTTAAGACATTTGCATTCAGTGTCTTTGAGATTAATCTCTAACTTCTTGATT 2142
QY 541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
Db 2143 GGTGGAGGCTTCTTATTTCTATTAATCTGACAGTGGCATAGTGTCAAAAAACCAAC 2202
QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580

Db	2203	AAATTGATCATCTGTGTTGGCCACCGTTCCTCCAACTGCTGGAAGATGATACCCAA	2262
Qy	581	TrpHisGlyAspAspPheLeuAspIysLeuAsnLeuIysGluSerAspAspSerValAsn	600
Db	2263	TGGCATGTGAGATGATTTTCAAGATTAAGCTTAAACCTGAAGAGAGTGTGATGACTCTGAA	2322
Qy	601	ThrGluAspAspArgIleLeuIysProCysSerThrProSerAspIysLeuValIleAspIys	620
Db	2323	ACAGAAAGCAGAGATCTTAAACCAAGTTCACACCCCACTGACAGTGTGTGATGACAAAG	2382
Qy	621	LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluValArgThrGly	640
Db	2383	TTGGTGGTGAACTTTGGGAAATCTTCTGCAAGAAATTTTCACAGATGAAGCCGAAAGCGGT	2442
Qy	641	GlnGluIysGlnPheArgArgGlyIysGluIleTyrAsp	652
Db	2443	CAGGAAAAACAATTGAGAGGGGAAAGAAATGGGAC	2478
RESULT 2			
AAAC92350			
ID	AAC92350 standard; cDNA, 2119 BP.		
XX			
AC	AAC92350;		
XX			
AC	26-MAR-2001 (first entry)		
DT			
XX			
DE	Human haemopoietin receptor protein NR10.3 encoding cDNA SEQ ID NO:16.		
XX			
KW	Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;		
KW	immunoregulation; hematopoietic cell regulation; transmembrane;		
KW	immune disorder; hematopoietic disorder; autoimmune disease; allergy;		
XX	metal allergy; pollen allergy; ss.		
OS	Homo sapiens.		
XX			
PN	WO200075314-A1.		
XX			
PD	14-DEC-2000.		
XX			
PF	01-JUN-2000; 2000MO-JP003556.		
XX			
PR	02-JUN-1999; 99JP-00155797.		
PR	30-JUL-1999; 99JP-00217797.		
XX			
PA	(CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.		
XX			
PI	Maeda M, Yaguchi N;		
XX			
DR	WPI; 2001-061720/07.		
DR	P-PSDB; AAB51244.		
XX			
PT	Hematopoietin receptor protein NR10 for screening potential ligands for		
PT	treatment of immune and hematopoietic disorders such as autoimmune		
PT	diseases and allergies.		
XX			
PS	Claim 1; Fig 13-14; 127bp; Japanese.		
XX			
CC	The present sequence encodes a human haemopoietin receptor protein		
CC	(NR10), specifically designated NR10.3. NR10 occurs as a transmembrane		
CC	protein and a soluble protein. NR10 is a haemopoietin receptor molecule		
CC	which participates in immunoregulation and haematopoietic cell regulation		
CC	in vivo, and is useful in searching for haematopoietic factors capable of		
CC	binding to the receptor. NR10 can be used for the identification of		
CC	substances for the treatment and prevention of immune and hematopoietic		
CC	disorders including autoimmune diseases and allergies such as metal and		
CC	pollen allergy		
XX			
SQ	Sequence 2119 BP; 643 A; 459 C; 504 G; 513 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	4.33e-316	Length:	2119
Score:	3451.00	Matches:	650
Percent Similarity:	99.85%	Conservative:	1

DB:	US-10-006-265-2 (1-652) × AAC92350 (1-2119)	Best Local Similarity: 99.69%	Query Match: 99.05%	Mismatches: 1	Gaps: 0
QY	1 MetLysLeuSerProGlnProSerCysAlaIleuLeuGlyMetMetTrpThrTrpAlaLeu	20			
DB	11 ATGAAGCTCTCTCCACAGCTTCAATGTTAACTGGGAGAAATGATGGAACCTGGGCACACG	70			
QY	21 TrpMetLeuProSerLeuCysIlePheSerLeuAlaAlaLeuProAlaIleAspProGluLeu	40			
DB	71 TGGATGCTCCCTCACTCTGCAGAAATTCAGCTGGGAGCTCTCCAGCTAAAGCTAGAAC	130			
QY	41 ILeSerCysValIYrYrYrArgIysAneLeuThrCysThrTrpSerProGlyIleGlu	60			
DB	131 ATTTCCTGTGCTACTACTATAGGAAAATTAACTGCACCTGGAGCTCCAGAAAGGAA	190			
QY	61 ThrSerTrpThrGlnTrpThrValIleAspGlnTrpYrAlaPheGlyGluIleHisAspAsn	80			
DB	191 ACCAGTTATACCCAGTACACAGTTAAGAACTTAACGCTTTTGGAGAAAACATATATAT	250			
QY	81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg	100			
DB	251 TGTACACCAATAGTTCTTACAGTGAATTCGTGCTCTGCTCTTTTCTCTTCACAGA	310			
QY	101 ILeThrIleProAspAsnTrpThrIleGluValGluAlaGluAsnGlyAspGlyValIle	120			
DB	311 ATAAGCATCCAGATTAATTAATACCTTAGGAGGAGCTGAATAATGAGTGTAAAT	370			
QY	121 LysSerHisMetThrTrpTrpArgLeuGluAsnIleAlaIlePheGlnProPheGlyIle	140			
DB	371 AAATCTCATATAGACATACATCGAGATTAGAGAACTAGCGAAACCTGAACCTAAGATT	430			
QY	141 PheArgValIleAspProValLeuGlyIleIleAspMetCileGlnIleGluTrpIleAspPro	160			
DB	431 TTCGTGTGAACCAAGTTTGGGACATCAACAGAAATGATTCATTAATGATTAAGCT	490			
QY	161 GluLeuAlaProValIleSerSerAspLeuIleTrpThrLeuArgPheArgThrValAsnSer	180			
DB	491 GAGTTGGGGCGCTGTTTCACTGATTAAATTAACACATTCGATTCAGGACAGTCAACGT	550			
QY	181 ThrSerTrpMetCileValIleAsnPheAlaIleAsnArgIleAspIleAsnGlnThrTrpAsn	200			
DB	551 ACCAGCTGAGTGAAGTCAACTTCGCTAAGCAACCTAAGATTAATAAACCAACCTAACAAC	610			
QY	201 LeuThrGlyLeuGlnProPheThrGluTrpValIleAlaIleAspGlyValIleGlu	220			
DB	611 CTCACGGGGCGTGCAGCCCTTTTACAGAAATATCTACATGCTGCGATGCGGTCAAGAG	670			
QY	221 SerIlePheTrpSerAspTrpSerGlnGlyIleAspMetCileGlnIleGluAlaPro	240			
DB	671 TCAGAAATCTCGAGTGAATGAGCTGAGCCAGAAATTAATGGAATGACTGAGGAAGAGCTCA	730			
QY	241 CysGlyLeuGluLeuTrpArgValIleLeuAspProAlaGluAlaAspGlyArgArgProVal	260			
DB	731 TGTGGCCCTGGAACGTGGAGAGTCTCTGAAACCACTGAGCGGATGGAAGAGGCCAGTGTG	790			
QY	261 ArgLeuLeuTrpIleValIleAspGlyValaProValLeuGlnIleGlnIleGlnIleGlnIle	280			
DB	791 CGGTGTGTATGGAAGAAAGGCAAGAGAGAGCCCAAGCTCTTAAGAGAAACCTTGGCTAACAAC	850			
QY	281 IleTrpTrpTrpProGluSerAsnThrAsnLeuThrGluTrpMetAsnThrThrAsnGln	300			
DB	851 ATATGATGATCTACAGAAAGCAACCTAATCTCACAGAAACATAGACATCTAACAG	910			
QY	301 GlnLeuGluLeuHisLeuGlyIleGluSerPheTrpValSerMetIleSerTrpAsnSer	320			
DB	911 CAGCTTGAACGTGACATCGGAGCGAGAGGCTTTTGGGAGTCTATGATTTCTTAATATCT	970			
QY	321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlnIleLysSerPheGln	340			
DB	971 CTGTGGAAAGTCTCAGTGGCCACCTGATGAGATTCAGTATTTCAAGAAAAATCAATTTGAG	1030			

QY	34	Cye11egi1uwa1metg1na1aCyeVa1A1a61u1sp6gi1ne1uVa1V1a1y1trp1g1n1ser	360
Db	1031	TGCATTGAGGTCATAGCAGAGCCCTGGCTGTCTAGAGCACAGCTAGTGTGTAATGGCAAGC	1090
QY	361	Se1a1e1u1sp1a1a1sn1Th1r1Tp1Me11egi1u1Trp1Phe1Pro1a1p1Va1a1sp1Se1gi1u1Pro	380
Db	1091	TCTGCTCTAGACGTAACACTTGGATGATTGAATGGTTTCCGAGATGTGACTCAGAGGCC	1150
QY	381	Th1r1Th1r1e1u1ser1Trp1gi1u1Se1r1a1Ser1gi1na1Th1r1a1n1Trp1Th11egi1n1a1p1y1s	400
Db	1151	ACCACCCCTTCTCTGGGAATCTGTGTCTCCAGGCCACGAACTGAGCATCCAGCAAGATTAA	1210
QY	401	Leu1y1s1Pro1Phe1Trp1Cy1s1Ty1r1Asn11e1Se1r1a1Ty1r1Pro1Me11e1u1H1a1s1p1y1Va1gi1y	420
Db	1211	TTTAAACCTTTCTGTGCTATTAACACTCTGTGTATTCCAATGTGTGCATGACAAAGTTGGC	1270
QY	421	gi1u1Pro1Ty1Se1r11egi1na1Ty1r1A1a1y1s1gi1u1y1a1Pro1Se1r1gi1u1y1Pro1gi1u1Th1r	440
Db	1271	GAGCCATATTCATCCACAGGCTTATGCCAAABAAGCGTTCCATCAGAAAGTCTGAGAGCC	1330
QY	441	Ly1s1Va1gi1u1a1n11egi1y1a1Ly1e1Th1r1Va1Th1r1e1Th1r1Trp1y1s1gi1u1e1Pro1y1s1e1r	460
Db	1331	AAGGTGGAGCAATTTGGCGTGAAACGGTCAAGATCATGTGAAAGAGATTCCAAAGAGT	1390
QY	461	gi1u1y1r1y1s1gi1y1i1e1e1Cy1a1s1n1Ty1r1Th1r1e1Phe1Ty1r1gi1na1a1gi1u1y1gi1y1s1y	480
Db	1391	GAGGAAAGGGGTATCATCTGCACATCAACCATCTTTATCCAAAGCTGAAAGGTGAAAGAAAG	1450
QY	481	Ph1e1Se1r1y1Th1r1Va1a1sn1Se1Se1r1e1u1gi1n1Ty1r1gi1u1Se1r1e1u1y1a1r1y1s	500
Db	1451	TTCTCCAAAGACAGTCAATTCACAGCATCTTGACAGTACGGCTCTGGAGTCCCTGAACGAAG	1510
QY	501	Th1Se1r1Ty1r1e1Va1gi1n1a1Me1Ca1a1sn1Th1Se1r1a1gi1y1gi1Th1r1a1n1gi1y1Th1Se1r	520
Db	1511	ACCTCTTAACATTTGTCAGGTCAATGGCCAGCACAGTGGCGGGAAACCAAGCGGACCGAC	1570
QY	521	11e1a1n1Phe1y1s1Th1r1e1Se1r1Ph1e1Se1r1a1Phe1gi1u1e11e1u11e1Th1Se1r1e1u1e1	540
Db	1571	ATTAATTTCAAGACATGTGTCAATCAAGTGTCTTGAGATTATCTCATTAATCTTCTGTGATT	1630
QY	541	gi1y1gi1y1e1u1e1u1e11e1u1e11e1e1u1Th1r1Va1a1Ty1r1gi1y1e1u1y1a1s1Pro1sn	560
Db	1631	GGTGGAGGCCCTTCTTATTTCTCATTAATCTGCACAGTGGCATATGTGCTCAAAAAACCCAC	1690
QY	561	Ly1e1u1Th1r1h1s1e1u1Cy1Trp1Pro1Th1r1Va1Pro1a1n1Pro1a1gi1u1Se1r1e11e1a1Th1r	580
Db	1691	AAATTTGACTCATCTGTGTGTGGCCACCGCTTCCCAACCTGCTGAAGATGATATGACCCACA	1750
QY	581	Trp1h1egi1y1a1Pa1Phe1y1a1s1y1y1e1u1a1n1e1u1y1s1gi1u1Se1r1a1Pa1a1s1Se1r1Va1a1n	600
Db	1751	TGGCATGGAGATGATTTCAAGATTAAGTTAAACCTGAAGAGATCTGATGACTCTGTGAAC	1810
QY	601	Th1r1gi1u1a1Pa1gi1e1e1u1y1e1Pro1Cy1Se1r1Th1r1Pro1Se1r1a1P1y1s1e1u1Va111e1a1P1y1s	620
Db	1811	ACAGAAGCACAGATCTTTAAACCATGTTCCACCCCAAGTGCACAGTTGCTATTCACAG	1870
QY	621	Leu1y1Va1a1a1n1Phe1gi1y1a1n1Va11e1u1gi1n1u11e1Phe1Th1r1a1Pgi1u1a1a1y1Th1r1y1	640
Db	1871	TTGTGTGTGAACCTTTGGGAATGTCTTCGCAAAATTTTCCACAGATGAAGCCAGACGGGT	1930
QY	641	gi1n1gi1u1y1s1gi1n1Phe1a1r1y1r1gi1y1y1e1u1Trp1a1p	652
Db	1931	CAGGA-AAACCAATTTAGAGGGGAAATAAATGGGAGC	1965

ABAS3808	RESULT 3
ID	ABAS3808 standard; CDNA; 2503 BP
XX	
AC	ABAS3808;
XX	
DT	01-MAY-2002 (first entry)
XX	

DE Human zcytor17 cDNA sequence SEQ ID NO:53.

KM Zcytor1, chromosome 5, Sgll; cytokine receptor; immunomodulatory;
KM antiinflammatory; antiviral; antineumatic; antiarthritic; cyrostatic;
KM muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;
KM infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease
KM autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KM inflammatory disease; pancreatitis; inflammatory bowel disease; ss.

OS Homo sapiens.

PN WO200200721-A2

PD 03-JAN-2002.

PF 26-JUN-2001; 2001WO-US020484.

PR 26-JUN-2000; 2000US-0214282P

PR 08-FEB-2001; 2001US-0267963P

PA (ZYMO) ZYMOGENETICS INC.

PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;

XX

DR P-PSDB; ABB05741.

PT Isolated polynucleotide encoding a

PT splenic, blood or bone disorders.

PS Example 1; Page 199-203; 235pp; English.

CC The present invention describes a cytokine receptor designated zcytor17.

CC antirheumatic, antiarthritic and muscular activities. The zcytor17

CC inflammatory, splenic, blood or bone disorders. Agonists or anti-

CC for stimulating lymphocyte proliferation, such as in the treatment of

CC infections. They are also useful for inducing cytotoxicity and for

CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple

CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to

CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the

XX
XX

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Pred. No.:	6.92e-316	Length:	2903
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Percent Similarity:	99.85%	Conservative:	1
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Query Match: 99.05% Indels: 1

QUESTION

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Abstract

[illegible]


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Db      617 ATTTCTGCTGCTACTACTATAGAGAAAATTTAACTGCACTTGAGTCCAGAGAAAGAA 676
Qy      61  ThrSerTyrThrGlnTyrThyValIlysaGthrTyrAlaPheGlyGluLysHisAspAsn 80
Db      677 ACCAGTTATACCCAGTACACAGTTAAAGAACTTACGCTTTTGGAGAAAACATCATATAT 736
Qy      81  CysThrTrpAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db      737 TGTACACCAATAGTTCTACAGAGTGAATACTGCTGCTCTTTTCTTTCTTCCACAAAGA 796
Qy      101  IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db      797 ATAAAGATCCAGATAAATTATACATGAGGTGAGAGCTGAAATAGAGATGCTATATT 856
Qy      121  LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
Db      857 AAATCTCATATGACATACCTGAGATTAAGAAACATAGCGAAACTGAACCACTAAGATT 916
Qy      141  PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
Db      917 TTCGTGTGAACCAAGTTTGGGCATCAACGAATGATTCAAATTGAATGAATGAAGCTT 976
Qy      161  GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
Db      977 GAGTTGGCGCTGTTTCACTGATTTAAATACACACTTCGATTCAGACAGTCAACAGT 1036
Qy      181  ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db      1037 ACCAGCTGAGTGAAGTCAACTCCCTAAGAAACCTAAGATAAACCAACCAACGTAACAC 1096
Qy      201  LeuThrGlyLeuGlnProPheThrGluLysTyrValIleAlaLeuArgCysAlaValLysGlu 220
Db      1097 CTCACGGGGCTGACGCTTTTAAACGAATATGTCATAGCTCGCGATGCGCTCAAGAG 1156
Qy      221  SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluValPro 240
Db      1157 TCAAAGTTCTGAGAGTGAAGTGAAGCCAAAGAAAATGAGAAATGACAGAGAAAGACTCCA 1216
Qy      241  CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
Db      1217 TGTGGCCTGGAAGCTGGAAGTCTCGAAACCACTGAGCGGAGTGAAGAAAGGCAAGTGT 1276
Qy      261  ArgLeuLeuTrpLysValAsnGlyAlaArgValaProValLeuGluLysThrLeuGlyTyrAsn 280
Db      1277 CGGTGTATATGAAGAAAGAGAGAGAGCCCACTGAGAGAAACCTTGCGCTACAC 1336
Qy      281  IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluTrpMetAsnThrThrAsnGln 300
Db      1337 ATATGCTACTATCCAGAAAGCAACATCACTCACAGAAACAAATGAACATCACTAACAG 1396
Qy      301  GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSer 320
Db      1397 CAGCTTGAAGTGCATCTGAGAGCGAGAGCTTTTGGGTGTATGATTTCTTATATATCTT 1456
Qy      321  LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
Db      1457 CTTGGGAAGTCTCAAGTGGCCACCTGAGGATTCAGCATATTCAGAAATAATCAATTCAG 1516
Qy      341  CysIleGluValMetGlnAlaCysValAlaGluAsnGlnLeuValValLysTrpGlnSer 360
Db      1517 TGCATTAGATCATGCAAGCCTGCGCTTCTAGACACCGCTAGTGTGTAAGTGGCAAGC 1576
Qy      361  SerAlaLeuAspValaAsnThrTrpMetIleGluTrpPheProAspValaAspSerGluPro 380
Db      1577 TCTGCTCTAGACGTAACATCTTGATGATGATGATGATTCGAGATGTGAGCTCAGAGCC 1636
Qy      381  ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
Db      1637 ACCACCCCTTCTGGAATCTGTGCTCAGGCCACGAAGTGAAGATCAGACCAAGATAA 1696
Qy      401  LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420

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Db      1697 TTAACCTTCTGTGCTATATACATCTGTGTATCCAAATGTTGACAGCAAGTTGGC 1756
Qy      421  GluProTyrSerIleGlnAlaTyrAlaLysGluLysValProSerGluGlyProGluThr 440
Db      1757 GAGCATATTCATCCAGGCTTAATGCAAAAGCCGCTTCATGAGAGGTCCTGAGACC 1816
Qy      441  LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
Db      1817 AAGGTGAGAACATTTGGCGTGAAGACGGTCAAGTACATCAAGAAAGATTCCTCAAGGT 1876
Qy      461  GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
Db      1877 GAGAGAAAGGGTATCATCTGCACTCAACCATCTTTAACAAGCTGAAGGTGAGAAAGGA 1936
Qy      481  PheSerLysThrValaAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
Db      1937 TTCCTCAAGACAGCAATTCAGCATCTTGAGATGAGCGCTGAGAGTCCCTGAACGAAAG 1996
Qy      501  ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSer 520
Db      1997 ACCTCTTACATTTCTGAGTATGCGATGCGACGACCAAGTCTGGGGAGAACCAAGGACCAAC 2056
Qy      521  IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db      2057 ATAAATTTCAAGACATTTGTCAATTCAGTGTCTTGAGATTAATCCCATTAATCTCTGATT 2116
Qy      541  GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValaLysTyrGlyLeuLysLysProAsn 560
Db      2117 GGTGAGAGCCCTTCTTATCTCATATATCTGACAGTGGCATATGTGTCAAAAACCCAAAC 2176
Qy      561  LysLeuThrHisLeuGlyTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db      2177 AAATTTGACTCATCTGTGTGGCCCAACCTTCCCAACCTGCTGAAAGTATGATGCCACA 2236
Qy      581  TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
Db      2237 TGGCATGAGATGATTTCAAGATTAACCTAAACCTGAAGAGTGTGATGACTGTGTAAC 2296
Qy      601  ThrGluAsnArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
Db      2297 ACAGAAACAGGATCTTAACCAATGTTCCACACCCCAAGTGCACAAAGTGTGATGACAAAG 2356
Qy      621  LeuValAlaAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
Db      2357 TTGGTGTGAACCTTGGAATGTTCTCAAGAAATTTTCAAGATGAAGCCAGACGGGT 2416
Qy      641  GlnGluLysGlnPheArgArgGlyLysGluTrpAsp 652
Db      2417 CAGGA-AAACATTTAAGAGGGGAAAAGAAATGGGAC 2451

RESULT 4
ADD68146
ID ADD68146 standard; cDNA; 2903 BP.
XX
AC ADD68146;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human zcytor17 cDNA SEQ ID NO:4.
XX
se; gene; human; zcytor17; antiinflammatory; dermatological;
XX immunosuppressive; antimicrobial; vaccine; inflammatory disease;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX atopic dermatitis; eczema; psoriasis; endotoxaemia; septiccaemia;
XX toxic shock syndrome; infectious disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 497..2485
FT CDS /*tag= a
FT /product= "zcytor17"
XX

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PN W02003060090-A2.
 XX 24-JUL-2003.
 XX
 PF 21-JAN-2003; 2003WO-US001984.
 XX
 PR 18-JAN-2002; 2002US-0350325P.
 PR 25-APR-2002; 2002US-0375323P.
 PR 19-DEC-2002; 2002US-0435315P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Kuiper JL, Dasovich MM, Grant FJ, Hammond AK;
 PI Novak JE, Gross JA, Dillon SR;
 XX
 DR WPI: 2003-618179/58.
 DR P-PsDB; ADB68147.
 XX
 PT New zcytor17 ligand polypeptides, useful for treating inflammatory
 PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
 PT disease, atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia.
 XX
 PS Example 3; SEQ ID NO 4; 372bp; English.
 XX
 CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A
 CC polypeptide of the invention has antiinflammatory, dermatological,
 CC immunosuppressive, and antimicrobial activity, and may have a use in a
 CC vaccine. The polypeptide is useful for treating inflammatory diseases,
 CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia, toxic
 CC shock syndrome or infectious diseases. The present sequence is used in
 CC the exemplification of the invention.
 XX
 SO Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,92e-316 Length: 2903
 Score: 3451.00 Matches: 650
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.69% Mismatches: 1
 Query Match: 99.05% Indels: 1
 DB: 10 Gaps: 0

US-10-006-265-2 (1-652) x ADB68146 (1-2903)

QY 1 MetIleuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrrAlaLeu 20
 DB 497 ATGAAGCTCTCTCCCAAGCCTTCATGTGTTAACTGGGGATGATGTGAGACTGGCACTG 556
 QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
 DB 557 TGGATGTCCTTCACCTCTGCAATTCAGCTGGCAGCTCTGCAGAGTAAGCCTGAGAAC 616
 QY 41 IleSerCysValIleTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 DB 617 ATTTCTGTGTCTACTACTATAGAAAATTTTAACTGCACCTGGAGTCCAGAAAAGGAA 676
 QY 61 ThrSerTyrThrGlnIleTyrThrValLysArgThrTrrAlaPheGlyGluLysHisAspAsn 80
 DB 677 ACCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTGAGAAAAACATGATTAAT 736
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 DB 737 TGTACAAACCAATAGTTCTACAACTGAAATCGTGCTTCGTCCTTTTCCCTTCCAAAG 796
 QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 DB 797 ATAACATCCCAATATATATATACATTTGAGGTGGAAGCTGAAATGGAATGATGTATATT 856
 QY 121 LysSerHisMetThrTyrTrrPArgLysGluAsnIleAlaLysThrGluProProlLysIle 140
 DB 857 AAATTCATATGACATATCTGAGATTATGAGAACATAGCGAAACATGAAACCACTTAAGATT 916

QY 141 PheArgValIleProValIleuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 DB 917 TTCGGTGTGAAACCAATTTTGGGCATCAAAACCAATGATTCAATGATGAATTAAGCCCT 976
 QY 161 GluLeuAlaProValIleSerSerAspLeuLysTyrThrIleArgPheArgThrValAsnSer 180
 DB 977 GAGTTGGCGCCTGTTTCACTGATTTAAATACACCTTCGATTCAGGACAGTCAACAGT 1036
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 DB 1037 ACCAGCTGATGAGAGTCAACTCTCCCTAAGAACCGTAAAGATTAACCAACGATCAAC 1096
 QY 201 LeuThrGlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLysGlu 220
 DB 1097 CTCACGGGCGCTCAGCCTTTTACAGAAATATGTCATATGCTCGATGTCGGGTCAAGAG 1156
 QY 221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGluGluAlaPro 240
 DB 1157 TCAAAGTTCTGAGAGTACCTGAGGCCAAGAAAAATGGGAATGACTGAGAGAGAGCTCCA 1216
 QY 241 CysGlyLeuGlnLeuTrpArgValIleuLysProAlaGluAlaAspGlyArgArgProVal 260
 DB 1217 TGTGGCTTGAACCTGTGAGAGTCTTGAAACCACTGAGGCCGAGTGAAGAGCCAGTGTG 1276
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValIleuGluLysThrLeuGlyTyrAsn 280
 DB 1277 CGGTGTTATGAGAAAGCAAGAGAGCCCAAGTCTTGAAGAAAACATTTGGCTATCAAC 1336
 QY 281 IleTrpTyrTyrProGlnSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 DB 1337 AATATGTACTATCCAGAAAGCAACCTAACCTCAGAAACATGAACTACTAACCCAG 1396
 QY 301 GlnLeuGluLeuHisLeuGlyLysGlnSerPheTrpValSerMetIleSerTyrAsnSer 320
 DB 1397 CAGCTTGAACCTGACATCTGGAGGCCAGAGCTTTTGGGTGTATGATTTCTTAATATTCT 1456
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 DB 1457 CTTGGGAAGTCTCCAGTGGCCACCCGAGAGATTCCAGCTATTCAAGAAAAATCATTTGAG 1516
 QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSer 360
 DB 1517 TGCATTGAGGTATGAGAGCCCTGCTGTGAGAACCACTAGTGTGAAATGGCAAAAC 1576
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 DB 1577 TCTGCTTACAGCTGAACCTTGATGATTGAATGTTTCCGAGTGAATCCAGAGCCC 1636
 QY 381 ThrThrLeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
 DB 1637 ACCACCTTTCTCGGGAATCTGTGTCTCAGGCCACAGAACTGAGACGATCCAGCAAGATAAA 1696
 QY 401 LeuLysProPheTrpCysTyrAsnIleSerValIleTyrProMetLeuHisAspLysValGly 420
 DB 1697 TTAAACCTTTCTGTGGCTATTAACATCTCTGTGTATCCAAATGTGATCAAAAGTTGGC 1756
 QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGlnGlyProGluThr 440
 DB 1757 GAGCCATATTCATCCAGGCTTATGCCAAAGAGAGGCTTCCATCCAGAGGCTCTGAGACC 1816
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 DB 1817 AAGGTGAGAAACATTTGGCGTGAAGAGCGTCAAGATCACTGAAAGAGATTCACCAAGAT 1876
 QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGly 480
 DB 1877 GAGAGAAAGGATATCATCTGCAACTACACACTTTTTCACCAAGCTGAGAGTGAAGAAAGA 1936
 QY 481 PheSerLeuThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLys 500
 DB 1937 TTCTCCAAACAGTCAATTCAGCATTTGCAAGTACAGGCTGAGAGTCCCTGAAACCAAAAG 1996
 QY 501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520

QY	101	ePhr eP eP oA eA eN Th Th l eG u a l a a g u a n e G y a s g y a l l e	120
Db	797	ATAACGATCCAGAAATATTATATCACTTAAGGGAGAGCTGAAAAAGGAGATGGTAAAT	856
QY	121	LYS eS eR I s eM eT Th T Y T P A T g l eU a n l eA l a y s Th G l P o P o l y s l e	140
Db	857	AAATCTCATTAAGACATACTGGAGATTAGAAACATAGGAAAACTGAACCTTAAGATT	916
QY	141	P heA g V a l V s P o V a l eU g y l e y a g y e c l e g n l e g U T P l e y s P o	160
QY	917	TTCCGTGTGAACCCAGTTTGGGCTCAAGAAAGAAATTCAAATTGAATGATTAAGCT	976
Db	977	GAGTTGGGGCCCTGTTTTCATCTGATTTAAATAATACACACTTCGATTCAGACAGTCAACGT	1036
QY	181	Th S e T P Me e G u V a l A s n P heA l a y s A n A g l y a s P y a s n G l n Th T Y A s n	200
Db	1037	ACCGACTGGATGGAAAGTCAACTTCGCTTAAGAACCTTAAGATATTAACCAACGTAAC	1096
QY	201	Leu Th g l eU a n P o P he Th g l u T Y a l l eA l eU a g P heA g T Th V a l A s n e T	220
Db	1087	CTCACGGGGCTCGACCTTTACAGAAATATGTCATAGCTCTGCGATGGCGGTCAAGAG	1156
QY	221	S e T Y s P he T P S e A s P T P S e G l n l u y s e G y e T Th G l u g l u a l a P o	240
Db	1157	TCAAAAGTTCTGAGAGTACGTGGAGCCAAAGAAAAATGGGAATGACTGAGAGAAAGTCTCA	1216
QY	241	Cy e g l eU a n eU T P A T g V a l eU y s P o a l a a e P g l Y A g A P o V a l	260
Db	1217	TGTGGCCCTGGAACTGTGGAGAGTCTTGAAACACAGCTGAGGGAGAGGAAGAAAGGCCACTGT	1276
QY	261	A g L eU eU T P L y L e A l A a g l Y a l A P o V a l eU g l y e T Th L eU g l Y T Y A s n	280
Db	1277	CGGTTGTTATGGAGAGAACGCAAGAGAACCCCAAGTCTTAAGAGAAACACTTGGCTACAC	1336
QY	281	l l e T P Y T Y P P G l U s e T A s n Th A s n eU Th g l U Th Met A s n Th Th A s n G l n	300
Db	1337	ATATGGTACTATCCAGAAAGCAACCTAACTCCAGAGAAACAATACACATCACTAAC	1396
QY	301	G l n eU g l eU eU H s L eU g l Y G l U s e P he T P V a l S e T Y A s n e T	320
Db	1397	CAGCTTGAACCTGCATCTGGAGAGCGAGAGCTTTGGGAGTCTATGATTTCTTATATATCT	1456
QY	321	L eU g l Y S e P P o V a l A Th L eU a g l eP o a l e g n l U y s e P he G l n	340
Db	1457	CTTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCAGACTATTCAGAGAAAAATCATTTCA	1516
QY	341	Cy e l l e g l U a l Me G l n A l C y S V a l a g l U a P G l n eU V a l Y e T P G l n e T	360
Db	1517	TGCATTGAGGTCATGACAGAGCCCTGCTTCTAGAGCCAGCTAGTGTGTAAAGTGGCAAGC	1576
QY	361	S e R a l eU a P V a l A s n Th T P Me l l e g U T P P he P o A s P V a l A s P e G l U P o	380
Db	1577	TCTGTCTAAGAGTGAACACTTGGATGATTTGAATGCTTTCCGAGTGGAGCTCAAGGCC	1636
QY	381	Th T Th L eU S e T P G l U S e V a l S e G l n a l a Th A s n T P Th l e G l n a s P y s	400
Db	1637	ACCAACCCCTTCTCTGGGAATCTGTGTCTAGGCAAGCACTGACACATCCACAGATATAA	1696
QY	401	L eU y s P o P he T P C y e T Y A s n l eS e V a l Y P P o Me L eU H s A S P y S V a l G l	420
Db	1697	TTAAAACTTTCTGGTGTCTAATACATCTCTGTATCCAAATTTGCATGACAAAGTTGGC	1756
QY	421	G l U P o Y S e l l e G l a l Y T A l a y s G l U Y a l P S e G l U Y P G l U Th T	440
Db	1757	GAGCCATATTCATCCATCCAGCTTAATGCCAAAGAGGCTTTCATCCAGAGGTCCTGACAC	1816
QY	441	L y S V a l G u a n l e g l V a l Y e Th T A l T Th T P Y S G l U l e P o l y S e T	460
Db	1817	AAGGTGAGAACATTGGGTGTAAAGGGTCAAGATCAATGGAAGAAAGATTTCCAAAGGT	1876

QY	461	GIuNrgYvsGyllelleCyvAsenTYThrlIepheTYrgNlaGluGlyGly 480
Db	1877	GAGGAAAGGGTATCATCTGTGCACTACCACTTTTACCAAGCTGAAAGGGGAAAAAGG 1936
QY	481	PheserYsTrValAasSerSerleleuGlnTYrglyeuGInSerleuLYsARgLYs 500
Db	1937	TTCTCCAAAGACAGTCATTTCCAGCATCTTGCGAGTACGGCCCTCGAGTCCCTGAAACGAAG 1996
QY	501	ThiSerTYrlleValGlnValMeValAsnThiSerAlaGlnTYrhaGlyTYrhaGlyTYrSer 520
Db	1997	ACCTCTTACATGTTTCAGGTGATGGCCAGCACCGTGTGGGGGAAACCAACGGGACGAGC 2056
QY	521	ILeAsnPeLYsTrhIeuserPheSerValPheGlnIlelleleuIeThSerleuIle 540
Db	2057	ATAAATTTCAAGACATGTCTCATTAAGTCTTGAAGATATCTCATPAACTTCTTGAT 2116
QY	541	GIyGlyGlyLeuLeuIlelelleleleuThrValAlaTYrglyLeuLYsProAsn 560
Db	2117	GGTGGAGGCGCTTCTTATTTCTCATTAATCTGACAGTGGCGATAGTGTCTCAAAAAACCAAC 2176
QY	561	LysLeuThrhIseuCYsTrpProThValProAsnProAlaGInSerSerIleAlaThr 580
Db	2177	AAATTTGACTCATCTGTGTGGCCACCGTCCCAACCTGCTGAAATGATATGACACA 2236
QY	581	TrpHISGlyAspAspPheLYsAspLYsLeuAsnLeuLYsGInSerAspAspSerValAsn 600
Db	2237	TGGATGAGAGTGAATTCACAGATTAACCTTAACCTGAAAGAGTGTGATGATCTGTGAAC 2296
QY	601	ThrGluAspARgIleleuLYsProCYsSerThrProSerAspLYsLeuValIleAspLYs 620
Db	2237	ACAGAGACAGGATCTTAAACCATGTTCCACCCCGTGAACAAGTGGTATTGACAAAG 2356
QY	621	LeuValValAsnPheGlyAsnValleuGlnIlePheThrAspGluAlaArgThrGly 640
Db	2357	TTGGTGGTGAACCTTTGGGAATGTTCTGCAAGAAATTTTCCACAGATGAAGCCAGAACGGGT 2416
QY	641	GIInGlyuYsGInPheARgARgLYsLYsGluTrpAsp 652
Db	2417	CAGGA-AAACATTTAGAGGGGAAAAAGAAATGGGAC 2451
RESULT 6		
ABA93803		
ID	ABA93803	standard; cDNA; 2529 BP.
AC	ABA93803;	
XX		
DT	01-MAY-2002	(first entry)
XX		
DE	Human zcytor17 cDNA sequence SEQ ID NO:45.	
XX		
KW	Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;	
KW	antifungal activity; antiviral; antirheumatic; antiarthritic; cyostatic;	
KW	muscular; lymphoid; immune; inflammatory; splenic; blood; bone;	
KW	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;	
KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;	
KW	inflammatory disease; pancreatitis; inflammatory bowel disease; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200200721-A2.	
PD		
XX	03-JAN-2002.	
PF	26-JUN-2001; 2001WO-US020484.	
XX		
PR	26-JUN-2000; 2000US-0214282P.	
PR	29-JUN-2000; 2000US-0214955P.	
PR	08-FEB-2001; 2001US-0267963P.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Sprescher CA, Presnell SR, Gao Z, Whitmore TE, Kujiiper JJ, Maurer MF;	

XX MPI: 2002-090519/12.
 DR P-PSDB: ABB05738.
 XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 XX
 PS Claim 2: Page 190-194; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antineumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral
 CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 2529 BP; 764 A; 530 C; 576 G; 659 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,93e-315 Length: 2529
 Score: 3441.00 Matches: 648
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.69% Mismatches: 1
 Query Match: 98.77% Indels: 1
 DB: 6 Gaps: 0

US-10-006-265-2 (1-652) x ABA93803 (1-2529)

QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetThrTPThrTPAlaLeuTPMet 22
 Db CTCTCTCCCTCCAGCCTTCACTGTGTAACTCGGAGATGATGTGACCTCGGACCTGTGATG 188
 QY 23 LeuProSerLeuCysIlePheSerLeuAlaLeuProAlaIleProGluAsnIleSer 42
 Db CTCCCTCTCACTCTGCAAAATTAGCCTGACCTGACCTGCAAGCTGAAGCTGAAGCAATTTCC 248
 QY 43 CysValTyrTyrTyrAspLeuThrCysThrTPSerProGluIleGluThrSer 62
 Db TGTGTCTACTACTAGGAAATTTAACTGCACTTGAAGTCCAGAAAGAAACCACT 308
 QY 63 TyrThrGlnTyrThrValIleArgThrTyrAlaPheGlyGluIleAspAsnCysThr 82
 Db TATACCCAGTACAGATTAGAACTTACCTTTTGGAAAAAATCATGATTAATTGTCA 368
 QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
 Db ACCAATAGTTCTACAAAGAAATCGTCTCTGCTCTTTTTCCTTCCAAAGATAACG 428
 QY 103 IleProAspAsnTyrThrIleGluValGluIleAsnIleAspGluValIleIleSer 122
 Db ATCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 488
 QY 123 HisThrTyrTyrPArgLeuGluAsnIleAlaIleThrGluProProIlePheArg 142
 Db CATATGACATCTAGATTAAGAACTATGCAAACTGAACCACTTAAGATTTTCCGT 548
 QY 143 ValIleProValIleGluIleIleArgMetIleGlnIleGluIleIleIleProGluIleu 162
 Db GTGAAACCAAGTTTGGGATCAACGAATGATTAATTAATTAATTAATTAATTAATTAATTAAT 608
 QY 163 AlaProValSerSerAspLeuIleTyrThrLeuArgPheArgThrValAsnSerThrSer 182

Db GCCTCTGTTTCATCGATTTAAATAACACACTTCGATTACAGACAGTCAACGATCACAGC 668
 QY 183 TrpMetGluValAsnPheAlaIleAsnArgIleAspIleAsnGlnThrTyrAsnLeuThr 202
 Db TGGATGAAAGTCAACTTCGCTTAACACCGTAAAGATTAATAACCAACCTACACCTCAGC 728
 QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIleGluSerIle 222
 Db GGGCTGACGCTTTTACGAATATGTCAATAGCTTCGCAATGCGGTCAAGAGTCAAG 788
 QY 223 PheTrpSerAspTrpSerGlnIleIleMetGlyMetThrGlnGluIleProCysGly 242
 Db TTTCGAGTGAAGTCAAGCAAGAAATGGGAATGACTGAGAAAGCTCCATGTGGC 848
 QY 243 LeuGluLeuTrpArgValIleuIleIleProAlaGluAlaIleAspGluValArgGluArgLeu 262
 Db CTGAACCTGTGAAAGTCTGAAACCAAGCTGAGCGATGAAAGAGCCAGTCCGCTGG 908
 QY 263 LeuTrpIleValAspIleValAlaProValLeuGluIleIleThrLeuGlyTyrAsnIleTrp 282
 Db TTATGAGAAAGGCAAGAGAGCCCTCACTGAGAAACCACTTGGCTACACATATAG 968
 QY 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnIleu 302
 Db TACTATCCAGAAACCAACCTACCTCAAGAAACATGAACACTTACACAGAGCTT 1028
 QY 303 GluLeuHisLeuGlyIleGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
 Db GACCTGATCTGGAGAGCGAGAGCTTTGGGTCTCTATGATTTCTTAATTTCTTGGG 1088
 QY 323 LysSerProValAlaThrIleArgIleProAlaIleGlnIleIleIleSerPheGluCysIle 342
 Db AAGTCTCAAGTGGCCACCTGAGATTCACCTATTCAGAAATCACTTCAAGTCACTT 1148
 QY 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValIleTyrGlnIleSerIle 362
 Db GAGGTCAATGACGCTCGCTGTGTGAGGACCAAGCTAGTGGTGAAGTGGCAAGCTCTGCT 1208
 QY 363 LeuAspValAsnThrTyrMetIleGluTrpPheProAspValAspSerGluProThrThr 382
 Db CTAGACCTGAACACTTGAATGATTAATGATTTCCGATGTGACCTAGACCCACCAACC 1268
 QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspIleLeuIle 402
 Db CTTCCTGGAAATGTGTCTCAGGCCACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1328
 QY 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspIleValGluPro 422
 Db CTTTCTGGTGTCTAATCACTCTGTGTATCAATGTGATGCAAAAGTTGGAGGCA 1388
 QY 423 TyrSerIleGlnAlaTyrAlaIleGluIleValProSerGluGlyProGluThrIleVal 442
 Db TATTCATTCACGCTTATGCAAAAGAGCGTTCATCAGAGGCTCTGAGAACCAAGGTG 1448
 QY 443 GluAsnIleGlyValIleThrValThrIleThrTrpIleGluIleProIlePheSerGluArg 462
 Db GAGAAACATGTGCGTGAAGAGCGTACATCAACATGAAAGATTTCCAAAGAGGAGA 1508
 QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluIleGlyIleGlyPheSer 482
 Db AAGGATTCATCTGCACTACCATCTTTTACCAACTGAAGTGAAGAAAGATTTCTCC 1568
 QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluIleSerLeuIleArgIleThrSer 502
 Db AAGACATCAATTCACATCTTGCAATAGGCTGAGAGTCCGGAACCAAGAACCTCT 1628
 QY 503 TyrIleValGluValMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSerIleAsn 522
 Db TACATTTTCAAGGTCAGGCAAGCAAGTGTGGGGGAACCAAGGGAACCAAGCATTAAT 1688
 QY 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyIle 542
 Db TTCAAGACATTTGATTCATTCAGTCTTTGAGATTAATCTCATTAATCTTCTGATTTGGTGA 1748

QY 543 GATLeuLeuLeuLeuLeuLeuLeuValAlaTyrGlyLeuLeuLeuProLeuLeuLeu 562
 DB 1749 GGGCTTCTTATTTCTATTTCCGACAGTGGCATATGCTCTCAAAAAACCAACCAATTG 1808
 QY 563 ThrHisLeuCySerTrpProThrValProLeuProAlaGlySerSerLeuAlaThrTPHis 582
 DB 1809 ACTCATCTGTGTGGCCACCGCTTCCCAACCTGTGAAAGTAGTATAGCCATCATGGCAT 1868
 QY 583 GlyAspAspPheLeuAspLeuLeuLeuLeuLeuLeuGlySerAspAspSerValAlaThrGlu 602
 DB 1869 GGAGATGATTTCAAGATTAAGATTAACCTGAAGAGTCTGATACCTGTGAACACAGAA 1928
 QY 603 AspArgIleLeuLeuProCySerSerThrProSerAspLeuLeuValIleAspLeuVal 622
 DB 1929 GACAGATCTTAAACCAATGTTCCACCCGAGACAGATGTTGATTTGACAAAGTTGGTG 1988
 QY 623 ValAspPheGlyAsnValLeuGlnGlnIlePheThrAspGluAlaArgThrGlnGln 642
 DB 1989 GTGACCTTGGGAATGTTCTGCAAGAAATTTTCACAGATGACCAAGACGGTCAAGA- 2047
 QY 643 LysGlnPheArgArgGlyLysGluTTPAsp 652
 DB 2048 AAACAATTGAAGAGGGAAGAAAGATGGAC 2077
 RESULT 7
 ADL26671
 ID ADL26671 standard; cDNA; 2529 BP.
 AC ADL26671;
 DE 20-MAY-2004 (first entry)
 XX Human cytokine receptor zcytor17 DNA seqid 108.
 XX
 XX antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;
 KW antibacterial; immunosuppressive; cell proliferation inhibitor;
 KW immune response inhibitor; inflammatory response inhibitor;
 KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KW cytokine-binding domain; class I cytokine receptor; haematopoietic cell;
 KW zcytor171g-induced proliferation; zcytor171g-induced differentiation;
 KW hematopoietic progenitor cell; zcytor171g-induced inflammation;
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; atopic dermatitis; psoriasis; endotoxaemia;
 KW septicemia; toxic shock syndrome; zcytor17; human; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX US2003215838-A1.
 PN
 XX 20-NOV-2003.
 PD
 XX 21-JAN-2003; 2003US-00351157.
 PF
 XX 18-JAN-2002; 2002US-0350325P.
 PR 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX
 XX (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUIJ/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNELL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX
 PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR,
 XX

DR WPI: 2003-876545/81.
 DR P-PSDB; ADL26672.
 XX
 PT Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.
 XX
 PS Disclosure; SEQ ID NO 108; 2059p; English.
 XX
 CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (CI) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing haematopoietic cells and hematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor171g-induced proliferation or differentiation
 CC of hematopoietic cells and hematopoietic progenitor cells; reducing
 CC zcytor171g-induced inflammation; treating a mammal afflicted with an
 CC inflammatory disease in which zcytor171g plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC psoriasis. The disease is acute inflammatory disease such as
 CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
 CC An immune response inhibiting composition is useful for inhibiting an
 CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (I) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a human zcytor17 cytokine receptor that can be used
 CC in a comparison with other zcytor17 receptors.
 XX
 SQ Sequence 2529 BP; 764 A; 530 C; 576 G; 659 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4,93e-315 Length: 2529
 Score: 3441.00 Matches: 648
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.69% Mismatches: 1
 Query Match: 98.77% Indels: 1
 DB: 11 Gaps: 0
 US-10-006-265-2 (1-652) x ADL26671 (1-2529)
 QY 3 LeuSerProGlnProSerCyValAsnLeuGlyMetTrpThrTrpAlaLeuTrpMet 22
 DB 129 CTCTCTCCCAACCTTCAATGTTAACTGGGAGATATGTGACCTGGGACATGTGGAG 188
 QY 23 LeuProSerLeuCyValPheSerLeuAlaLeuProAlaLeuProGluAsnIleSer 42
 DB 189 CTCCTCTCACTGCAAAATTCAGCTGGCAGCTGTCCAGCTAAGCAATTTCC 248
 QY 43 CyValTrpTrpTrpTrpArgLysAsnLeuThrCySerTrpMetProGlyLysGluThrSer 62
 DB 249 TGTGTCTACTACTATAGAAAATTTAACTGCTGAGTCCAGGAAAGAAACCACT 308
 QY 63 TyrThrGlnTrpThrValLysArgThrTrpAlaPheGlyGlyLysHisAspAsnCySer 82
 DB 309 TATACCACTATACAGCTTAAGAACTTACGCTTTTGGAGAAAACATATATATGTACA 368
 QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThr 102
 DB 369 ACCAATAGTTTACAAAGTGAATCGTGTCTCTTTTCTCTTCCCAAGAAATTAAG 428
 QY 103 IleProAspAsnTrpThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
 DB 429 ATCCGAGATTAATTAATCAATTGAGGTGAGAGCTGAAGAAAGAGATGTATTAATATCT 488

QY 123 HIsMetThrTyrTrpArgLeuGluuAsnIleAlaIysThrGluProProIlePheArg 142
 DB 489 CATATGACATATCGAGATTAGAGAACATAGGAAACCACTGACCTTAAGTTTTCCT 548
 QY 143 ValIysProValLeuGlyTlleYsaArgMetIleGlnIleGluTrpIleYsaProGluLeu 162
 DB 549 GTGAACCAAGTTTGGGATCAACCAATGATTCAAAATTGAATGATTAAGCTGAGTGG 608
 QY 163 AlaProValSerSerAspLeuIleYsaThrLeuArgPheArgThrValAsnSerThrSer 182
 DB 609 GCGCTGTTTCACTCGATTATAAATACACACTTCATTCAGGACGTCACGTCACGAC 668
 QY 183 TrpMetGluValAsnPheAlaIysAsnArgIleYsaAspIleYsaAsnGlnThrTyrAsnLeuThr 202
 DB 669 TGGATGGAAGTCACTTCGCTAGAACCGTAAAGATTAATAACCAACGACGACCTCAG 728
 QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIleGluSerIleYs 222
 DB 729 GGGCTGACGCTTTTACAGAAATATGTCAATAGCTGACATGTGCGGTCAAGAGTCAAG 788
 QY 223 PheTrpSerAspTrpSerGlnGluIleYsaMetGlyMetThrGluGluAlaProCysGly 242
 DB 789 TTCGAGTGAAGTGAAGCAAGAAATAAGGAATGACTGAGAGAAAGAAAGCTCATGTGAC 848
 QY 243 LeuGluLeuTrpArgValLeuIleYsaProAlaGluAlaAspGlyArgArgProValArgLeu 262
 DB 849 CTGGAACCTGTGAGAGTCTTGAACCAAGCTAGAGGGGATGGAAGAAAGGCTGCGGTG 908
 QY 263 LeuTrpIleYsaIleArgGlyAlaProValLeuGluIleYsaThrLeuGlyTyrAsnIleTrp 282
 DB 909 TTATGAGAAGAGGCAAGAGAGAGCCCACTGCTAGAGAAACACTTGGCTACAACTATAGG 968
 QY 283 TyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnIleu 302
 DB 969 TACTATCCAGAAAGCAACACTCACTCAAGAAACAACTCACTCACTCACTCACTCACT 1028
 QY 303 GluLeuHIsleuGlyGlyIleYsaPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
 DB 1029 GAACCTGATCTGGAGGCGCAAGCTTTTGGGTGTATGATTTCTTAATAATTCCTTTGG 1088
 QY 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluIleYsaSerPheGlnCysIle 342
 DB 1089 AAGTCTCCAGTGGCCACCTGAGATTCAGCTATTAAGAAATAATCAATTCAGTGCAT 1148
 QY 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValIleTrpGlnSerSerAla 362
 DB 1149 GAGGTCAAGCAGGCTGCTGCTGAGGACCAAGCTAGTGTGAATGTGCAAAAGCTCTCT 1208
 QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
 DB 1209 CTTAGCGTGAACCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1268
 QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpTrpIleGlnGlnAspIleYsaLeuYs 402
 DB 1269 CTTTCTCGGAATCTGTCTCAAGCCCAAGACTGAGATCCAGCAAGATTAATAA 1328
 QY 403 ProPheTrpCysTyrAsnIleSerValIleYsaProMetLeuHIsAspIleValIleGluPro 422
 DB 1329 CTTTCTGCTGTATTAACATCTGTGTATCAAAAGTGTGACAAAGTGTGCGAGCCA 1388
 QY 423 TyrSerIleGlnAlaTyrAlaIleGluIleValProSerGluIleProGluThrIleYsaVal 442
 DB 1389 TATTCATCCAGGCTTATGCCAAAGAGCGTTTCCATCAAGAGGTTCTGAGACCAAGGTG 1448
 QY 443 GluAsnIleGlyValIleYsaThrValThrIleThrTrpIleGluIleProIleYsaSerGluArg 462
 DB 1449 GAGAAACATGGCGTGAACCGTCAAGTCAATGAAAGAGATTCACCAAGAGTGAAGA 1508
 QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluIleGlyIleYsaPheSer 482
 DB 1509 AAGGTATACATCTGCACTACCACTTTTACCAAGCTGAAGGAGGAAAGAGATTCCTCC 1568
 QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuIleYsaArgIleYsaThrSer 502

DB 1569 AAGACAGTCAATTCAGCATCTTGACAGTACGCGCTGAGGTCCCTGTAAGCAAGAACCTCT 1628
 QY 503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyTyrThrAsnGlyThrSerIleAsn 522
 DB 1629 TACATTTGTCAGGTCATGCGACCAAGTCTGGGGGAAACCAAGGACCAAGCATTAAT 1688
 QY 523 PheIleYsaThrLeuSerPheSerValPheGluIleIleLeuIleThrSerIleIleGlyGly 542
 DB 1689 TTCAGACATTTGTCATGAGTGTCTTTGAGATTATCTCATTAACCTTCTGTATGTGGA 1748
 QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuIleYsaIleYsaProAsnIleYsaLeu 562
 DB 1749 GCGCTTCTTATTCATTAATCTGACAGTGCATATGTGTCCTCAAAAACCAACAAATTTG 1808
 QY 563 ThrIleLeuCysTrpProThrValIleProAsnProAlaGluSerSerIleAlaThrTrpHis 582
 DB 1809 ACTCATCTGTGTGGCCACCGTTCACCAACCTGTGAAAGTATAGCCACATGGCAT 1868
 QY 583 GlyAspAspPheIleYsaIleYsaLeuAsnLeuIleYsaIleYsaAspAspSerValAsnThrGlu 602
 DB 1869 GGAATGATTTCAAGATTAAGCTTAACCTGAAGAGTGTGATGACTGTGAAACACAGA 1928
 QY 603 AspArgIleLeuIleYsaProCysSerThrProSerAspIleYsaLeuValIleAspIleYsaVal 622
 DB 1929 GACAGGATCTTAACCAACATGTTCCACCCCGACGACAAAGTTGGTGAATGACAAATG 1988
 QY 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
 DB 1989 GTGAACCTTGGGAATGTTCTCAAGAAATTTTCAACATGAAGCAGAAACGGTCAAGA - 2047
 QY 643 LysGlnPheArgArgGlyIleGluTrpAsp 652
 DB 2048 AAACATTTAGAGAGGAGAAAGATGGAC 2077
 RESULT 8
 AB083363
 ID AB083363 standard; cdna: 4315 BP.
 AC AB083363;
 DT 20-JAN-2003 (first entry)
 XX
 DE Human NR10.3 splicing variant encoding cDNA SEQ ID NO:1.
 XX
 KW NR10; splicing variant; haematopoietic receptor; immunomodulator;
 KW haemostatic; haematopoietic factor; immunological disease;
 KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FH 7..2052
 FT /*tag= a
 FT /product= "NR10.3"
 XX
 WO200277230-A1.
 PD 03-OCT-2002.
 PE 22-MAR-2002; 2002WO-JP002769.
 PR 26-MAR-2001; 2001JP-00087298.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Maeda M, Yaguchi N, Hasegawa M;
 XX
 DR WPI; 2003-018925/01.
 DR P-PSDB; ABP54363.
 XX
 PT NR10 splicing variants of haematopoietic receptor proteins and encoded
 genes, applicable in searching haematopoietic factors and developing

PT remedies for immunological and hematopoietic diseases.
XX
PS Example 2; Fig 1-2; 250pp; Japanese.
XX
CC The present invention describes hematopoietic receptor NR10 splicing
CC variants (1). (1) have immunomodulator and hemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC hematopoietic factors, and developing remedies for immunological and
CC hematopoietic diseases. The hematopoietic receptor genes participate
CC in vivo immunomodulation and hematopoietic cell regulation, and in the
CC search for hematopoietic factors capable of functionally binding to the
CC receptors. The present sequence encodes the human NR10.3 protein from the
CC present invention
XX
SQ Sequence 4315 BP; 1187 A; 1008 C; 1061 G; 1059 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,07e-314 Length: 4315
Score: 3441.00 Matches: 648
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 98.77% Indels: 1
DB: 8 Gaps: 0
US-10-006-265-2 (1-652) x AB083363 (1-4315)
QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTpmet 22
Db CTCTCTCCCGAGCCTTCATGTGTTCACCTGGGATGATGTGAACCTGGGACCTGTGGATG 129
QY 23 LeuProSerLeuCysIysPheSerLeuAlaAlaLeuProAlaIysProGluAsnIleSer 42
Db CTCGCCCTCACTCGAAATTCAGCCTGGAGCTCTGCAGCTAAGCCTGAGAACATTCC 189
QY 43 CysValIleTrpTrpArgIysAsnLeuThrCysThrTrpSerProGlyIleGluThrSer 62
Db TGGGTCTACTACATATGAGAAATTTAAACCTGCATTGAGTCCAGGAAAGGAAACCACT 249
QY 63 TyrThrGlnIleThrValIysArgTrpTrpAlaPheGlyGluIysHisAspAsnCysThr 82
Db TATTAACCACTGACAGTTAAGAAACTTACGCTTTGGAGAAACATGATTAATTGTACA 309
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
Db ACCAATAGTCTCAAGTGAATAATCGTTCGTCCTTTTCCCTTCCAGAAATACG 369
QY 103 IleProAspAsnTrpThrIleGluValGluAlaGluAsnGlyAspGlyValIleIysSer 122
Db ATCCCAATATATATACCATTTGAGTGAAGCTGAAATGAGATGGTGTAAATTAATCT 429
QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaIleThrGluProProIlePheArg 142
Db CATATGACATACCTGAGATTTAGAAACATAGCCAAACCTAACCACTTAAGATTTCCGT 489
QY 143 ValIysProValLeuGlyIleIysArgMetIleGlnIleGluTrpIleIysProGluLeu 162
Db GTGAACCAAGTTTGGGCATCAACAGATGATTCAATTGAATGAATAAAGCCGAGTTG 549
QY 163 AlaProValSerSerAspLeuIleIysTrpThrLeuArgPheArgThrValAsnSerThrSer 182
Db GGCCTGTTTCATCTGATTTTAAATACACTTCGATTCCAGACAGCAACAGTACACAGC 609
QY 183 TrpMetGluValAsnPheAlaIysAsnArgIysAspIysAsnGlnIleThrTrpAsnLeuThr 202
Db TGAATGAAATCAACTTCGCTAAGAACCCGTAAGATTAACCAACAGTCAACCTCAGC 669
QY 203 GlyLeuGlnProPheThrGluTrpValIleAlaLeuArgCysAlaValIysGluSerIys 222
Db GGGCTGAGCCTTTACAGAAATATGTATAGCTCTGGAGTGTGGCTCAAGAGTCAAG 729
QY 223 PheTrpSerAspTrpSerGlnIleGlyIysMetGlyMetThrGluGluGluAlaProCysGly 242
Db TTCTGAGTGACTGGAGCCAAAGAAATGGAATGACTGAGGAAGAAAGCTCATGTGCGC 789

QY 243 LeuGluLeuTrpArgValIleuIysProAlaGluAlaAspGlyArgArgProValArgLeu 262
Db CTGGAACCTGTGAGAGTCTTGAACACAGCTGAGGGCGGATGGAAGAACGCAAGCGCTTG 849
QY 263 LeuTrpIysValAlaArgGlyAlaProValIleGluIysThrLeuGlyTyrAsnIleTrp 282
Db TTAATGAAAGAGCAAG 909
QY 283 TyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnIleu 302
Db TACTATCCGAAAGCAACCTAATCTCACAGAAACATATACATTAACGACGACTT 969
QY 303 GluLeuHisLeuGlyIleGluSerPheTrpValIleSerMetIleSerTyrAsnSerLeuGly 322
Db GAACCTCATCTGGAGGCGAGAGCTTTTGGGTGTATATTTCTTAATTTCTTGGG 1029
QY 323 IysSerProValAlaThrLeuArgIleProAlaIleGlnGluIysSerPheGlnCysIle 342
Db AAGTCTCCAGTGGCCACCTGAGAGATTCAGCTATTCAAGAAATCATTTTCAGTCAAT 1089
QY 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValIleTrpGlnSerSerAla 362
Db GAGGTATGCAAGCCCTGCGTCTGAGACCAAGCTAAGTGAAGTGGCAAGCTGTGCT 1149
QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db CTAGAGCTGAACACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1209
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspIysLeuIys 402
Db CTTTCTGGGAAATCTGTGTCTCAGGCAAGAACATGCAATCAGCAATCAATTAATTAATA 1269
QY 403 ProPheTrpCysThrAsnIleSerValTyrPrometLeuHisAspIysValGlyGluPro 422
Db CTTTGTGTGCTATTAACATCTCTGTATCCAAAGTTCAGAACAAAGTGGCGAGCA 1329
QY 423 TyrSerIleGlnAlaIleValIysGluGlyValProSerGluGlyProGluTrpIysVal 442
Db TATTCATCCAGGCTTATCCAAAGAGCGTTCATCAAGAGTCTCTGAGACCAAGGTG 1389
QY 443 GluAsnIleGlyValIysThrValThrIleThrTrpIysGluIleProIysSerGluArg 462
Db GAGAACATTTGGCGTGAAGCGGTCAAGATCAATGAGAAAGAGATTCCTCAAGGTGGA 1449
QY 463 IysGlyIleIleCysAsnTrpThrIlePheTyrGlnAlaGluGlyIysGlyPheSer 482
Db AAGGTATCATCTGCACTACACCATCTTTTACCAAGCTGAAGGTGAAGAGATTTCTCC 1509
QY 483 TyrThrValAsnSerSerIleLeuGlnIleGlyLeuGluSerLeuIysArgIysThrSer 502
Db AAGACAGCATATTCACGACATCTTGCAGTACGGGCTGAGATCCCTGAAAGAAAGACTCT 1569
QY 503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSerIleAsn 522
Db TACATGTTCAAGTATGCGCACCAAGCTGCGGGGAAACCAACCGGACAGCATAAAT 1629
QY 523 PheIysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyIys 542
Db TTCAAACATTTGATTCAGTGTCTTTGAGATTTCCTATTAATCTCTGTGATGTGGA 1689
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuIysIysProAsnIysLeu 562
Db GGCCTTCTTATTTCTATTCTCTGACAGTGGCATATGTCTCAAAAAACCAACCAATTTG 1749
QY 563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
Db ACTCATCTGTGTGGCCACCGTTCCAAACCTGCGTGAAGATGATACCATGCGCAT 1809
QY 583 GlyAspAspPheIysAspIysLeuAsnLeuIysGluSerAspAspSerValAsnTrpGlu 602
Db GGAGATGATTTCAAGATTAAGCTTAAACCTGAAGAGATGATGATGATGATGATGATGAT 1869

Qy 603 AsparagileLeuLyseProCySerThrProSerAspLyLeuValIleAspLyLeuVal 622
 Db 1870 GACAGGATCTTAAACCATGTTCCACCCCACTGACAGTGTGATTCACAGTTGGTG 1929
 Qy 623 ValAspPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
 Db 1930 GTGAACCTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAGCCAGAACGGGTCAAGA- 1988
 Qy 643 LysGlnPheAspArgGlyGlyLeuGluTrpAsp 652
 Db 1989 AAACAAATTTAGAGGAGGAAAGAAATGGGAC 2018
 RESULT 9
 ABA93767
 ID ABA93767 standard: cDNA; 2386 BP.
 AC ABA93767;
 XX 01-MAY-2002 (first entry)
 DT
 XX Human zcytor17 cDNA sequence SEQ ID NO:1.
 DE
 XX Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antirheumatic; antiarthritis; cytostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; bone;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
 XX Homo sapiens.
 OS
 XX MO200200721-A2.
 PN 03-JAN-2002.
 XX 26-JUN-2001; 2001MO-US020484.
 PF 26-JUN-2000; 2000US-0214282P.
 XX 29-JUN-2000; 2000US-0214955P.
 PR 08-FEB-2001; 2001US-0267963P.
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuiper JL;
 PI Maurer WF;
 XX WPI; 2002-090519/12.
 DR P-PSDB; ABB05730.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 XX
 PS Claim 2; Page 161-166; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiarthritis and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral
 CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93767 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention
 CC
 XX Sequence 2386 BP; 711 A; 525 C; 575 G; 575 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.67e-314 Length: 2386
 Score: 3435.00 Matches: 647
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.69% Mismatch: 1
 Query Match: 98.59% Indels: 1
 DB: 6 Gaps: 0
 US-10-006-265-2 (1-652) x ABA93767 (1-2386)
 Qy 3 LeuSerProGlnProSerCysValAsnLeuGlyMetCysTrpThrAlaLeuTrpMet 22
 Db 138 CTCTCTCCCAAGCCTTCACTGCTTAACTGGGAGATGATGATGACCTGGCATCTGGATG 197
 Qy 23 LeuProSerLeuCysLysPheSerLeuAlaIleuProAlaLysProGluAsnLysSer 42
 Db 198 CTCCCTCCTCCTGCAAAATTCAGCTGGCAGCTCTGCGCAGCTTAAGCTGAAGACATTTCC 257
 Qy 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
 Db 258 TGTGCTACCTACTATAGGAAATTTAACTGCACTGAGTCCAGAGAAAGAAACAGT 317
 Qy 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsnCysThr 82
 Db 318 TATACCCAGTACAGAGTTAAGAACTTAACCTTTGGAGAAACATGATATTTGTACA 377
 Qy 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArgLysThr 102
 Db 378 ACCAATAGTCTTACAAGGAAATCGTGCTCGAGCTCTTTTCCCTTCAAGATAACG 437
 Qy 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspArgValIleLysSer 122
 Db 438 ATCCAGATTAATTTATACATTTGAGTGGAGTGGAACTGAAATGAGATGTGTAATTAATCT 497
 Qy 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProLysIlePheArg 142
 Db 498 CATATGACATCTGAGATTTGAGAACATGACGAAATGAAACCACTTAATTTCCGT 557
 Qy 143 ValLysProValLeuGlyLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
 Db 558 GTGAACCAAGTTTGGGCATCAACGAATGATCAAAATGAAATGATTAACCTGAGTTG 617
 Qy 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
 Db 618 GCGCCTGTTTATCTGATTTAAATATACACACTTGCATTCAGACAGCAACAGTACCAAGC 677
 Qy 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGluThrTyrAsnLeuThr 202
 Db 678 TGGATGGAATGCACTTCGCTAAGAACCGTAAAGATTAACCAACGTAACCTCACG 737
 Qy 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
 Db 738 GGGCTGAGCCTTTTACGAATATGTCATAGCTCTGCGATGTGGCTCAAGAGTCAAG 797
 Qy 223 PheTrpSerAspTrpSerGlnGlyMetCysLysThrGluGluGluAlaProCysGly 242
 Db 798 TTCGGAGTGCCTGAGCAAGAAATGGGAATGACTGGAAGAACCTCCATGTGGC 857
 Qy 243 LeuGluLeuTrpArgValLleuLysProAlaGluAlaAspGlyArgAspProValArgLeu 262
 Db 858 CTGAAACTGTGGAAGATCTGTAACCAAGCTGAGCGGATGGAAGAACGCGATCGGTTG 917
 Qy 263 LeuTrpLysLysAlaArgLysAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
 Db 918 TTAATGAAGAAAGCAAGGAGGAGCCCAAGTCTTAAGAAACATTTGGCTCAATATGG 977
 Qy 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrAsnGlnGluLeu 302
 Db 978 TACTATCCAGAAACCAACACTACCTCACAGAAACAAATGAACATTAACCAACAGCTT 1037
 Qy 303 GluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322

Db 1038 GAACATCATCTGGAGCGAGACCTTTGGGTCATATGATTTCTTAATATCTCTGGG 1097
 QY 323 LYSSEProValAlaThrLeuArgIleProAlaIleGlnGluYssSerPheGlnCysIle 342
 Db 1098 AAGCTCCAGTGGCCACCTGAGAGATTCCAGCTATTCACAAAATCATTTCCGTGATT 1157
 QY 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValIleYsTrpGlnSerSerAla 362
 Db 1158 GAGGTATGACAGGCGCTGCGTTGCTGAGAGACACAGTGTGTGAAGTGGCAAAAGCTCTGGCT 1217
 QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
 Db 1218 CTAGAGCTGAACCTTGAGATGATGATGTTCCGATGTGACCTCAGAGCCACCAACC 1277
 QY 383 LeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspValLeuVal 402
 Db 1278 CTTTCTGGGAATCTGTGTCTCAGGCCACGAATCGAACATCCAGCAAGTAAATTAAAA 1337
 QY 403 ProPheTrpCysTrpAsnIleSerValTrpProMetLeuHisAspValGlyGluPro 422
 Db 1338 CTTTCTGGGCTATTAACATCTGTGTATCCAAATGTGTGATGACAAAGTTGGCGAGCCA 1397
 QY 423 TrpSerIleGlnAlaTrpAlaValGlyGluValProSerGluGlyProGluTrpValVal 442
 Db 1398 TATTCATCCAGGCTTAATGCAAAAGAGGCTTCCATCAAGAGCTCTGAGACCAAGTGG 1457
 QY 443 GluAsnIleGlyValIleYsThrValThrIleThrTrpLeuGluIleProYssSerGluArg 462
 Db 1458 GAGAACATTGGCTGTAAGACGTCACGATCACTGAAAGAGATTTCCCAAGATGTGAGAA 1517
 QY 463 LysGlyIleIleCysAsnTrpThrIlePheTrpGlnAlaGluIleGlyIleGlyPheSer 482
 Db 1518 AAGGTATCATCTGCAACTACACATCTTTTCAAGCTGAAGTGGAAAAAGATTCTCC 1577
 QY 483 LysThrValAsnSerSerIleLeuGlnTrpGlyLeuGluSerLeuValGlyTrpThrSer 502
 Db 1578 AAGACAGTCAATTCCAGCATCTTGAGTACGGCTGGAGTCCCTGAAACCAAAAGACCTCT 1637
 QY 503 TyrIleValGlnValMetAlaAsnTrpSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
 Db 1638 TACATTTTCAGGTTCATGGCCACAGACAGTCTGGGGGAACCAACGGACCATTAAT 1697
 QY 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
 Db 1698 TTCACGATTCATTCAGTGTCTTTGACATTATCTCTCAATCTCTCGATTGGTGGG 1757
 QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaIleValGlyLeuValSerProAsnValLeu 562
 Db 1758 GGCCTTCTTAATTCATTTATCTCGACAGTGGCATATGCTCAAAAAACCAACCAATTTG 1817
 QY 563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
 Db 1818 ACTCATCTGTGTGGCCACCGCTTCCCAACCTGCTGAAAGTATAGCCACATGGCAT 1877
 QY 583 GlyAspAspPheLysAspLysLeuAsnLeuValGluSerAspAspSerValAsnThrGlu 602
 Db 1878 GAGAGATGATTTCAAGGATTAAGCTAAACCTGAAGAGATCTGATGCTGGAACACAGAA 1937
 QY 603 AspArgIleLeuLysProCysSerTrpProSerAspLysLeuValIleAspValLeuVal 622
 Db 1938 GACAGAGATCTTAACCAATGTTCCACCCACAGAACAGTGTGTGATGCAAGTTGGTGG 1997
 QY 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
 Db 1998 GTAAACTTGGGAATGTTCTGCAAGAAATTTTCACGATGAAACAGAAAGGGGTCAAGA 2056
 QY 643 LysGlnPheArgArgGlyLysGluTrp 651
 Db 2057 AACCAATTTAGAGGGGAAAAAGATGG 2083
 RESULT 10
 ADL26673
 ID ADL26673 standard; cDNA; 2402 BP.

XX ADL26673;
 AC 20-MAY-2004 (first entry)
 XX
 DT Human cytokine receptor zcytor17 DNA seqid 110.
 XX
 DE antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;
 XX immunosuppressive; cell proliferation inhibitor;
 XX antibacterial; immunosuppressive; cell proliferation inhibitor;
 KW immune response inhibitor; inflammatory response inhibitor;
 KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KW cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
 KW zcytor171g-induced proliferation; zcytor171g-induced differentiation;
 KW hematopoietic progenitor cell; zcytor171g-induced inflammation;
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 KW septicemia; toxic shock syndrome; zcytor17; human; gene; ss.
 XX
 OS Homo sapiens.
 OS
 PN US2003215838-A1.
 XX
 PD 20-NOV-2003.
 XX
 PF 21-JAN-2003; 2003US-00351157.
 XX
 PR 18-JAN-2002; 2002US-0350325P.
 PR 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX
 PA (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUIJ/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNEL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX
 PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
 XX
 DR MPI: 2003-876545/81.
 DR P-PSDB; ADL26674.
 XX
 PT Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.
 XX
 PS Disclosure; SEQ ID NO 110; 205PP; English.
 XX
 CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing hematopoietic cells and hematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor171g-induced proliferation or differentiation
 CC of hematopoietic cells and hematopoietic progenitor cells; reducing
 CC zcytor171g-induced inflammation; treating a mammal afflicted with an
 CC inflammatory disease in which zcytor171g plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC psoriasis. The disease is acute inflammatory disease such as
 CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.

CC An immune response inhibiting composition is useful for inhibiting an
CC immune response in a mammal exposed to an antigen or pathogen. An
CC inflammatory response inhibiting composition is useful for suppressing an
CC inflammatory response in a mammal with inflammation. An antibody that
CC specifically binds to (1) is useful for detecting the presence of a
CC multimeric or heterodimeric cytokine receptor in a biological sample.
CC This sequence encodes a human zcytor17 cytokine receptor that can be used
CC in a comparison with other zcytor17 receptors.

XX Sequence 2402 BP; 713 A; 532 C; 580 G; 577 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,696-314	Length:	2402
Score:	3435.00	Matches:	647
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.69%	Mismatches:	1
Query Match:	98.59%	Indels:	1
DB:	11	Gaps:	0

US-10-006-265-2 (1-652) x ADL26673 (1-2402)

Qy	3	LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet	22
Db	138	CTCTCTCCCGAGCCCTTCACTGTTTAACTGGGAGATGATGGACCTGGGCACTGTGGATG	197
Qy	23	LeuProSerLeuCysValPheSerLeuAlaLeuProAlaLeuProGlnAsnLeuSer	42
Db	198	CTCCCTCACTCTGCAAAATTCAGCTGGAGCTCTGCCAGCTGAGAACCTTTTCC	257
Qy	43	CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlnThrSer	62
Db	258	TGTGTCTACTACTATAGAAAAATTTAAGCTGCACTTGGAGTCCAGAAAGAAACCGT	317
Qy	63	TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsnCysThr	82
Db	318	TATACCCGATCACAGTTAAGAACTTAACGCTTTGGAGAAAAACATGATATTGTACA	377
Qy	83	ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgLleThr	102
Db	378	ACCAATACTTTCACAGTAAATGCTGCTGCTGCTTTTCTTCCCAAGATTAACG	437
Qy	103	IleProAspAsnTyrThrIleGluValGlnAlaGluAsnGlyAspGlyValIleLysSer	122
Db	438	ATCCAGATATTTATACCATTTGAGGTGAGCTGAAATGAGATGCTGTAATTAATCT	497
Qy	123	HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg	142
Db	498	CATATGACATACGTGAGATTAGAGAACATACGAAACCTGAACCACTAATATTTCCGT	557
Qy	143	ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGlnLeu	162
Db	558	GTAAGAACAGTTTGGGATCAACGAAATGATTCAAATTTGAATGATTAACCTGAGATTG	617
Qy	163	AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer	182
Db	618	GCGGCTGTTTCACTGATTTAAATACACACTTCGATTCAAGACAGTCAACAGTACAGC	677
Qy	183	TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr	202
Db	678	TGGATGAGAACTCACTTCGTAAGAACCGTAAGATTAACCAACGTAACAACCTCAGC	737
Qy	203	GlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLysGlnSerLys	222
Db	738	GAGGCTGAGCCTTTTACAGATATGTCATACCTCTGCATGTGGCTCAAGAGTCAAG	797
Qy	223	PheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGlnGlnGlnAlaProCysGly	242
Db	798	TTCTGGAGTGACTGAGGCAAGAAAAATGGGAATGACTGAGAAAGCTCCATGTGGC	857
Qy	243	LeuGlnLeuTrpArgValLeuLysProAlaGlnAlaAspGlyArgArgProValArgLeu	262
Db	858	CTGGAACGTGGAGAGTCTGAAACCAAGCTGAGCGGATGAGAAAGGCGAGTGGTGG	917

Qy	263	LeuTrpLysLysAlaArgGlyAlaProValLeuGlnLysThrLeuGlyTyrAsnIleTrp	282
Db	918	TTATGAAAGAAAGGCAAGAGAGCCCACTCTTACAGAAAAACATTTGGTACATATAGG	977
Qy	283	TyrTyrProGlnSerAsnThrAsnLeuThrGlnThrMetAsnThrTyrAsnGlnLeu	302
Db	978	TACTATCCAGAAAGCAACACTAATCTCAAGAAACATGAACTACTAACCAGACGCTT	1037
Qy	303	GluLeuHisLeuGlyGlyGlnSerPheTrpValSerMetIleSerTyrAsnSerLeuGly	322
Db	1038	GAACGTACCTGGAGAGGAGGAGCTTTGGTGTCTATGATTTCTTAAATTTCTTGGG	1097
Qy	323	LysSerProValAlaThrLeuArgIleProAlaIleGlnGlnLysSerPheGlnCysIle	342
Db	1098	AAGTCTCCAGTGGCCACCTTAGAATTCACCTTTCAGAAAAATCATTTCACTGCAAT	1157
Qy	343	GluValMetGlnAlaCysValAlaGlnAspGlnLeuValLysTrpGlnSerSerAla	362
Db	1158	GAGGTCAATGACAGGCTGGTGTCTGAGGACCAAGCTAATGATGGCAAAAGCTCTGCT	1217
Qy	363	LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr	382
Db	1218	CTAGACGTGAACACTTGGATGATTAATGATTTCCGAGATGGACTCAGAGCCCAACCC	1277
Qy	383	LeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys	402
Db	1278	CTTTCTGGAAATCTGTGTCTCAGGCCACGAATCTGACATCCAGAACATTAATTA	1337
Qy	403	ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyLysPro	422
Db	1338	CTTTCTGGTGTCTAATCATCTGTGTATCAATGTTGATGCAAAAGTTGGAGGACCA	1397
Qy	423	TyrSerIleGlnAlaTyrAlaLysGlnGlyValProSerGlnGlyProGlnThrLysVal	442
Db	1398	TATTCATCCAGGCTTATGCAAAAGAGGCGTTCCATCAGAGGCTCTGAGAACCAAGGTG	1457
Qy	443	GluAsnIleGlyValLysThrValThrIleThrTrpLysGlnIleProLysSerGluArg	462
Db	1458	GAGAACATTTGGCTGAAAGAGCGTACATGATCAATGAAAGATTTCCAGAGATGAGGA	1517
Qy	463	LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGlnGlyLysGlyPheSer	482
Db	1518	AAGGTATCATCTGCAACCTACACATCTTTTACCAACTGAGTGAAGAAAGATTTCTCC	1577
Qy	483	LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer	502
Db	1578	AAGACATCAATTCACACATCTTGCAGTACGAGCTGAGAGTCCCTGAAACCAAAAGACCTCT	1637
Qy	503	TyrIleValGlnValMetAlaAsnThrSerAlaGlyLysThrAsnGlyThrSerIleAsn	522
Db	1638	TACATTTTCAGTCAATGAGCCAGCAACAGTCTGGGGAAACCAACGGGACCATTAAT	1697
Qy	523	PheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerLeuIleGlyLys	542
Db	1698	TTCAAGACATTTGATTCATGATGCTTTGAGATTAATCTCTTAATCTTCTGATTTGGGA	1757
Qy	543	GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu	562
Db	1758	GACCTTCTTATTTCAATTAATCTGACAGTGCATATGCTCAAAAAAACCAAAATTTG	1817
Qy	563	ThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrpHis	582
Db	1818	ACTATCTGTGTGGCCACCTGTTCCAAACCTGCTGAAGATGATTAAGACACATGGCAT	1877
Qy	583	GlyAspAspPheLysAspLysLeuAsnLeuLysGlnLysSerAspAspSerValAsnThrGlu	602
Db	1878	GGAGATGATTTCAAGATTAAGATTAAGCTTAAGAGATCTGATGTAACACAGAA	1937
Qy	603	AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal	622
Db	1938	GACAGATCTTAAACCATATGTTCCACCCCAAGTGAACAAAGTTGATGTAACAGTTGGTG	1997
Qy	623	ValAsnPheGlyAsnValLeuGlnGlnIlePheThrAspGlnLysArgThrGlnGln	642


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Db      372 TGACAAACCAATAGTCTTACAAAGTGAATAATCGTCTCGTCTCTTTTCTCTTCCACAGA 431
Qy      101 ILeThrIleProAspAsnTyrThrIleGluValIleGluValAsnGlyAspGlyValIle 120
Db      432 ATAAAGATCCCAAGATTAATTAATCAATGAGGTGAGAGCTGAATAAGAGATGGTGTAAATT 491
Qy      121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaIleThrGluProProlysisIle 140
Db      492 AAATCTCATATGACATACTGGAGATTAGAGAACATAGCGAAACCTGAACCACTTAAGATT 551
Qy      141 PheArgValIleProValIleuGlyIleIleYsArgMetIleGlnIleGluTrpIleYsPro 160
Db      552 TTCCGTGTGAACACCGTTTGGGCATCAACCGAATGATTCAAATGATGATTAAGCCT 611
Qy      161 GluLeuAlaProValSerSerAspLeuIleYsThrIleuArgPheArgThrValAsnSer 180
Db      612 GAGTGGGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTGAGACAGTCAACGT 671
Qy      181 ThrSerTrpMetGluValAsnPheAlaIleYsAsnArgIleAspIleYsAsnGlnThrTyrAsn 200
Db      672 ACCAGCTGATGAGAGTCAATCTCCCTAAGAACCTTAAGATTAACCAACGTAAC 731
Qy      201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIleGlu 220
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Qy      261 ArgLeuLeuTrpIleYsAlaArgGlyValaProValIleuGlyIleYsThrLeuGlyTyrAsn 280
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Qy      281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
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Qy      301 GlnLeuGluLeuHisIleuGlyGlyIleuSerPheTrpValSerMetIleSerTyrAsnSer 320
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Qy      321 LeuGlyIleYsSerProValAlaThrIleuArgIleProAlaIleGlnGluIleYsSerPheGln 340
Db      1092 CTTGGGAAGTCTCCAGTGGCCACCTGAGATTCAGCTATTCAGAAAAATCATTTGAG 1151
Qy      341 CysIleGluValIleMetGlnAlaCysValAlaGluAspGlnLeuValValIleTrpGlnSer 360
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Qy      381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspIleYs 400
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Qy      401 LeuIleYsProPheTrpCysTyrAsnIleSerValIleYsProMetLeuHisAspIleYsAla 420
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Qy      421 GluProTyrSerIleGlnAlaTyrAlaIleYsGluGlyValaProSerGluGlyProGluThr 440
Db      1392 GAGCCATTTTCATTCAGGCTTATGCCAAAGAGGCGTTTCATTCAGAGGCTCGAGACC 1451
Qy      441 LysValIleGluAsnIleGlyValIleYsThrValThrIleThrTrpIleGluIleProIleYsSer 460
Db      1452 AAGGTGGAACATTGGCGTGAAGCGGTCAAGATCAATGGAAGAGATTCCTCCAGAGGT 1511

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Qy      601 ThrGluAspArgIleLeuIleYsProCysSerThrProSerAspIleYsLeuValIleAspIleYs 620
Db      1932 ACAGAAAGCAGGATCTTAAACATGTTCCACCCCAAGTGAAGATGATGACAG 1991
Qy      621 LeuValValaAsnPheGlyAsnValIleuGlnIlePheThrAspGluAlaArgThrGly 640
Db      1992 TTGGTGTGAACTTTGGGAATGTTCTGCAAGAAATTTTCACAGATGAAGCCAGAACGGGT 2051
Qy      641 GlnGluIleYsGlnPheArgArgGlyIleYsGluTrp 651
Db      2052 CAGGA-AAACATTTAGAGGGGGAAGAAATGG 2083

RESULT 12
ID ACF36434 standard; cDNA; 2481 BP.
XX ACF36434;
XX AC
XX 18-DEC-2003 (first entry)
XX DE Human type-1 cytokine receptor, GLM-R encoding cDNA.
XX KW GLM-R; type-1 cytokine receptor; gene therapy; gene mapping; human;
XX transgenic; gene; 88.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 63..2261
XX FT /*tag= a
XX FT /product= "GLM-R"
XX FT /note= "type-1 cytokine receptor"
XX FT sig_peptide 63..119
XX FT /*tag= b
XX FT mat_peptide 120..2258
XX FT /*tag= c
XX PN MO2003072740-A2.
XX PD 04-SEP-2003.
XX PF 24-FEB-2003; 2003WO-US005616.
XX PR 25-FEB-2002; 2002US-0359806P.

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XX (GETH) GENENTECH INC.
 PA De Sauvage FJ, Ghilardi NP, Goddard A, Godowski PJ, Grimaldi CJ;
 PI Gurney AL, Wood WI;
 XX MPI; 2003-712721/67.
 DR P-PSDB; ABR82790.
 XX
 XX New isolated nucleic acid molecule encoding a GLM-R polypeptide, useful
 PT for treating disorders characterized by the over or under abundance of
 PT monocytes or macrophages.
 XX
 XX Claim 3; Fig 1; 156pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC type-1 cytokine receptor GLM-R polypeptide. The nucleic acid molecules,
 CC polypeptides, antibodies, agonists or antagonists, and compositions are
 CC useful for treating disorders characterized by the over or under
 CC abundance of monocytes or macrophages. The nucleic acid molecules are
 CC useful as hybridization probes, in chromosome and in gene mapping, and in
 CC generating antisense RNA or DNA. The present sequence represents a cDNA
 CC encoding a human GLM-R polypeptide
 XX
 SQ Sequence 2481 BP; 729 A; 553 C; 603 G; 596 T; 0 U; 0 Other;

Alignment Scores:

Prod. No.:	1 77e-314	Length:	2481
Score:	3435.00	Matches:	647
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.69%	Mismatches:	1
Query Match:	98.59%	Indels:	1
DB:	10	Gaps:	0

US-10-006-265-2 (1-652) x ACF36434 (1-2481)

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 DB 90 CTCCCTTCACTGCAAAATTCAGCTGCGAGCTCTGCAAGCTGAAGCAATTTCC 149
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 DB 150 TGTGTCTACTACTATGAGAAAATTTAACTGCACTTGAGTCAAGAAAGAAACAGT 209
 QY 63 TyrThrGlnTyrThrValaLeuArgThrTyrAlaPheGlyGlyLeuYshsAspAsnGlySer 82
 DB 210 TATATCCAGTACACAGTTAAAGAACTTACGCTTTTGGAGAAAACATGATTAATTGACA 269
 QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPheLeuProAlaGlyLeuTrp 102
 DB 270 ACCAATAGTTCACAGTGAAGTAAATCGTCTGCTCTTTTCCCAAGAAATACG 329
 QY 103 IleProAspAsnTyrThrIleGlyValaGluAlaGluAsnGlyAspGlyValaIleLeuSer 122
 DB 330 ATCCCAATATTAATTAACATTTGAGGTGAGAGCTGAAAATGAGATGTTAATTAATCT 389
 QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLeuThrGluProGlyIlePheArg 142
 DB 390 CATATGACATACATGAGATTAGAGAACATGCGAAAACCTAAGATTTTCCGT 449
 QY 143 ValLeuProValaLeuGlyIleLeuArgMetIleGlnIleGluTrpIleLeuProGlyLeu 162
 DB 450 GTGAAACCAATTTGGGCATCAACGATGATTCATTAATGATTAAGCTGAGTTG 509
 QY 163 AlaProValSerSerAspLeuLeuTyrThrLeuArgPheArgThrValaAsnSerThrSer 182
 DB 510 GCGCCTGTTTCACTGATTTAAATTAACACCTTGATTCAGACAGCAAGCAAGTACAGC 569
 QY 183 TrpMetGluValaAsnPheAlaLeuArgGlyAspLeuAsnGlnThrTyrAsnLeuThr 202

DB 570 TGGATGGAAGTCACACTCCCTTAAGAACCTTAAGATTAATAAACCAACGTAACACCTCACG 629
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 DB 630 GGGCTGAGACCTTTTACAAATATGATGATGCTCTGCGATGTGGCTCAAGAGTCAAG 689
 QY 223 PheTrpSerAspTrpSerGlnGlyMetThrGluGluGluAlaProCysGly 242
 DB 690 TTCTGAGAGATGAGGAGCCAAAGAAAATGGAAATGACATGAGGAAGAACTCATGTGCG 749
 QY 243 LeuGluLeuTrpArgValaLeuLeuProAlaGluAlaAspGlyArgArgProValaArgLeu 262
 DB 750 CTGGAACCTGTGAGAGTCTGAAACCAAGCTGAGCGGAGGAAGAAAGGCAAGTCCGTG 809
 QY 263 LeuTrpLeuValaAlaArgGlyAlaProValaLeuGluLeuThrLeuGlyTyrAsnIleTrp 282
 DB 810 TTAATGAGAAAGCAAGAGAGAGCCCAAGTCTAGAGAAAACCTTGGCTACACATATCG 869
 QY 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
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 QY 323 LysSerProValaIleThrLeuArgIleProAlaIleGlnGlySerPheGlnCysIle 342
 DB 990 AAGTCTCCAGTGGCCACCTGAGAGATCCAGCTATTAAGAAAATCATTTCAAGTGCATT 1049
 QY 343 GluValaMetGlnAlaCysValaAlaGluAspGlnLeuValaValaLeuTrpGlnSerSerAla 362
 DB 1050 GAGGTGATGCAAGCGCTGCGTCTGAGGACCAAGCTAAGTGTGAAGTGGCAAGCTCTGCT 1109
 QY 363 LeuAspValaAsnThrTrpMetIleGluTrpPheProAspValaAspSerGluProThrThr 382
 DB 1110 CTAGACGTGAAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1169
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 DB 1170 CTTCCTGGAGAACTGTGTCTCAAGGCGACCACTGACATCAAGCAATTAATTAATA 1229
 QY 403 ProPheTrpCysTyrAsnIleSerValaTyrProMetLeuHisAspLeuValaGlyLeuPro 422
 DB 1230 CTTTCTGGTGTGATTAACATCTCTGTATCAAGTTCATGACAAAGTGGCGAGCA 1289
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 DB 1350 GAGAACATTTGGGTGAAGCGGTCAAGATCACTGGAAGAAAGATTCCTCAAGAGTGAAGA 1409
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QY 303 GJLueHISleuGIyGIyGluSerPheTrpValSerMetIleSerTYrAsnSerleuGIy 322
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DB 1330 TATTCATCAGGCTTATGCGCAAGAGCGTCCATCAGAAAGCTCTTGAGCAAGAGT 1389
QY 443 GIuAsnIleGIyValLysThrValThrIleThrTrpLysGIuIleProLysSerGIuArg 462
DB 1390 GAGAAATGTCGCGTGAAGAGCGTCAAGATCAATGAAAGATGATCCCAAGATGAGAGA 1449
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QY 623 ValAsnPheGIyAsnValLeuGlnGluIlePheThrAspGlnAlaArgThrGIyGlnGIu 642
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QY 643 LysGlnPheArgArgGIyLysGIuTrp 651
DB 1989 AAAACAATTAAGAGGGGAGAAAGATGG 2015

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RESULT 14

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AB083364
ID AB083364 standard; cDNA; 5271 BP.
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AC AB083364;
XX
XX 20-JAN-2003 (first entry)
XX
DE Human NR10.4 splicing variant encoding cDNA SEQ ID NO:3.
XX
XX NR10, splicing variant; haematopoietin receptor; immunomodulator;
XX haemostatic; haematopoietic factor; immunological disease;
XX haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2301
FT FT /tag=a
FT FT /product="NR10.4"
XX
XX
XX MO200277230-A1.
XX
XX PD 03-OCT-2002.
XX
XX PF 22-MAR-2002; 2002WO-0P002769.
XX
XX PR 26-MAR-2001; 2001JP-00087298.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Maeda M, Yaguchi N, Hasegawa M;
XX PI
XX
XX WPI; 2003-018925/01.
XX DR P-PSDB; ABP54364.
XX
XX PT NR10 splicing variants of haematopoietin receptor proteins and encoded
XX genes, applicable in searching haematopoietic factors and developing
XX remedies for immunological and haematopoietic diseases.
XX
XX PS Claim 1; Fig 4-5; 250pp; Japanese.
XX
XX CC The present invention describes haematopoietic receptor NR10 splicing
XX variants (1). (1) have immunomodulator and haemostatic activities. The
XX proteins and encoded genes are applicable in searching for novel
XX haematopoietic factors, and developing remedies for immunological and
XX haematopoietic diseases. The haematopoietin receptor genes participate in
XX in vivo immunomodulation and haematopoietic cell regulation, and in the
XX search for haematopoietic factors capable of functionally binding to the
XX receptors. The present sequence encodes the human NR10.4 protein from the
XX present invention
XX
XX SO Sequence 5271 BP; 1312 A; 1302 C; 1318 G; 1339 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,28e-314 Length: 5271
Score: 3435.00 Matches: 647
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 98.59% Indels: 1
DB: 8 Gaps: 0

US-10-006-265-2 (1-652) x AB083364 (1-5271)
QY 3 LeuSerProGlnProSerCyValAsnLeuGIyMetMetTrpThrTrpAlaLeuTrpMet 22
DB 70 CTTCTCTCCACGCTTCAATGTTAACTGGGAGATGATGAGACCTGGGCACTGTGATG 129
QY 23 LeuProSerLeuCyLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
DB 130 CTCCTCTCACTCTGCAAAATTCAGCTGCGAGCTCTGCCAGCTGAGCAATTTCC 189
QY 43 CyValTYrTYrTYrArgLysAsnLeuThrCySerThrTrpSerProGIyLysGIuTrpSer 62

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XX 22-MAR-2002; 2002WO-JP002769.
 PF
 XX 26-MAR-2001; 2001JP-00087298.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Maeda M, Yaguchi N, Hasegawa M;
 PI WPI; 2003-018925/01.
 XX P-PSDB; ABP54366.
 DR
 XX NR10 splicing variants of hematopoietin receptor proteins and encoded
 PT gene, applicable in searching hematopoietic factors and developing
 PT remedies for immunological and hematopoietic diseases.
 XX
 PS Claim 1; Fig 10-12; 250pp; Japanese.
 CC The present invention describes haematopoietic receptor NR10 splicing
 CC variants (I). (I) have immunomodulator and haemostatic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietin receptor genes participate in
 CC in vivo immunomodulation and haematopoietic cell regulation, and in the
 CC search for haematopoietic factors capable of functionally binding to the
 CC receptors. The present sequence encodes the human NR10.5 protein from the
 CC present invention
 XX
 SQ Sequence 3072 BP; 849 A; 721 C; 755 G; 747 T; 0 U; 0 Other:
 Alignment Scores:
 Pred. No.: 1,67e-311 Length: 3072
 Score: 3405.00 Matches: 647
 Percent Similarity: 94.05% Conservative: 1
 Best Local Similarity: 93.90% Mismatches: 1
 Query Match: 97.73% Indels: 41
 DB: Gaps: 1
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 QY 183 TTPMETGLUVALASNPHEALALYSASNAARGLYSASPGLYASNGLTHRTYRSLNLEUTR 202
 DB 610 TGGATGGAAGTCAACTTCGCTTAAGAACCGTAAAGGATGAAACCAACGTRACACTCAGC 669
 QY 203 GLYLEUGLNPProPheThrGluTYRValIleAlaLeuArgCysAlaValIlySGluseTlys 222
 DB 670 GGGCTGACGCTTTTRACAAATRTGTCATAGCTCTGCCATGTGCGGTCAAGAGTCAAAAG 729
 QY 223 PHEPTRSEASPTRPserGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242
 DB 730 TTCTGAGAGTACTGGAGCCCAAGAAAAATGGGAATGACTGAGGAAGAACTCATGTGCGC 789
 QY 243 LEUGLLEUTRArgValLeuLysProAlaGluValAspGlyArgArgProValArgLeu 262
 DB 790 CTGGAACTGTGAGAGTCTTGAAACCAAGCTGAGCGGATGGAAAGAGGCCAGTGCCTTG 849
 QY 263 LEUTRPLYSLeuAlaArgGlyAlaProValLeuGluLysThrLeuGlyTYRAsnIleTP 282
 DB 850 TTAATGAAAGAGGCAAGAGAGCCCAAGTCTTGAAGAAAACCTTGCTRACAACTATGG 909
 QY 283 TYTYRProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
 DB 910 TACTATCCAGAAAGCAACACTAACTCAGAGAAACATGAAACACTACTAACCGACGACTT 969
 QY 303 GLULeuHleLeuGlyGlyLysSerPheTPRValSerMetIleSerTYRAsnSerLeuGly 322
 DB 970 GAACGTGATCTGGAGAGCGAGAGCTTTGGTGTCTATATATTTCTATTAATTTCTTGGA 1029
 QY 323 LYSERProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342
 DB 1030 AAGTCTCCAGTGGCCACCCTGAGAGATTCAGACTATTCAAGAAAAATCATTTCAAGTCATT 1089
 QY 343 GLUValMetGlnAlaCysValAlaGluAspGlnLeuValValIlySTRPGLNserSerAla 362
 DB 1090 GAGGTATGACAGGCGCTGCTGCTGAGACACAGCTAGTGTAAGTGCAAGGCCAAAGCTGTGCT 1149
 QY 363 LEUAspValAsnThrTPRMetIleGluTPRPherProAspValAspSerGluProTPRThr 382
 DB 1150 CTAGAGCTGAACACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1209
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 DB 1210 CTTTCTGGGAATCTGTGCTCAGGCCACGAATGACATCCAGAAAGTAAATTAA 1269
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 DB 1270 CTTTCTGGTGTATTAACATCTGTGATCCAAATGTCATGCAAAAGTGGCGAGCCA 1329
 QY 423 TYRSErIleGlnAlaTYRAlaLysGluGlyValProSerGluGlyProGluTPRThrLysVal 442
 DB 1330 TATTCATCCAGGCTTATCCAAAGAGGCGTTCCTCAAGAGGTCCTAGACCAAGGGTG 1389
 QY 443 GLUAsnIleGlyValIlyThrValThrIleTPRPLYSGLIleProLysSerGluArg 462
 DB 1390 GAGAACATTTGGGTGAAGCGGTCAAGATCAATGAAAGAAATGCCCAAGAGTGAAGA 1449
 QY 463 LYSGLYIleIleCysAsnTYRThrIlePheTYRGINaIleGluGlyLysGlyPheSer 482
 DB 1450 AAGGATCATCTGCAATACCAACATCTTTTACCAAGCTGGAAGTGAAGAAAGATCTCC 1509
 QY 483 LYSThrValAsnSerSerIleLeuGlnTYRGLYLeuGluLysLeuLysArgLysTPRThrSer 502
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 QY 503 TYRILEValGlnValMetAlaAsnThrSerAlaGlyGlyTYRAsnGlyThrSerIleAsn 522
 DB 1570 TACATTTGTTCAAGTCAAGGTCACAGCAAGTCTGGGGGAACCAAGCGGACACAGCAAT 1629
 QY 523 PHELYThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:59:57 ; Search time 300.186 Seconds
(without alignments)
3553.966 Million cell updates/sec

Title: US-10-006-265-2
Perfect score: 3484
Sequence: 1 MKLSPQSPSCVILGMWMTWL.....FTDEARTGQEKQFRGKEMD 652

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BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Database : Issued Patents NA:
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5: /cg2_6/ptodata/1/ina/PTCUS.COMB.seq:*
6: /cg2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	682.5	19.6	2995	4	US-09-700-820C-17
2	679.5	19.5	3085	3	US-08-795-473B-4
3	679.5	19.5	3085	3	US-09-439-856-4
4	679.5	19.5	3085	4	US-09-023-655-1131
5	678.5	19.5	2369	1	US-07-797-556-1
6	678.5	19.5	2369	1	US-08-308-881-1
7	678.5	19.5	2369	2	US-09-058-263-1
8	678.5	19.5	2369	2	US-09-059-099-1
9	678.5	19.5	2369	3	US-09-058-264-1
10	678.5	19.5	2369	4	US-09-455-962-1
11	678.5	19.5	2369	5	PCT-US95-06530-1
12	677.5	19.4	2754	2	US-08-825-558-5

13	677.5	19.4	2754	3	US-09-312-611-5	Sequence 5, Appli
14	636.5	18.3	1977	2	US-08-825-558-3	Sequence 3, Appli
15	636.5	18.3	1977	3	US-09-312-611-3	Sequence 25, Appli
16	616	17.7	3477	4	US-09-313-942-25	Sequence 23, Appli
17	616	17.7	3507	4	US-09-313-942-23	Sequence 1066, Ap
18	505.5	14.5	2943	4	US-07-923-976-3	Sequence 7, Appli
19	505.5	14.5	2943	4	US-09-023-655-1086	Sequence 1066, Ap
20	503.5	14.5	3024	1	US-07-923-976-7	Sequence 7, Appli
21	487	14.0	2563	6	5422248-1	Sequence 5, Appli
22	487	14.0	2563	6	5422248-1	Sequence 5, Appli
23	464.5	13.3	3293	1	US-07-923-976-1	Sequence 1, Appli
24	461	13.2	2855	1	US-07-923-976-5	Sequence 5, Appli
25	401.5	11.5	3182	1	US-07-923-976-5	Sequence 5, Appli
26	401.5	11.5	3182	1	US-07-943-843-1	Sequence 1, Appli
27	401.5	11.5	3182	1	US-08-347-003-1	Sequence 1, Appli
28	401.5	11.5	3591	1	US-07-943-843-5	Sequence 1, Appli
29	401.5	11.5	3591	1	US-08-347-003-5	Sequence 5, Appli
30	401.5	11.5	5245	4	US-09-949-016-4210	Sequence 4210, Ap
31	401.5	11.5	5252	4	US-09-949-016-338	Sequence 338, App
32	377	10.8	4040	2	US-08-685-118-1	Sequence 1, Appli
33	377	10.8	4040	2	US-08-915-435-1	Sequence 1, Appli
34	377	10.8	4040	2	US-08-914-520-1	Sequence 1, Appli
35	377	10.8	4040	4	US-09-949-016-1887	Sequence 1887, Ap
36	362	10.4	4171	2	US-09-058-263-5	Sequence 5, Appli
37	362	10.4	4171	2	US-09-058-263-5	Sequence 5, Appli
38	362	10.4	4171	3	US-09-058-264-5	Sequence 5, Appli
39	362	10.4	4171	3	US-09-455-962-5	Sequence 5, Appli
40	362	10.4	4171	4	PCT-US95-06530-5	Sequence 3, Appli
41	362	10.4	4171	5	US-07-943-843-3	Sequence 3, Appli
42	281	8.1	2498	1	US-08-347-003-3	Sequence 3, Appli
43	281	8.1	2589	1	US-08-653-740-6	Sequence 6, Appli
44	244	7.0	2589	1	US-09-073-594-6	Sequence 6, Appli
45	244	7.0	2589	2		

ALIGNMENTS

RESULT 1
US-09-700-820C-17
; Sequence 17, Application US/09700820C
; Patent No. 6610485
; GENERAL INFORMATION:
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Saito, Makiyohi
; APPLICANT: Ohmoto, Yoshihiko
; TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
; FILE REFERENCE: 06501-070001
; CURRENT APPLICATION NUMBER: US/09/700, 820C
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/138652
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/279876
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 17
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) .. (2839)
US-09-700-820C-17

Alignment Scores:
Pred. No.: 2,846-65
Score: 682.50
Percent Similarity: 47.24%
Best Local Similarity: 28.35%
Query Match: 19.59%
DB: 4
Length: 2995
Matches: 180
Conservative: 120
Mismatch: 282
Indels: 54
Gaps: 17


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COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,473B
FILING DATE: 11-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-795-473B-4

Alignment Scores:
Pred. No.: 6,45e-65 Length: 3085
Score: 679.50 Matches: 175
Percent Similarity: 46.75% Conservative: 113
Best Local Similarity: 28.41% Mismatches: 261
Query Match: 19.50% Indels: 67
Gaps: 16

US-10-006-265-2 (1-652) x US-08-795-473B-4 (1-3085)
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Db 631 CCGAAGAAACCTTAAGAAATTTGAGTGCATGTGAAACGACGGAGAAAGAAATGAGTGTGAG 690
QY 55 TrpSerProGlyLyLeGluThrSerTyTyr---ThrgInTyThVallys-----Arg 70
Db 691 TGGGATGGTGGAGAGGAAACACACATTCGAGACAACTTCATTAATCTGAATGGGCA 750
QY 71 ThrTyAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 751 ACACACAAGTTTGGCATGTGCAAAACGTAACCCCACTCATGACACTGTGAT 810
QY 85 SerSerThrSerGluAsnArgLaseRcYsSerPhePheLeuProArgLethrIlePro 104
Db 811 TATTCTACT-----GTGTATTTTGTG----- 831
QY 105 AspAsnTyThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
Db 832 ---AACATTGAAGTCTGGGTAGACAGAGATGCCCTTGGGAAGTTACATCAGATCAT 888
QY 124 MetThrTyTyrTPArgLeuGluAsnIleAlaLysThrGluProGlySlePheArgVal 143
Db 889 ATCAATTTTGATCCGTATATATAAGTG---AAGCCCAATCCCGCACATATATTATCAGG 945
QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 946 ATCAACTCAGAGAACTGTCTAGTATCTTAATAATGACATGGAACCAACCAAGTATTAAAG 1005
QY 164 ProValSerSerAspLeuLysTyThrLeuArgPheArgThValAsnSerThrSerTrp 183
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QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThTyAsnLeuThrGly 203
Db 1063 AGCCGAGATTCTCT---CTGTGAAGACACAGCATCCACCCGATCTTCATTCCTGTCGAAGAC 1119
QY 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222

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Db 1120 CTTAAACCTTTACAGAAATATGTGTTTAGATTCGCTGTATGACGAAGATGTAAGGGA 1179
QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaProCys--- 241
Db 1180 TACTGAGCTGACTGTGAGTGAAGAAAGCAAGTGGGATCACCCTTGAAGATGACACTTAA 1239
QY 242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
Db 1240 GCACCAAGTTCTGTGTATATAATATGATCCATCTCAGGCTTACAGAACTTACAA 1299
QY 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyraAsnIle 281
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QY 282 TrpTyTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThraGlnGln 301
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Db 1414 CTGACAGTAAATCTCAAAATGATCGCTATCTGACGACCTTACAGTAAAGAAATCTTGT 1473
QY 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
Db 1474 GCGAATACGATGACGCTGTTTAACTATCCCTGCTGTGACTTCAAGACTACACCT 1533
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Db 1534 GTAAATGATCTTAAAGCATTCCTCCCAAAATATACATGATTAAGTGGTGAATGAGCTACTCA 1593
QY 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
Db 1594 AGCGAATCTGTAAAGAAATATATACTGATGATGTGTGTGTTATTCAGATTAAGACCTGCT 1653
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Db 1654 ATCAAGACGTGCAACAAAGAAAGATGATACCGTGATGCCACTTATTAAGAGGAACTTA 1713
QY 402 LysProPheTrpCysTyraAsnIleSerValTyTyrProMetLeuHisAspLysValGlyGlu 421
Db 1714 GCAGAGACAAATGTTATTTATTAACAGTTACTCCAGATATATGCGATGAGCAACGAAAGC 1773
QY 422 ProTySerIleGlnAlaTyraLysLeuGluGlyAlaProSerGluGlyProGluThrLys 441
Db 1774 CCGTATCCATPAAGGATACCTTAAACACCTCCACTTCAAGGACCTTACTGTTGG 1833
QY 442 ValGluAsnIleGlyValLysLeuThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db 1834 ACAAAAAGTAGGAGAAAAGAAAGCTGTCTTAGAGTGGACCAACTTCCTGTGATGTT 1893
QY 462 ArgLysGlyIleIleCysAsnTyThrIlePheTyrglnAlaGluGlyLysGlyPhe 481
Db 1894 CAGATGATTTATCAGAAATTAATATATTTATATAGAACCATCATGGAATGAATGAAT 1953
QY 482 SerLysThrValAsnSerSerIleGlnTyrglyLeuGluSerLeuLysLysArgLysThr 501
Db 1954 GCTGGAATGGGATTCCTCCACACAGAAATATCATTTGCTCTTACATGATGACACA 2013
QY 502 SerTyriLeValGlnValMetAlaAsnThrSerAlaGlyIleTyraAsnGlyThSerIle 521
Db 2014 TTGTCATGATGATCAATGACGACATACACATGAAAGTGGAGAGAGTGCACGAATTC 2073
QY 522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
Db 2074 ACTTTACTATCCCAAGATTTGCTCAAGAGAAATTAAGCAATAGTGTGCTGTGTC 2133
QY 542 GlyLysLeuLeuIleLeuIleIleLeuThrValAlaTyrglyLeuLysLysProAsnLys 561
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QY 562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581

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 / Sequence 4, Application US/09439856
 / Patent No. 641009
 / GENERAL INFORMATION:
 / APPLICANT: Galun, Elchan
 / APPLICANT: Nahot, Orit
 / APPLICANT: Blum, Herbert E.
 / TITLE OF INVENTION: A Pharmaceutical Composition for Treating
 / TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
 / NUMBER OF SEQUENCES: 10
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Davidson, Davidson and Kappel, LLC
 / STREET: 1140 Avenue of the Americas
 / CITY: New York
 / STATE: New York
 / COUNTRY: USA
 / ZIP: 10036
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: MS-DOS EDITOR
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/439,856
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/795,473
 / FILING DATE: 11-FEB-1997
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Davidson, Clifford M.
 / REGISTRATION NUMBER: 32,728
 / REFERENCE/DOCKET NUMBER: 963.1007
 / TELEPHONE: (212)-997-1037
 / TELEFAX: (212)-997-1028
 / INFORMATION FOR SEQ ID NO: 4:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 3085 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: unknown
 / US-09-439-856-4
 Alignment Scores:
 Pred. No.: 6,45e-65 Length: 3085
 Score: 679.50 Matches: 175
 Percent Similarity: 46.75% Conservative: 113
 Best Local Similarity: 28.41% Mismatches: 261
 Query Match: 19.50% Indels: 67
 DB: 3 Gaps: 16
 US-10-006-265-2 (1-652) x US-09-439-856-4 (1-3085)
 Qy 35 ProAlaLysProGluLeuIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
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Qy 55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
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 Qy 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
 Db 751 ACACACAACTTGTGCATTTGCAAGCAAAACCTGACACCCCACTCACTGATTTGAT 810
 Qy 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
 Db 811 TATTCTACT-----GTGATTGTTC----- 831
 Qy 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
 Db 832 ---AACATGAAGTCTGGGTGAAGAGAAATGCCCTTGGAAGGTTCATCATCAT 888
 Qy 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheAspVal 143
 Db 889 ATCAATTTTGATCTGTATATTAAGTG--AAGCCCAATCCGCACATATTTATTCAGTG 945
 Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
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 Qy 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
 Db 1006 AGTGTATATAA---CTAAATATATAACATTCAATATAGACCAAGATGCTCAACTGG 1062
 Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
 Db 1063 AGCCAGATTCCT---CCTGAACACACAGCATCCACCCGATCTTCATCTGCTCCAAAGAC 1119
 Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
 Db 1120 CTTAAACCTTTTACAGATATATGTGTTAGATTCCTGATGATGAAGAAATGATGAAGCA 1179
 Qy 223 PheTrpSerAspTrpSerGlnLysMetGlyMetThrGluGluGluAlaProCys--- 241
 Db 1180 TACTGAGTACTGGAGTGTAAGCAAGCAAGTGGATCACCTATGAAGATGACATTA 1239
 Qy 242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
 Db 1240 GCACCAAGTTCTGTATTAATAATAGATCCATCCATCAAGGCTACAGAACTGACAA 1299
 Qy 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
 Db 1300 CTGCTGTGAAGACATGCTCCCTTTTGAAGCAATGCAAAATCTTGATTTGAAGTG 1359
 Qy 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 301
 Db 1360 ACTCTCAAAAGATGGAATACACATTACAAATTAACAGTTAATGCCACA-----AAA 1413
 Qy 302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
 Db 1414 CTGACAGTAAATCTCAAAATATCGCTATCTACGCAACCTTAACAGTAAGAAATCTTGT 1473
 Qy 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
 Db 1474 GGCAAATCAGATGACGCTCTTTTAATCTATCCCTGCTGATCTTCAACCTACACCT 1533
 Qy 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSerSer 361
 Db 1534 GTAATGATCTTAAGACATCTCCCAAAAGATAACAGCTTTGGTGAATGAGACTATCA 1593
 Qy 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
 Db 1594 AGGGAATCTGTAAAGAAATATATACTTGAAGTGTGTGTATTCAGATGAACACCTGT 1653
 Qy 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
 Db 1654 ATCACAGACTGGCAAGAAAGATGTCACCGCATCGCACTTATTAAGAGGAACTTA 1713
 Qy 402 LysProPheTrpCysTyrAsnIleSerValTyrPrometLeuHisAspLysValGlyGlu 421

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Db      1714 GCAGAGCAAAATGCTATTGTGTAACAGTTACTCCAGTATAGCTGATGAGACCAAGAAC 177
Oy      442  ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrIys 441
Db      1774 CCTGAATCCATTAAGGCAATACCTTAACAAGCTCCACCTTCCAAAGAACTACTGTGGG 183
Oy      442  ValGluAenIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db      1834 ACAAATAAGTAGGGAAGAAAACGACAGCTGCTTAGAGTGGGACCACTTCCTGTGATGTT 1893
Oy      462  ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPhe 481
Db      1894 CAGAATGGATTATACGAATAATATCTATATTATATAGAACCATCATTTGGAAATGAAACT 1955
Oy      482  SerLysThrValAsnSerSerIleLeuGlnIrrGlyIleGluGluSerLeuLysArgLysThr 501
Db      1954 GCTGGAAATGGAGATTCTTCCACACAGAAATATACATTGTCTCTTTGACTAGTACACA 2011
Oy      502  SerTyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
Db      2014 TTGTTCATAGTAGAATGCAATGACAGCATACAGATGAAAGGGGAGAGATGTCACAAATTC 2073
Oy      522  AsnPheLysThrLysSerPheSerValIleGluIleIleLeuIleThrSerLeuIleGly 541
Db      2074 ACTTTTACTACCCCAAGGTGGCTCAAGAGAAATTTGAAGCCATATGTCGTGCTTTGGC 2133
Oy      542  GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysPheAsnLys 561
Db      2134 TTAGCATTCCTATTTAGCAACACTCTTGGGAGTGCGTTCGCTTAAATAGGAAACCTA 2199
Oy      562  LeuThrHisLeuCysTyrProThrValProAsnProAlaGluSerSerIleAlaThrTyr 581
Db      2194 ATTAAAAAACATCTGGCCTTATGTTCCAGATCTCTCAAGAGCATATTTGCCAGTGG 2253
Oy      582  -----HisGlyAspAsnPheLysAspLysLeu----- 590
Db      2254 TCACCTCACACTCCTCAAGGACAAATTTTATTCAAAAGATCAATGATTCAGATGCG 2313
Oy      590  ----- 590
Db      2314 AATTTCATGATGTAAGTGTGTGGAAATAGAACGAATAGCAAAAAGCCTTTTCAGAA 2373
Oy      591  AsnLeuLysGluSerAsp-----AspSerValAsnThrGlu 602
Db      2374 GATCTGAATCATTTGGACCTGTTCAAAAAAGGAAAAAATTAATATCTGAA 2421

RESULT 4
US-09-023-655-1131
; Sequence 1131, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM-TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023.655
; FILING DATE: HERewith
;

```

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ. ID NO: 1131:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3085 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g18653
 JS-09-023-655-1131

US-09-023-655-1131

Alignment Scores:	
Pred. No.:	6,456-65
Score:	679.50
Percent Similarity:	46.75%
Best Local Similarity:	28.41%
Query Match:	19.50%
DB:	4
	19
	67
	16

US-10-006-265-2 (1-652) x US-09-023-655-1131 (1-3085)

[illegible]

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QY 223 PheTrpSerAspTrpSerGlnGlnIuysMeGlyMetThrGlnGlnIuuaIProCys--- 241
Db 1180 TACTGGAGTGCATCGATGAGAAAGCAAGTGGATCATCCATTAAGATAGACCATTA 1239
QY 242 GlyLeuGlnLeuTrpArgValLeuLysProAlaGlnAlaAspGlyArgArgProValArg 261
Db 1240 GCACCAAGTTCTTCGATATAAAATAGATCCATCCATACCTCAAGCTTACAGACCTGACAA 1299
QY 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGlnLysThrLeuGlyLysAsnIle 281
Db 1300 CTGCTGTGGAAGACATTTGCTCTTGAAGCAACCAAGAAATCTTGGATTATGAAAGTG 1359
QY 282 TrpTrpTrpProGlnSerAsnThrAsnLeuThrGlnThrMetAsnThrThrAsnGlnGln 301
Db 1360 ACTCTCAACAAGATGAAATACATCAATTAACAATAATACAGTAAATGCGACCA-----AAA 1413
QY 302 LeuGlnLeuHisLeuGlnGlyGlnSerPheTrpValSerMetLysSerLysAsnSerLeu 321
Db 1414 CTGACAGTAAATCTCAAAATGATCCCTATCTAGCAACCTTAACAGTAAAGAAATCTTGT 1473
QY 322 GlyLysSerProValAlaThrLeuArgGlyProAlaIleGlnGlnLysSerPheGlnCys 341
Db 1474 GGCATAATCAGATCAGCTGTTTAACTATCCCTGCTGCTGCTTCAAGCTTCACTCACTCCT 1533
QY 342 IleGlnValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
Db 1534 GTAAATGATCTTAAGATCTCCCAAAAGATACATGCTTTGGGTGAATGATGATCTCCCA 1593
QY 362 AlaLeuAspValAsnThrTrpMetIleGlnTrpPheProAspValAspSerGluProThr 381
Db 1594 AGGGAATCTGTAAAGAAATATATATCTGATGCTGTGTATATCAGTAAAGCACTCTGT 1653
QY 382 ThrLeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
Db 1654 ATACAGACTGGCAACAAGATGCGTACCGTGCATCCACTTATTAAAGGAACTTA 1713
QY 402 LysProPheTrpCysTrpAsnIleSerValLysProMetLeuHisAspLysValGlyGln 421
Db 1714 GCAGAGCAAAATGCTATTATGATACAGTATACCTCAAGTATATGCTATGACCAAGGAGC 1773
QY 422 ProTrpSerIleGlnAlaLysAlaLysGlnGlyValProSerGlnGlyProGlnThrLys 441
Db 1774 CCTGAATCCATAAGGATACCTTAAACAAGCTCCCACTTCAAGAGCACTTCTGTCCG 1833
QY 442 ValGlnAsnIleGlyValLysThrValThrIleThrTrpGlnLysIleProLysSerGlu 461
Db 1834 ACAAAAAGATGAGAAAAACAAGCTGCTTGAAGTGGACCACTTCTGTGATGTT 1893
QY 462 ArgLysGlyLysIleCysAsnTrpThrIlePheTrpGlnAlaGlnGlyLysGlyPhe 481
Db 1894 CAGAAATGATTTATCAGAATTTATCTATTTTATGAAACCATTCATTTGAAATGAACCT 1953
QY 482 SerLysThrValAsnSerSerIleLeuGlnTrpGlyLeuGlnSerLeuLysArgLysThr 501
Db 1954 GCTGTGATGTGGATCTTCCACACAGATATACATTCCTTGTAGCTAGTGCACA 2013
QY 502 SerTrpIleValGlnIleMetAlaAsnThrSerAlaGlyGlyThrAsnGlnThrSerIle 521
Db 2014 TTGTACTGTGTAGATGATGCAATGACATACAGATGAAAGTGGAGGTGCCAATTC 2073
QY 522 AsnPheLysThrLeuSerPheSerValPheGlnLysIleLeuLeuThrSerLeuIleGly 541
Db 2074 ACTTTTACTACCCCAAAAGTTTGTGCAAGAGAAATGAACCATATGTCGCTGTTTGC 2133
QY 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaLysGlyLeuLysProAsnLys 561
Db 2134 TTAGCATTTCTATGCAACTCTTCTGGAGTGTGTTCTGTTTATATAGCGAGACTTA 2193
QY 562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrp 581
Db 2194 ATTAAAAACAACATCTGGCTTAATGTTCCAGATCTTCAAAAGATCATATATGCCAGTGG 2253
QY 582 -----HisGlyAspAspPheLysAspLysLeu----- 590

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Db 2254 TCACCTCACACTCTCCAAAGCACACATTTTAAATCAAAAAGATCAAAATGATTCAGATGCG 2313
QY 590 ----- 590
Db 2314 AATTTCAGTATGATGATGCTTGTGAAATAGAACCAATGACAAAAGCCTTTCCAGAA 2373
QY 591 AsnLeuLysGlnSerAsp-----AspSerValAsnThrGln 602
Db 2374 GATCTGAATCATTTGACCTGTTCAAAAAGAAAATTAATCATCTGAA 2421

RESULT 5
US-07-797-556-1
; Sequence 1, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Geating, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; TITLE OF INVENTION: Inhibitory Factor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,556
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2369 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; TISSUE TYPE: human placenta
; IMMEDIATE SOURCE:
; CLONE: B10G/pDC303
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 244..2369
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 310..2369
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 244..309
; US-07-797-556-1

Alignment Scores:
Pred. No.: 5,36e-65 Length: 2369
Score: 678.50 Matches: 169
Percent Similarity: 48.44% Conservative: 110
Best Local Similarity: 29.34% Mismatches: 258

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Query Match: 19.47% Indels: 39
 DB: 1 Gaps: 14
 US-10-006-265-2 (1-652) x US-07-797-556-1 (1-2369)

QY 35 ProAlaLysProGluAsn1LeSerCysVal1YrYrYrArgLysAsnLeuThrCysThr 54
 DB 619 CCAGAAAAACCTAAATAATTTAGCTGCAATTCGAAACGAGGAAATAAAGGTGTG 678
 QY 55 TTPSerProGlyLysGluThrSerYr---ThrGlnYrThrValLys-----Arg 70
 DB 679 TGGGATGGGAGGAGGAAACACACTGGAGACAACTTCACTTAAATCTGAATGGCA 738
 QY 71 ThrYrAlaPheGlyGlu-----LysHisAap-----AsnCysThrAsn 84
 DB 739 ACACAGAAAGTTCGATTCGAAACGAAACCGTACACCCCACTGACCTGTTAT 798
 QY 85 SerSerThrSerGluAsnArgLaseCysSerPhePheLeuProArg1LeThrIlePro 104
 DB 799 TATTCTACT-----GTGTAATTTGTC----- 819
 QY 105 AspaenYrThrIleGluValGluAgluAsnGlyAapGlyValIleLysSer---His 123
 DB 820 ---AACATTGAAGTCTGGGTAGAGACAGAGATGCCCTGGAGAGATTACATCATCAT 876
 QY 124 MetThrYrYrThrArgLeuGluAsn1LeAlaLysThrGluProProLysIlePheArgVal 143
 DB 877 ATCAATTTTGATCTCTGATATATTAAGTG---AAGCCCAATCCGCCCATTAATTTATCATGTG 933
 QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
 DB 934 ATCAACCTAGAGAGAACTGCTAGTATCTTAAATAGCATGAGACCAACCAAGTATTAG 993
 QY 164 ProValSerSerAspLeuLysYrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
 DB 994 AGTGTATTAATA---CTAAATATATAACATTCATATAGAGCCAAAGATGCCCTCAACTGG 1050
 QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrYrAsnLeuThrGly 203
 DB 1051 AGCCGATTTCTCT---CTGAAGACACACACATCCACCACCATCTTCACTGCTCAAGAC 1107
 QY 204 LeuGlnProPheThrGluYrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
 DB 1108 CTTAACCTTTTACGATATGTGTGTAGATTCCTGTATGAGAGAAAGATGTAAGGGA 1167
 QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaProCys--- 241
 DB 1168 TACTGAGTGAAGTGAAGAGAACCAAGTGGATCACTATGAAGATAGACCATCTAA 1227
 QY 242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
 DB 1228 GCACCAAGTTCTGTATTAATAATATCATCTCCATCTCAAGGCTACAGAACTGTACAA 1287
 QY 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyYrAsnIle 281
 DB 1288 CTCGTGTGGAAGACATTCCTCTTTTGAAGCAATGAAATAATTTGATTTAGCAAGTG 1347
 QY 282 TrpYrYrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 301
 DB 1348 ACTCTACAAAGATGGAATCATCATTTACAAATTCACAGTTAATGACCA-----AAA 1401
 QY 302 LeuGluLeuHisLeuGlyLysGluSerPheTrpValSerMetIleSerYrAsnSerLeu 321
 DB 1402 CTGACAGTAATCTTCACAAATGATGCTATCTAGCAACCCCTAAACAGTAAGAAATCTGT 1461
 QY 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
 DB 1462 GGCAATATAGATGACGCTGTTTAACTATCCCTGCTGTGACTTCAAGCTACATCACTCT 1521
 QY 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
 DB 1522 GTAATGATCTTAAAGCATTCCTCCAAAGATAAACATGCTTGGGTGATGATGACATCTCA 1581

QY 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
 DB 1582 AGGGAATCTGTAAAGAAATATATACTTGAAGTGTGTGTATCATGATTAAGACCTCTGT 1641
 QY 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGluAspLysLeu 401
 DB 1642 ATCAGACAGCTGCAACAAGAGATGTGACCTGATCGCACCTATTATTAAGAGGAACTTA 1701
 QY 402 LysProPheTrpCysYrAsnIleSerValYrProMetLeuHisAspLysValGlyGlu 421
 DB 1702 GCAGAGACAAATGCTATTTGATTAACACTTTCACAGATTCCTGATGAGACCAAGAAC 1761
 QY 422 ProYrSerIleGlnAlaYrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
 DB 1762 CTTGAATCATTAAGGATCACTTAAACACTCCACTTCACCTTCAAGAGCTACTGTTGG 1821
 QY 442 ValGluAsnIleGlyValLysYrThrIleThrTrpLysGluIleProLysSerGlu 461
 DB 1822 ACAAAAAAGAGGAGAAAAAGAGCTGTCTTAGAGTGCACCAACTTCTGTGATGTT 1881
 QY 462 ArgLysGlyIleIleCysAsnYrThrIlePheYrGlnAlaGluGlyLysGlyPhe 481
 DB 1882 CAGATGATTTATCAGAAATTAATATATATTTATAGAACCATCATTTGAGAAATGAACT 1941
 QY 482 SerLysThrValAsnSerSerIleLeuGlnTrpGlyLeuGluSerLeuLysArgLysThr 501
 DB 1942 GCTGTGAATGTGAGATTTCTTCCACACAGAAATATCATTTGCTCTTTGATCAAGTAC 2001
 QY 502 SerTrpIleValGlnValMetAlaAsnThrSerAlaGlyIleYrAsnGlyThrSerIle 521
 DB 2002 TTGTATACATGATGATGAGATGAGACATACACAGATGAGGTGGAGAGATGCTCAAGATTC 2061
 QY 522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
 DB 2062 ACTTTTCTTACCCCAAGTTGTCTCAAGAGAAATTGAAGCATAGTGTGCTGTTGC 2121
 QY 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaYrGlyLeuLysLysProAsnLys 561
 DB 2122 TTAGCATTTCTTATGACAACTCTTGTGAGTGTGCTGTTCCTTTAATTAACGAGACTTA 2181
 QY 562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
 DB 2182 ATTAATAAAACACATCTGGCCATAGTTCCAGATCTTCAAAAGATCATATTGCCAGTGG 2241
 QY 582 -----HisGlyAspAspPheLysAspLysLeu 590
 DB 2242 TCACCTCACTCTCTCAAGGACAAATTTTAAATCAAAAGATCAATG 2289

RESULT 6
 US-08-308-881-1
 ; Sequence 1, Application US/08308881
 ; Patent No. 5783672
 ; GENERAL INFORMATION:
 ; APPLICANT: Mosley, Bruce
 ; APPLICANT: Cosman, David J.
 ; TITLE OF INVENTION: Receptor for Oncostatin M
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple 7.1
 ; SOFTWARE: Microsoft Word, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/308,881
 ; FILING DATE: 12-SEP-1994
 ; CLASSIFICATION: 435

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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
? JS-08-308-881-1

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QY 522 AenphelyThrlseuSerPheSerValPheGluIlelleLeuIleThrSerleuIleGly 541
 DB 2062 ACTTTACTACCCCAAGTTTCTCAGAGAAATTGAAGCACTAGTCTGCTGTTGC 2121
 QY 542 GlyGlyLeuLeuIleleuIlelleLeuThrValAlaTyGlyLeuIleValProAlaIle 561
 DB 2122 TTACGATTCCTTATTCACAACACTCTCTGGAGAGTCTGTTGCTTAAATGAAGACCA 2181
 QY 562 LeuThrHisLeuCyTrpProThrValProAlaProAlaGluSerSerleuIleThrTrp 581
 DB 2182 ATTAATAAACACATCTGGCTTAATGATTCAGATCCTTCAAGATCATATATGCCAGTGG 2241
 QY 582 -----HisGlyAspAspPheIleValAspIleValLeu 590
 DB 2242 TCACCTCACACTCTCCAGGACCAATTTATTAATCAAAAGATCAATG 2289

RESULT 7
 US-09-058-263-1
 ; Sequence 1, Application US/09058263
 ; Patent No. 5891997
 ; GENERAL INFORMATION:
 ; APPLICANT: Mosley, Bruce
 ; APPLICANT: Cosman, David J.
 ; TITLE OF INVENTION: Receptor for Oncostatin M
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple 7.1
 ; SOFTWARE: Microsoft Word, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/058,263
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/308,881
 ; FILING DATE: 12-SEP-1994
 ; APPLICATION NUMBER: US 08/249,553
 ; FILING DATE: 26-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seese, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2614-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; TELEX: 756822
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2369 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; TISSUE TYPE: human placenta
 ; IMMEDIATE SOURCE:
 ; CLONE: B10G/pDC303
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 244..2369
 ; FEATURE:
 ; NAME/KEY: mat_peptide

LOCATION: 310..2369
 ;
 ; NAME/KEY: sig_peptide
 ; LOCATION: 244..309
 ; US-09-058-263-1

Alignment Scores:
 Pred. No.: 5,366-65
 Score: 678.50
 Percent Similarity: 48.44%
 Best Local Similarity: 29.34%
 Query Match: 19.47%
 DB: 2
 Gaps: 14

US-10-006-265-2 (1-652) x US-09-058-263-1 (1-2369)

QY 35 ProAlaIleProGluIleValSerCyValIleThrValGlyAsnLeuThrCyThr 54
 DB 619 CCAGAAAACCTAAATAATTTGATGTTGATGTAACGAGGAAATAAGAGTGTAG 678
 QY 55 TrpSerProGlyIleGluThrSerTy---ThrGluThrValIle-----Arg 70
 DB 679 TGGATGTGTGAAGGAAACACACTTGAAGCAAACTTAAATAATCGAATGGCA 738
 QY 71 ThrTyAlaPheGlyGlu-----LysHisAsp-----AsnCyThrThraen 84
 DB 739 ACACACAAGTTTCTGATTCGTAAGCAAGCAACCTGACCCCACTTCATGCTTGTAT 798
 QY 85 SerSerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThrIlePro 104
 DB 799 TATTTCTACT-----CTGTATTTTGTCT----- 819
 QY 105 AsparnTyThrIleGluValGluAlaGluAsnGlyValIleLysSer---His 123
 DB 820 ---AACATTGAAGCTGGGTGAAGACAGAGATCCCTTGGGAAGTTACATCATGAT 876
 QY 124 MetThrTyTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
 DB 877 ATCAATTTGATCCTGATATTAAGTGC---AAGCCCAATCCGACCATATTTATCACTG 933
 QY 144 LysProValleuGlyIleLysArgMetIleGluIleGluTrpIleLysProGluLeuAla 163
 DB 934 ATCAACTCAGAGAAAGTGTAGATATCTTAAATTTGACATGACCAACCAAGATTAAAG 993
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 QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGluThrTyraenLeuThrGly 203
 DB 1051 AGCCAGATTCCT---CCTGAAGACACAGATCCACCGATCTTATTCATGTCAGAAC 1107
 QY 204 LeuGlnProPheThrGluTyValIleAlaLeuArgCyValAlaValIleGluSerLys--- 222
 DB 1108 CTTAAACCTTTTAAAGATATATGTTTAAAGATTCGCTGATGAAGAAAGATGTAAGGGA 1167
 QY 223 PheTrpSerAspTrpSerGluGluLysMetGlyMetThrGluGluAlaProCy--- 241
 DB 1168 TACTGAGAGTCACTGAGTGAAGAAAGCAAGTGGATCACTATGAAGATAGACCTCTTAA 1227
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Db      1462 GGGAAATCGAATCGACCTGTTTAACTATCCCTGCGCTGACCTTCAAGCTACTCAACCT 1521
Qy      342 1leGluValMetGln1aCysVal1aGluAspGlnLeuVal1ValylStrPginSer 361
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Qy      362 AlaleuAspVal1aSerThrTrpMet1leGluTrpPheProAspVal1aSerGluProThr 381
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Qy      402 LysProPheTrpCysTrpYraen1leSerVal1TrpMetLeuHisAspLysVal1GlyGlu 421
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Qy      522 AsnPheLysThrLeuSerPheSerVal1PheGlu1le1leLeu1leThrSerLeu1leGly 541
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Qy      542 GlyGlyLeuLeu1leLeu1le1leLeuThrVal1AlaTrpGlyLeuLysLysProAsnLys 561
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Qy      562 LeuThrHisLeuLysTrpProThrVal1ProAsnProAlaGluSerSer1leAlaThrTrp 581
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Qy      582 -----HisGlyAspAspPheLysAspLysleu 590
Db      2242 TCACCTCACACTCCTCCAGACGCAATTTAATTCAAAAGATCAATG 2289

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? COUNTRY: USA
? ZIP: 98101
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Apple 7.1
? SOFTWARE: Microsoft Word, Version 5.1a
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/059,099
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/308,881
? FILING DATE: 12-SEP-1994
? APPLICATION NUMBER: US 08/249,553
? FILING DATE: 26-MAY-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Seese, Kathryn A.
? REGISTRATION NUMBER: 32,172
? REFERENCE/DOCKET NUMBER: 2614-A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 587-0430
? TELEFAX: (206) 233-0644
? TELEX: 756822
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2369 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA to mRNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
? TISSUE TYPE: human placenta
? IMMEDIATE SOURCE:
? CLONE: B10G/PDC303
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 244..2369
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 310..2369
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 244..309
?
? US-09-059-099-1
?
? Alignment Scores:
? Pred. No.: 5,36e-65 Length: 2369
? Score: 678.50 Matches: 169
? Percent Similarity: 48.44% Conservative: 110
? Best Local Similarity: 29.34% Mismatches: 258
? Query Match: 19.47% Indels: 39
? DB: 2 Gaps: 14
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Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
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Db 1582 AGGGAATCTGTAAGAAATATATCTGATGAGTGCTGTGTTATCAATAAGACACCTGCT 1641
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Db 1642 ATCAAGATCTGGAACAAGAAAGATGATCCGTCGATCCGACTATTTAAGGGGAACCTTA 1701
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Db 1702 GCAGAGACAAATGCTATTTGTAACAGTACTCCAGATATATGCTGATGAGACAGAAAGC 1761
Qy 422 ProTrpSerIleGlnAlaTrpAlaLysGluGlyValProSerGluGlyProGluThrLys 441
Db 1762 CCGTAATCAATTAAGCAATCACTTAACAGCTCACTTCCAAAGACCTATCTGTTGG 1821
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Db 1942 GCTGGAATGAGGATTTCTCCACACAGAAATATACATATGCTCTTGTAGCTAGTACACA 2001
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RESULT 9
US-09-058-264-1
; Sequence 1, Application US/09058264
; Patent No. 6010886
;
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,264
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE: human placenta
 TISSUE TYPE: human placenta
 IMMEDIATE SOURCE:
 CLONE: B10G/PDC303
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 244..2369
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 310..2369
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 244..309
 US-09-058-264-1

Alignment Scores:

Pred. No.:	5,36e-65	Length:	2369
Score:	678.50	Matches:	169
Percent Similarity:	48.44%	Conservative:	110
Best Local Similarity:	29.34%	Mismatches:	258
Query Match:	19.47%	Indels:	39
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US-10-006-265-2 (1-652) x US-09-058-264-1 (1-2369)

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QY 582 -----HisGlyAspAspPheLysAspLysLeu 590
DB 2242 TCACCTCACATCTCTCAAGGACAAATTTTATCAAAAGATCAATATG 2289

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RESULT 10

US-09-455-962-1
 ; Sequence 1, Application US/09455962
 ; Patent No. 6524817
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Mosley, Bruce
 ; APPLICANT: Cosman, David J.
 ; TITLE OF INVENTION: Receptor for Oncostatin M
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple 7.1
 ; SOFTWARE: Microsoft Word, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/455,962
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/058,264
 ; FILING DATE:
 ; APPLICATION NUMBER: US 08/249,553
 ; FILING DATE: 26-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seese, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2614-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ;
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2369 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; TISSUE TYPE: human placenta
 ; IMMEDIATE SOURCE:
 ; CLONE: B10G/pDC303
 ;
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 244..2369
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 ; NAME/KEY: mat_peptide
 ; LOCATION: 310..2369
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 ; NAME/KEY: sig_peptide
 ; LOCATION: 244..309
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 ; US-09-455-962-1
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 ; Alignment Scores:
 ; Pred. No.: 5,366-65 Length: 2369
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 ; Best Local Similarity: 29.34% Mismatches: 258
 ; Query Match: 19.47% Indels: 39
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 ;
 ; US-10-006-265-2 (1-652) x US-09-455-962-1 (1-2369)
 ;
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 DB 739 ACACACAACTTTCCTGATTCGACAAAGCAACAGTCACCCCACTCATGACCTTGTAT 798
 QY 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
 DB 799 TATTCTACT-----GTGATTTTGTTC----- 819
 QY 105 AspaenTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
 DB 820 ---AACATTGAAGCTGGCTGAGAGCAGAGAAATCCCTTGGGAGGTTACATCATCAT 876
 QY 124 MetThrTyrTTPArgLysGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
 DB 877 ATCAATTGTGATTCCTGATATTAAGTG---AAGCCCAATCCGCCACATAATTATCATGTG 933
 QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTyrIleLysProGluLeuAla 163
 DB 934 ATCAACTAGAGGAAGACTGTCAAGTATCTTAATAATTCATGACATGACCAACCAAGTATTAG 993
 QY 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTyr 183
 DB 994 AGTGTTATTAATA---CTAAATAATATACATTAATAATATGAGCAACAAAGATGCTCAACTGG 1050
 QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
 DB 1051 AGCCAGATTCTCT---CTGAAGACACAGCATCCACCGCATTTCAATTCATGCTCAAGAC 1107
 QY 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
 DB 1108 CTTAACCTTTTACAGATATATGTTTGAAGTTGCTGTATGAAGAGAAAGTATGAAGGA 1167
 QY 223 PheTTPSerAspTTPSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
 DB 1168 TACTGAGTGCATCGAGTGAAGAGCAAGTGGGATCATCTTATGAAATAGACCATCTTAA 1227
 QY 242 GlyLeuGluLeuTTPArgValLeuLysProAlaGluAlaAspGlyArgProValArg 261
 DB 1228 GCACCAAGTTTCTGTATTAATAATATGATCCATCCATCTCAAGGCTACAGAACTGTACAA 1287
 QY 262 LeuLeuTTPLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
 DB 1288 CTCGTGTGAAGACATTCCTCTTTTGAAGCCCAATGAGAAAATCTTGATTAAGAACTG 1347
 QY 282 TTPTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 301
 DB 1348 ACTCTCAAGATGGAATATCATTTTACAAATATACAGTTATGTCACAA-----AAA 1401
 QY 302 LeuGluLeuHisLeuGlyGlyGluSerPheTyrValSerMetIleSerTyrAsnSerLeu 321
 DB 1402 CTGACAGTAATCTCACAAATGATGCTATCTACAAACCTTACAGTAAGTAAGAAATCTTGT 1461
 QY 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
 DB 1462 GGCAAATCAAGTGAAGCTGTTTAACTATCTCCCTGCTGATCTTCAAGTCACTACACCT 1521
 QY 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTTPGlnSerSer 361
 DB 1522 GTATGATCTTAAGCATTCCTCCCAAGATTAACATGCTTGGGAGATGACATCACTCA 1581
 QY 362 AlaLeuAspValAsnThrTTPMetIleGluTyrPheProAspValAspSerGluProThr 381
 DB 1582 AGGGAATCTGTAAAGAAATATATATCTGAGTGTGTGTATTCAGATTAAGACACCTGT 1641
 QY 382 ThrLeuSerTTPGluSerValSerGlnAlaThrAsnThrPheIleGlnIleAspLysLeu 401

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Db      1642 ATCAGACTGCGACAGAGAGATGGTACCGTCATCGACCACTATTATTAAGAGGAACCTTA 1701
Qy      402  LysProPheThrPyrSerIleuValIleSerValIleProMetLeuHisAspLysValGlu 421
Db      1702 GCAGAGAGCAAAAGCTATTGTTGATTAACGATTACCTCCAGTATATCTGATGAGCAGGAAAGC 1761
Qy      422  ProTyrSerIleGlnIleAlaTyrAlaValGluGluValProSerGluGluProGluThrLys 441
Db      1762 CCGGATCCCAATTAAGGATATCTTAACAAGCTCCACCTTCCAAAGAGCTACTGTTCCG 1821
Qy      442  ValGluAsnIleGlyValLysThrValThrIleThrTyrLysGluIleProLysSerGlu 461
Db      1822 ACAAAAAGATGAGAAAAAGAAAGCTGTCTTAGAGGAGCAACCACTTCTGTGTGATGTT 1881
Qy      462  ArgLysGlyIleIleLeuSerValIleLeuThrIlePheThrGlnIleGluGlyValGlySerGly 481
Db      1882 CAGAAATGATTTATTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1941
Qy      482  SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
Db      1942 GCTGTGAATGTGATTTCTTCCACAGAGATATACATTTGCTTGTGACTAGTACACA 2001
Qy      502  SerTyrIleValGlnValMetAlaSerThrSerAlaGlyLysThrSerGlyThrSerIle 521
Db      2002 TTGTACATGTGTACAAATGGCAGATACACAGATGAAGTGGGAAGTGTCCAGAAATTC 2061
Qy      522  AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
Db      2062 ACTTTTACTACCCCAAGTTTGCTCAAGAGAAATGAAACCAATGCTGCTGCTTTC 2121
Qy      542  GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaIleGlyLeuLysLysProAsnLys 561
Db      2122 TTAGCATTTCTATTGACAACTCTTCTGGAGTCTGTCTGCTTATTAAGCAGACCTTA 2181
Qy      562  LeuThrHisLeuGlySerProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
Db      2182 ATTAATAAAACACATCTGGCTTAATGTTCCAGATCTTCAAAAGAGCTATATGCCAGTGG 2241
Qy      582  -----HisGlyAspAspPheLysAspLysLeu 590
Db      2242 TCACCTCACACTCTCCACAGGCAAAATTTTAATTCAAAAGATCAAAATG 2289

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REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/pDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
PCT-US95-06530-1

Alignment Scores:
Pred. No.: 5,366-65 Length: 2369
Score: 678.50 Matches: 169
Percent Similarity: 48.448 Conservative: 110
Best Local Similarity: 29.348 Mismatches: 258
Query Match: 19.474 Indels: 39
DB: 5 Gaps: 14

US-10-006-265-2 (1-652) x PCT-US95-06530-1 (1-2369)
Qy      35  ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
Db      619  CCAGAAAACCTAAATAATTTGATGTCATTGTAACGAGGAGAAATGAGGTGTAG 678
Qy      55  TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValys-----Arg 70
Db      679  TGGGATGTGGGAAGGAAACACACTTGAGACAACTTCACTTAATAATCTGAATGGCA 738
Qy      71  ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db      739  ACACACAGATGTTGCTGATTCGCAAGCAAAACGAGACACCCACCTCATGCTGTGAT 798
Qy      85  SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db      799  TATTTCTACT-----GTGATTTTGTCT----- 819
Qy      105  AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
Db      820  ---AACATTGAAGTCTGGGTAGAGAGCAAGATGCCCTTGGAAGGTATCATCAATCAT 876
Qy      124  MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
Db      877  ATCAATTTGATTCCTGATATATAAGG---AGCCCAATCCGCCACATATATTATCAGTG 933
Qy      144  LysProValLeuGlyIleLysArgMetIleGlnIleGlyTrpIleLysProGluLeuAla 163
Db      934  ATCAACTCAGAGAACTGTCTAGTATCTTAATAATTGACACCAACCAAGATATTAG 993
Qy      164  ProValSerSerAspLeuLysTyrThrIleAsnArgPheArgThrValAsnSerThrSerTrp 183
Db      994  AGTTTATATAATA---CTAAATAATATAACATTCATATATAGACCAAAAGATGCTCAACTTGG 1050

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Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
Db 1051 AGCCAGATTCCCT---CTGGAAGACACAGATCCACCACCTCTTCAATTCACCTGCAAGAC 1107
Qy 204 LeuGlnProPheThrGlyTyrValIleAlaLeuArgValAlaValLeuGlySerLys--- 222
Db 1108 CTTAAACCTTTTACAGAAATATGTGTTAGGATTCCTGATGAGAGAAATGTAAGGGA 1167
Qy 223 PheTyrSerAspTyrSerGlnGluLysMetGlyMetThrGlnGluAlaProCys--- 241
Db 1168 TACTGGAGTCTGAGTGAAGAGACAGAGGATCCCTATGAAGATGACACTTAA 1227
Qy 242 GlyLeuGluLeuTyrPargValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
Db 1228 GCACCAAGTTCTGTTATTAATAATATCCATCCCTACTCAAGGCTACAGAACTTACA 1287
Qy 262 LeuLeuTyrLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
Db 1388 CTCGTGTGAAGACATTCCTCTTTTGAAGCCCAATGAGAAATCTTGATTAATGAGTG 1347
Qy 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
Db 1348 ACTCTCACAGATGAGAAATCACATTACAAATTAACAGATTAAATGACCA---AAA 1401
Qy 302 LeuGluLeuHisLeuGlyGlyLysSerPheTyrValSerMetIleSerTyrAsnSerLeu 321
Db 1402 CTGACAGTAAATCTCACAAATGATGCTATCTAGAACCTTACAGTAAAGAAATTTGT 1461
Qy 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
Db 1462 GGCAATATGATGATGCGCTGTTTAACTATCCCTGCTGATCTTCAAGTCACTCACCT 1521
Qy 342 IleGluValMetGlnAlaCysValAlaGluLysGlnLeuValLysTyrGlnSerSer 361
Db 1522 GTAATGATCTTAAAGCATTCCTCCCAAGATTAACATGCTTGGTGAATGAGACTCA 1581
Qy 362 AlaLeuSerValAsnThrTyrMetIleGluTyrPheProAspValAspSerGluProThr 381
Db 1582 AGGGAATCTCTAAAGAAATATATCTTACTGATGCTGTGTATTCAGATTAAGACCCCTGT 1641
Qy 382 ThrLeuSerTyrGluSerValSerGlnAlaThrAsnTyrPheIleGlnAlaAspLysLeu 401
Db 1642 ATCACAGATCGCAACAAGAGATGTCGCGATCCGACTTCACTTAAAGAGGGAACCTTA 1701
Qy 402 LysProPheTyrPyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
Db 1702 GCAGAGAGCAAAATCTTTGATATACAGTACTCCAGATATGCGTAGAGCAACGAGAGC 1761
Qy 422 ProTyrSerIleGlnAlaTyrAlaLysGluValProSerGluGlyProGluThrLys 441
Db 1762 CTTGAATCTTAAGAGCATCTTAAACAGCTCCACCTTCCAAAGAGCACTACTGTTGG 1821
Qy 442 ValGluAsnIleGlyValLysThrValThrIleThrLysGluLysProLysSerGlu 461
Db 1822 ACAAAAAGAGAGGAAAGAAAGAGAGCTGCTTAGAGTGAGCAACAACCTCGTTGAGT 1881
Qy 462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481
Db 1882 CAGATGATTTATTCAGAAATTAATATATTTATATAGAACCATCATTTGAGAAATGAAACT 1941
Qy 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
Db 1942 GCTGTGAATGTGATTTCTTCCACACAGAAATATCATTTGCTCTTTGACTAGTACGACA 2001
Qy 502 SerTyrIleValGlnValMetAlaAsnThrSerAlaGlyThrAsnGlyThrSerIle 521
Db 2002 TTGTAATCATGTATGCAATGAGCATACACATGAGAGTGGAAGATGTCGCAAAATC 2061
Qy 522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
Db 2062 ACTTTTACTACCCCAAGTTTGTCTAAGAGAAATTAAGCAATAGTCTGCTGTTGGC 2121
Qy 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561

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Db 2122 TTAGATCTCTATTGACAACTCTTCTGGAGTGGCTGTCTGCTTAAATAGGAGACCTA 2181
Qy 562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
Db 2182 ATTAACAAACATCTGCTTAATGTTCCAGATCTTCCAAAGAGTCATATGGCCAGTGG 2241
Qy 582 -----HisGlyAspAspPheLysAspLysLeu 590
Db 2242 TCACCTCACTCTCCAGGACAAATTTATTCAAAGATCAAAATG 2289

RESULT 12
US-08-825-558-5
; Sequence 5, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623_0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; FAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2754
; US-08-825-558-5

Alignment Scores:
Pred. No.: 8.92e-65 Length: 2754
Score: 677.50 Matches: 175
Percent Similarity: 46.75% Conservative: 113
Best Local Similarity: 28.41% Mismatches: 261
Query Match: 19.45% Indels: 67
DB: Gaps: 16

US-10-006-265-2 (1-652) x US-08-825-558-5 (1-2754)
Qy 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
Db 376 CCGAAGAAACCTTAATAATTTGATGATGTGAACAGAGGAGAAAGAAATGAGCTGTGAG 435
Qy 55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
Db 436 TGGGATGTGTGAAGGAGAAACACACTTGAGACAAACTTCACTTAAATGTAATGGCA 495

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REFERENCE/DOCKET NUMBER: 0623.0530002
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2754 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2754
US-09-312-611-5

Alignment Scores:
Pred. No.: 8,92e-65 Length: 2754
Score: 677.50 Matches: 175
Percent Similarity: 46.75% Conservative: 113
Best Local Similarity: 28.41% Mismatches: 261
Query Match: 19.45% Indels: 67
Gaps: 16
DB: 3

US-10-006-265-2 (1-652) x US-09-312-611-5 (1-2754)

QY 35 ProAlaLysProGluAsnLysSerCyValTyrTyrArgLysAsnLeuThrCysThr 54
DB 376 CCAAGAAAAACCTAAATAATTTGATGTCATTTGAAAGAGGAGAAATGAGGTGTGAG 435
QY 55 TTPSerProGluLysGluThrSerTyr---ThrgInTyrThrValLys-----Arg 70
DB 436 TGGAGTGGTGAAGGAAACACACCTTGACGACAACTTCAATTAATCTGAATGGCA 495
QY 71 ThrTyrAlaPheGluLys-----LysHisAsp-----AsnCysThrThrAsn 84
DB 496 ACACGACAGTTGTCGATTCGAAACGAAACGTCACACCCCACTCATGCACTTGAT 555
QY 85 SerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProArgLleThrIlePro 104
DB 556 TATCTACT-----GTGATTTTGTGTC----- 576
QY 105 AspAsnTyrThrIleGluValGluValGluAsnGlyAspGlyValIleLysSer---His 123
DB 577 ---AACATTGAAGTGGGTAGAACGAGAAATGCCCTTGGAGGATTAACATCATCAT 633
QY 124 MetThrTyrTyrPArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
DB 634 ATCATTTTGCATCCGTATATAAGT---AAGCCCATCCGCCACATTAATTATCAAGTG 690
QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTyrPileLysProGluLeuAla 163
DB 691 ATCAACTGAGAGAACTGCTAGTATCTTAATAATGACATGAGCAACCAAGTATTAAG 750
QY 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTyr 183
DB 751 AGTGTATATAAT---CTAAATAATATAACTATCAATATAGACCAAGATGCCCTCAACTGG 807
QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
DB 808 AGCCGATTCCT---CTGGAAGACACAGATCCACCCATCTTCACTTCACTGCAAGAC 864
QY 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
DB 865 CTTAAACCTTTTACAGATATGTGTAGATTCCCTGTATGAAGAGAGATGTAAAGGA 924
QY 223 PheTTPSerAspTyrSerGlnGluLysMetGlyMetThrGluGluAlaProCys--- 241
DB 925 TACTGAGTGTAGCTGAGAGAACCAAGATGGATCACCCTATGAAGATTAAGCACTTAA 984
QY 242 GlyLeuGluLeuTyrPArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
DB 985 GCAACAATTTCTGTATATAATATAGATCCATCTCAAGGCTACAGAACTATACAA 1044

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QY 262 LeuLeuTyrPylsValArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
DB 1045 CTCGTGTGAAGACATTCCTCCCTTTTGAACCAATGAGAAATCTTGATTAAGAACTG 1104
QY 282 TTPTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
DB 1105 ACTCTCAACAATGGAATACATTTACAAAATTAACACAGTTAATGCCACAC-----AAA 1158
QY 302 LeuGluLeuHisLeuGlyGlyLysSerPheThrValSerMetLysSerTyrAsnSerLeu 321
DB 1159 CTGACAGTAATCTCACAAAATGATGCTATACCAACCTTAACAGTAAGAAATCTTGTT 1218
QY 322 GlyLysSerProValAlaThrLeuArgLleProAlaIleGlnGluLysSerPheGlnCys 341
DB 1219 GGCAAATCATGATGACAGCTGTGTAACTATCCCTCCCTGTGACCTTCAAGCTACACCT 1278
QY 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTyrPGLSerSer 361
DB 1279 GTAATGATCTTAAAGCATTTCCCAAGATTAACATGCTTTGGGTGGAATGACATCTCA 1338
QY 362 AlaLeuAspValAsnThrTyrMetIleGluTyrPheProAspValAspSerGluProThr 381
DB 1339 AGGGAATCTGTAAGAAATATATATCTGAGTGTGTGTATCATGATTAAGACACCTGT 1398
QY 382 ThrLeuSerTyrPGLSerValSerGlnAlaThrAsnThrPheIleGlnGlnAspLysLeu 401
DB 1399 ATCAACAAGCTTGCAACAAGAAAGATGTAACCTGTGATGCACCTTAAAGAGGAACTTA 1458
QY 402 LysProPheTyrPArgLysAsnLysSerValTyrProMetLeuHisAspLysValGly 421
DB 1459 GCAAGAGCAAAATGCTATTTTATTAACAGTTACTCAGATATATGCTGATGACACGGAAGC 1518
QY 422 ProTyrSerIleGlnAlaTyrAlaLysGluLysValProSerGluGlyProGluThrLys 441
DB 1519 CCGATATCATTAAGAGCATACCTTAACAAAGCTCACCTTCAAGAGCATATGATGCTGG 1578
QY 442 ValGluLeuIleGlyValLysThrValThrIleThrIleThrLysGluIleProLysSerGlu 461
DB 1579 ACAAAAAGATGAAGAAAGAAAGAAAGCTGTCTTAAGATGGACCAACTCCCTGTGATGTT 1638
QY 462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481
DB 1639 CAGAAATGATTTATCAGAAATTAATTAATTTATTAAGAACATCATTTGAAATGAAGAACT 1698
QY 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
DB 1699 GCTGGAATGTGATGATTTCCCAACAGAAATATATCATTTGCTCTTGTGACATGACACA 1758
QY 502 SerTyrIleValGlnValMetAlaAsnThrSerAlaGlyLysThrAsnGlyThrSerIle 521
DB 1759 TTGTACATGTGACCAATGCGACATACAGATGAGGTGGAGATGGTCCAGAAATTC 1818
QY 522 AsnPheLysThrLysSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
DB 1819 ACTTTTACTACCCCAAGTTTGTCTCAAGAGAAATTAAGCAATATGTCGCTGTTTGC 1878
QY 542 GlyLysLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
DB 1879 TTACATTTCCATTAAGACAACTCTTGGAGTGTGTCTGCTTAATAAGCGAGACTTA 1938
QY 562 LeuThrHisLeuCysTyrProThrValProAsnProAlaGluSerSerIleAlaThrTyr 581
DB 1939 ATTAAAAACACATCTGCTTAAGTTCCAGATCTTCAAAAGTCAATATTTGCCACAGTGG 1998
QY 582 -----HisGlyAspAspPheLysAspLysLeu----- 590
DB 1999 TCACCTCACTCTCCAAAGGACAAATTTTAATTAATCAAAAGATCAATATGATTCAGATGCC 2058
QY 590 ----- 590
DB 2059 AATTCACTGATGTAAGTGTGTGGAATTAAGAAACAAATGACAAAGCCCTTTCCAGAA 2118

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QY      591 AsnLeuLysGluSerAsp-----AspSerValAsnThrGlu 602
Db      2119 GATCTGAATATCATTTGGACCTGTTCTCAAAAGAAAATTAATACTGAA 2166

RESULT 14
US-08-825-558-3
/ Sequence 3, Application US/08825558
/ Patent No. 5965724
/ GENERAL INFORMATION:
/ APPLICANT: SHARKEY, ANDREW
/ APPLICANT: SMITH, STEPHEN K.
/ TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
/ STREET: 1100 NEW YORK AVENUE
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/825,558
/ FILING DATE: 19-MAR-1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ESMOND, ROBERT W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0623.0530001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)371-2600
/ TELEFAX: (202)371-2540
/ INFORMATION FOR SEO ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1977 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: Both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1974
/ US-08-825-558-3

Alignment Scores:
Pred. No.:      1,94e-60      Length:      1977
Score:          436.50       Matches:      163
Percent Similarity: 46.53%    Conservative: 105
Best Local Similarity: 28.30%  Mismatches:   237
Query Match:     18.27%      Indels:       72
                        Gaps:        15

US-10-006-265-2 (1-652) x US-08-825-558-3 (1-1977)
QY      35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
Db      376 CCAGAAAACCTTAATAATTTGAGTTGATGTGAACGAGGGAAGAAAATGAGAGTGTGAG 435
QY      55 TrpSerProGluLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
Db      436 TGGGATGGTGGAGGAAACACACTTGAGACAAACTTCCTTTAAATCTGAATGGGCA 495
QY      71 ThrTyrAlaPheGluGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db      496 ACACACAGATTTCGTGATTGCAAGCAAAACGTGACACCCCACTCATCTGTTGAT 555
QY      85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104

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Db      556 TATTTCTACT-----GTGTAATTTTGTG----- 576
QY      105 AspAsnTyrThrIleGluValGluIleGluAsnGlyAspGlyValIleLysSer---His 123
Db      577 ---AACATTGAAGTCTGGGTAGACAGAGAAATGCCCTTGGGAAGGTTACATCATCATCT 633
QY      124 MetThrTyrTrpArgLysGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
Db      634 ATCAATTTTGTATTCGTATATAAGTG---AAGCCCAATCCGCCACATTAATTTATCAGTG 690
QY      144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db      691 ATCAACTCAGAGAACTGTCTAGTATCTTAAATATGACATGGACCAACCAAGTATTAAG 750
QY      164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db      751 AGTGTTATATA---CTAATAATTAACATTCATTAATAGACCAAAAGATGCCCACTTG 807
QY      184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
Db      808 AGCCAGATTCTCT---CTGAAGACACAGCATCCACCCGATCTTCATCTCACTGCCAAGAC 864
QY      204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysValValLysGluSerLys--- 222
Db      865 CTTAAACCTTTTACAGAAATATGTGTAGATTCCTGTATGACAGAAAGATGTAAGGA 924
QY      223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
Db      925 TACTGAGTGACTGGAGTGAAGACAGAGTGGATCACCCTTAAGATAGACATCTAA 984
QY      242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
Db      985 GCACCAAGTTCTCGTATTAATAATAGATCCATCCATCAAGGCTACAGACTGACAA 1044
QY      262 LeuLeuTrpLysLeuAlaArgLysAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
Db      1045 CTCGGTGGAGAACATATGCCCTCTTTGAAGCCAAATGGAATAATCTGGATTAAGAAG 1104
QY      282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 301
Db      1105 ACTCTCACAAGATGGAAATCACTTTACAAATTTACACAGTTAAAGCCCA-----AAA 1158
QY      302 LeuGluLeuIleLeuGlyLysSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
Db      1159 CTGACAGTAAATCTCAAAATGATCGCTATCTAGCAACCTTAAGAAATCTTGT 1218
QY      322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
Db      1219 GGCAAATCGATGCGAGCTGTTTAACTATCCCTGCTGCTGACTTTCAAGCTACACCT 1278
QY      342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSer 361
Db      1279 GTAAATGATCTTAAGAGATCTCCCAAAAGATACATGCTTTGGGTGAAGAGTACTGCA 1338
QY      362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
Db      1339 AGGGAATCTGAAGAAATATATACTGAGTGCTGTGTGTATGACATGAAGACCCCTGT 1398
QY      382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
Db      1399 ATCAGAGACTGGCAACAGAGATGTACCCGTGACCTGCACTTAATTAAGAGGAATTA 1458
QY      402 LysProPheTrpCysTyrAsnIleSerValTyrPrometLeuHisAspLysValGluGlu 421
Db      1459 GCAAGAGCAAAATGCTATTGTATTAACAAGTTACTCCAGATATAGCTGATGAGACCAAG 1518
QY      422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
Db      1519 CCTGAATCATTAAGGCACTTAACAAAGCTCCACCTTCAAAAGGACCTATCTGTTCG 1578
QY      442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db      1579 ACAAAAAGATGAGGAAAAACGAAGCTGTCTTAGGTGGACCAATTCCTGTGATGTT 1638

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DB 1339 AGGGAATCTGTAAAGAAATATATATACCTGAGTGGTGTGTATACAGATTAAGCACCTGT 1398
QY 382 ThrLeuSerTrpGIuSerValSerGIuAlaThrAsnTrpThrIleGIuAspLysLeu 401
DB 1399 ATCAGACACTGGCAGACAGAAAGATGTACCGTGATCGACCTATTTAAGAGGAACTTA 1458
QY 402 LysProPheTrpCysTrpAsnIleSerValTrpProMetLeuHisAspLysValGIuGIu 421
DB 1459 GCGAGAGCAAAATGCTATTGATTAACGTTACTCCAGTATATGCTGATGACAGGAAAGC 1518
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DB 1519 CCGAATCCATTAAGGATACCTTAACAGATCCACCTCCAAAGACCTTACTGTTCCG 1578
QY 442 ValGIuAsnIleGIuValLysTrpValThrIleThrTrpLysGIuLysProLysSerGIu 461
DB 1579 ACAAAAAAGTAGGAAAAAGAGCTGCTTAAAGTGGAGCAACTCTCTGTGATGTT 1638
QY 462 ArgLysGIuLysIleCysAsnTrpThrIlePheTrpGIuAlaGIuLysGIuLysPhe 481
DB 1639 CAGAAATGATTTTACAGAAATTTATCTATTTTATTAAGAACCATCATGGAATGAACCT 1698
QY 482 SerLysThrValAsnSerSerIleLeuGIuTrpGIuLysLeuLysSerLysArgLysThr 501
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QY 502 SerTrpIleValGIuValMetAlaAsnThrSerAlaGIuLysThrAsnGIuThrSerIle 521
DB 1759 TTGTACATGTGTACGAGATGACATACAGATGAAGTGGAAAGTGTCCAGAAATTC 1818
QY 522 AsnPheLysThrLeuSerPheSerValPheGIuLysIleLeuLysThrSerLeuIleGIu 541
DB 1819 ACTTTTACTACCCCAAGTTT----- 1839
QY 542 GIuGIuLeuLeuIleLeuIleIleuThrValAlaTrpGIuLysLysProAsnLys 561
DB 1840 -----GAA 1842
QY 562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGIuSerSerIleAlaThrTrp 581
DB 1843 TTAAAAAACAC-ATCTGGCTTAATGTTCAGATCCTTCAAAAGATCATATTGCCAGTGG 1901
QY 582 -----HisGIuAspAspPheLysAspLysLeu 590
DB 1902 TCACCTCACACTCTCCAGAGCACAATTTTAATTCAAAAGATCAAAATG 1949

Search completed: February 23, 2005, 19:35:55
Job time : 343.186 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 09:15:27 ; Search time 1015.05 Seconds

(without alignments)
3796.488 Million cell updates/sec

Title: US-10-006-265-2

Perfect score: 3484

Sequence: 1 MKLSRQPSQVNLGMMWTAL.....FTDEARTQEQKFRGKEMD 652

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -OFMT=fastcap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNIT5=bits -START=1 -END=-1 -MATRIX=ploum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10006265_@CGN_1_1_1175@runat_18022005_094659_22236
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOC -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3484	100.0	2969	15	US-10-006-265-1
2	3451	99.1	2119	15	US-10-006-265-16
3	3451	99.1	2903	10	US-09-892-949-53
4	3451	99.1	2903	17	US-10-351-157-4
5	3451	99.1	2903	17	US-10-352-554-4
6	3451	99.1	2903	18	US-10-772-531-53
7	3441	98.8	2529	10	US-09-892-949-45
8	3441	98.8	2529	17	US-10-351-157-108
9	3441	98.8	2529	18	US-10-772-531-45
10	3435	98.6	2238	10	US-09-972-708-5
11	3435	98.6	2238	18	US-10-715-667-5
12	3435	98.6	2402	10	US-09-892-949-1
13	3435	98.6	2402	17	US-10-351-157-110
14	3435	98.6	2402	18	US-10-772-531-1
15	3435	98.6	2480	10	US-09-972-708-3
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17	2850	81.8	2295	10	US-09-892-949-68
18	2850	81.8	2295	17	US-10-351-157-38
19	2850	81.8	2295	17	US-10-352-554-38
20	2850	81.8	2295	18	US-10-772-531-68
21	2810	80.7	1986	10	US-09-892-949-55
22	2810	80.7	1986	17	US-10-351-157-122
23	2810	80.7	1986	18	US-10-772-531-55
24	2779	79.8	1557	17	US-10-351-157-70
25	2779	79.8	1557	17	US-10-352-554-70
26	2758	79.2	1947	10	US-09-892-949-47
27	2758	79.2	1947	17	US-10-351-157-121
28	2758	79.2	1947	18	US-10-772-531-47
29	2758	79.2	2196	10	US-09-892-949-4
30	2758	79.2	2196	17	US-10-351-157-120
31	2758	79.2	2196	18	US-10-772-531-4
32	2606	74.8	2445	14	US-10-227-884-91
33	2606	74.8	2445	14	US-10-230-163-91
34	2606	74.8	2445	14	US-10-330-338-91
35	2606	74.8	2445	14	US-10-218-631-91
36	2606	74.8	2445	14	US-10-230-414-91
37	2606	74.8	2445	14	US-10-232-124-91
38	2606	74.8	2445	14	US-10-216-159A-91
39	2606	74.8	2445	14	US-10-218-849-91
40	2606	74.8	2445	14	US-10-227-873-91
41	2606	74.8	2445	14	US-10-227-883-91
42	2606	74.8	2445	14	US-10-219-076-91
43	2606	74.8	2445	14	US-10-230-434-91
44	2606	74.8	2445	14	US-10-219-003-91
45	2606	74.8	2445	14	US-10-219-075-91

ALIGNMENTS

RESULT 1
US-10-006-265-1

Sequence 1, Application US/10006265
Publication No. US20030125520A1

GENERAL INFORMATION:
APPLICANT: Maeda, Masaetsugu
TITLE OR INVENTION: NOVEL HEMOPHILIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
CURRENT APPLICATION NUMBER: US/10/006, 265
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1

LENGTH: 2969
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (523) ... (2478)
US-10-006-265-1

Alignment Scores:

Pred. No.:	0	Length:	2969
Score:	3484.00	Matches:	652
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-10-006-265-2 (1-652) x US-10-006-265-1 (1-2969)

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QY 21 TrpMetLeuProSerLeuCysGlyPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db TGGATGCTCCCTCAGCTGCAAAATTCAGCTGGCAGCTGCGCAGCTAAGCTTGAGAAC 642
QY 41 LLeSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db ATTTCCGTCTCACTCACTAATAGAAAATTTAACTGCACTTGAGATCCAGAAAGAA 702
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysPheAspAsn 80
Db ACCAGTTATACCAGTACACAGTTAAGAACTTAAGCTTCCGAGAAAACATGATTAAT 762
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db TGTACAAACCAATAGTTCTTACAAAGTAAATCGGTCTCGCTCTTTTCTTCACAAAG 822
QY 101 LLeThrLLeProAspAsnTyrThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
Db ATTAACGATCCCAATTAATTTACATTGAGCTGGAAGCTAAAATGGAGATGGTAAATT 882
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnLLeAlaLysThrGluProGlyLLe 140
Db AAATCTCATATGACATCTGAGATTTAGAAACATAGCGAAACTGAACACCTTAAGATT 942
QY 141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
Db TTCGGTGTGAACCAAGTTTGGGCAATCAACGAATGATTCAAATGTGAATGAATAAAGCT 1002
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
Db GATTTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAACAGT 1062
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db ACCAGCTGAGTGAAGTCACTTCGTAAGAACCGTAAGATTAACCAACGTAAC 1122
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValLLeAlaLeuArgCysAlaValLysGlu 220
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QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
Db TCAAAGTCTCGAGTGACTGAAGCCAAAGAAAATGGGAATGACTGAGAGAAAGCTCCA 1242
QY 241 CysGlyLeuGluLeuTrpArgValLLeuLysProAlaGluAlaAspGlyArgArgProVal 260
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QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
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QY 281 LLeTrpTyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
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QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLLeSerTyrAsnSer 320
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QY 321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
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QY 341 CysLLeGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
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Db ACCACCTTCTCCGGGAATCTGTCTCAGGCCACAGAACTGACATCCAGCAAGATAAA 1722
QY 401 LeuLysProPheTrpCysTyrAsnLLeSerValTyrProMetLeuHisAspLysValGly 420
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QY 421 GluProTyrSerLLeGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
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QY 441 LysValGluAsnLLeGlyValLysThrValLTrpLLeThrLysGluLLeProLysSer 460
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QY 461 GluArgLysGlyLLeLLeCysAsnTyrThrLLePheTyrGlnAlaGluGlyLysGly 480
Db GAGAGAAAGGATATCATCTGCAACATCAACCACTTTTACCAAGCTGGAAGTGAAGAA 1962
QY 481 PheSerLysThrValAsnSerSerLLeLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
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QY 501 ThrSerTyrLLeValGlnValMetAlaAsnThrSerAlaGlyLLeThrAsnGlyThrSer 520
Db ACCTCTTACATTTGTCAGTCAATGGCAACACAGTGGGAGAAACCAAGGACACAGC 2082
QY 521 LLeAsnPheLysThrLeuSerPheSerValPheGluLLeLLeuLLeThrSerLeuLLe 540
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QY 541 GlyGlyGlyLeuLeuLLeLeuLLeLLeLeuThrValAlaTyrGlyLeuLysLysProAsn 560
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QY 561 LysLeuThrHisLeuCysTrpProThrValLLeProAsnProAlaGluSerSerLLeAlaThr 580
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QY 601 ThrGluAspArgLLeLeuLysProCysSerThrProSerAspLysLeuValLLeAspLys 620
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QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluLLePheThrAspGluAlaArgTrpGly 640
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Qy      641 GInGluLySGlnPheArgArgGlyLySGluTTPaap 652
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RESULT 2
US-10-006-265-16
; Sequence 16, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006,265
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2119
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11) ... (1996)
US-10-006-265-16

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Percent Similarity: 99.85%   Conservative: 1
Best Local Similarity: 99.69%   Mismatches: 1
Query Match: 99.05%         Indels: 1
DB: 15                  Gaps: 0

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Qy      41 TLeSerCyValTyrTyrTyrArgLysAsnLeuThrCySerTTPSerProGlyLysGlu 60
Db      131 ATTCTCTGCTCTACTACTATAGGAAAAATTAACTCCTGACCTTGAGTCCAGGAAAGGAA 190
Qy      61 TThSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
Db      191 ACCGATTATACCCAGTACACAGTTAAGAACTTACGCTTTTGGAGAAAAACATGATATAT 250
Qy      81 CySerThrAsnSerSerThrSerGluAsnArgAlaSerCySerPhePheLeuProArg 100
Db      251 TGTACAACCAATAGTTCACAGTGAATAATCGCTGCTCTTTTTCCTTCCACAGA 310
Qy      101 TLeThrLLeProAspPheTyrThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
Db      311 ATACAGATCCACAGATTAATATACCATTGAAGTGAAGCAAAATGAGAGATGCTGTATAT 370
Qy      121 LysSerHisMetThrTyrTyrArgLysGluAsnLLeAlaLysThrGluProProLysLLe 140
Db      371 AAATCTCATATAGACATCTGAGATTAAGAAACATAGGAAAACTGAACCTTAAGATT 430
Qy      141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTyrLLeLysPro 160
Db      431 TTCCGTGTGAAGAACAGTTTGGGCAATCAAGCAATGATTCAATGATGATTAAGGCT 490

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Qy      161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
Db      491 GAGTTGGGCGCTGTTCACTGATTTAAATACACACTTCGATTCAGACAGTCAACGT 550
Qy      181 ThrSerTTPMeTGlValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db      551 ACCAGCTGGATGGAAGTGAATCTCGCTAAGAACCGTTAAGATTAATAAACCAACATACAC 610
Qy      201 LeuThrGlyLeuGlnProPheThrGluTyrValLLeAlaLeuArgCyValLValLysGlu 220
Db      611 CTACGGGGCTGCAGCCCTTTTACAGAAATGTCTATAGCTCCCATGTGCGGTCAAGAG 670
Qy      221 SerLysPheTTPSerAspTTPSerGlnGlyLysMetGlyMetThrGlnGluAlaPro 240
Db      671 TCAAGTTCAGAGTGAAGTGAAGCAAGAAAAATGGAAATGACTGAGAGAAAGCTTCA 730
Qy      241 CySGlyLeuGluLeuTTPArgValLLeuLysProAlaGluAlaAspGlyArgArgProVal 260
Db      731 TGTGCGCTGGAACCTGTGAGAGTCTCTGAACCACTGAGCGGATGGAAGAGCGCACTG 790
Qy      261 ArgLeuLeuTTPLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
Db      791 CGGTTGTTATGAGAAAGGCAAGAGAGAGCCCACTCTAGAGAAAAACATTGGCTACAC 850
Qy      281 TLeTTPTyTyrTTPProGlnLysThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
Db      851 ATATGTAATCATCAAGAAAGCAACATTAACCTCACAGAAACATGAACATCACTAACCCAG 910
Qy      301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTTPValSerMetLLeSerTyrAsnSer 320
Db      911 CAGCTTAACCTGCATCTGGAGGCGGAGAGCTTTGGGTGTCTATGATTTCTTAATATCT 970
Qy      321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
Db      971 CTGGGAAAGTCTCCAGTGGCCACCCCTGAGATTCACAGTATTCAAGAAAAATCATTTTCAG 1030
Qy      341 CySerLLeGluValMetGlnAlaCyValAlaGluLysProGlnLeuValLValLysTrpGlnSer 360
Db      1031 TGCATGTGATCAGTCAAGGCTCGTGTGTGAGGACCAAGCTATGATGTGCAAAAGC 1090
Qy      361 SerAlaLeuAspValAsnThrTTPMetLLeGluTTPPheProAspValAspSerGluPro 380
Db      1091 TCTGCTCAAGCGTGAACACTTGGATGATTAATGCTTTCCGATGTGGACTCAGAGGCC 1150
Qy      381 ThrThrLeuSerTTPGlnLysSerValSerGlnAlaThrAsnTTPThrLLeGlnLysLys 400
Db      1151 ACCACCTTTCTCGGAATCTGTCTCAGGCCACGAATCGACATCCAGCAAGATATAA 1210
Qy      401 LeuLysProPheTTPCySerTyrAsnLLeSerValTyrProMetLeuHisAspLysValGly 420
Db      1211 TTAAAACTTTCTGTGCTATACATCTCTGTATCCAAATGTGACATGAACAAAGTTGGC 1270
Qy      421 GluProTyrSerLLeGlnAlaTyrAlaLysGluGlyValProSerGlnGlyProGlnThr 440
Db      1271 GAGCCATATTCATCCAGGCTTATGCCAAGAGGCGTTCCATATAGAAAGTCTGAGAAC 1330
Qy      441 LysValGluAsnLLeGlyValLysThrValThrLLeThrTTPLysGluLLeProLysSer 460
Db      1331 AAGGTGAGAAACATTTGGCGTGAAGACGTCACATCATCAAGAAAGAGATTCCCAAGAGT 1390
Qy      461 GluArgLysGlyLLeLLeCyAsnTyrThrLLePheTyrGlnAlaGluGlyLysGly 480
Db      1391 GAGAGAAAGGGTATCATCTGCATCAACATCTTTTACCAAGCTGAAGGGTGAAGAAAGGA 1450
Qy      481 PheSerLysThrValAsnSerSerLLeGlnTyrGlyLeuGlnLysSerLeuLysArgLys 500
Db      1451 TTCTCCAGACAGTCAATTTCCAGCATCTTGCAATGAGGCTCGAGTCCCTGAAACGAAG 1510
Qy      501 ThrSerTyrLLeValGlnValMetAlaAsnThrSerAlaGlyLysThrAsnGlyThrSer 520
Db      1511 ACCTCTTAACATTTGTTCAAGTCAATGCGCAGCACCGAGTCTGGGGGAAACCAAGGGACCGC 1570

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QY 521 ILeasnPhelysThreuserPheserValphegluilelleleuileThrserleulle 540
Db 1571 ATAAATTTCAAGACATTTGTATTCAGTGTCTTTGAGATTATCTCTAATCTTCTGATT 1630
QY 541 GLYGLYGLYleuileuilelleleuThValAlaTyGLYleuylsProasn 560
Db 1631 GGCGAGGCGCTCTTATTCATTATCTGACAGTGCATATGCTCTCAAAAAACCAAC 1690
QY 561 lvsleuThrsiaseuCsTProthrValProasnProhlaGluserSerilleaIatPr 580
Db 1691 AAATTTACTATCTGTGTGGCCACCGTTCCACCTGCTGAAGTATATAGCCACA 1750
QY 581 TrpHieGLYAspAspPheylsAspLySleuasnleuylsGLuserAspAspSerValasn 600
Db 1751 TGGCATCGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGTCTGATGACTGTGAAC 1810
QY 601 ThrGLuAspArglileuileuylsProCsSerThProserAspLySleuValIleAspLyS 620
Db 1811 ACAGAAAGACAGGATCTTAAACATGTTCCACCCCACTGACAAAGTTGGTGTGACAAAG 1870
QY 621 leuValValasnPhelgYasnValleuGluilelPheThrsApGluAlaArgThrgly 640
Db 1871 TTGGTGTGAACCTTGGGAAATGTTCTGCAGAAATTTTCACAGATGAAGCCAGAGCGGT 1930
QY 641 GlnGluLysGlnPheArgArglyLySGLuTrpAsp 652
Db 1931 CAGGA-AAAACATTTAGAGGAGGAAAAAGATGGGAC 1965

RESULT 3
US-09-892-949-53
; Sequence 53, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2903
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497) ... (2482)
US-09-892-949-53

Alignment Scores:

Pred. No.: 0 Length: 2903
Score: 3451.00 Matches: 650
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.05% Indels: 1
DB: 10 Gaps: 0

US-10-006-265-2 (1-652) x US-09-892-949-53 (1-2903)

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrPalaleu 20
Db 497 ATGAAGCTCTCTCCCGCCCTTATGTGTAACTGGGAGATGATGGAAGCTGGGCACTG 556

QY 21 TrpMetLeuProSerLeuCsLysPheSerLeuAlaAlaLeuProAlaLysProGluasn 40
Db 557 TGAATGCTCCCTTCACTCTGCAGAAATTCACCTCGGAGCGCTCTCCAGCTAAGCTAGAAC 616
QY 41 lIeserCysValTyTyTyTyArgLysAsnleuThrCysThrTrpSerProGlyLysGlu 60
Db 617 ATTTCTGTGTCTACTACTATAGAAAAATTTAACTGACACTGGAAGTCCAGAAAAAGGA 676
QY 61 ThrserTyThrgluTyThrValLysArgThrTyAlaPheGlyGluLysHisAspAsn 80
Db 677 ACCAGTTATACCAGTACACAGTAAAGAACTTACGCTTTTGGAGAAAAACATGATAT 736
QY 81 CysThrThrsAsnSerSerThrsGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 737 TGATCAACCAATAGTTCTTACAGATGAATAATCGTGTGCTCTTTTCTCTTCCACAGA 796
QY 101 lIethrIleProAspAsnTyThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db 797 ATTAGCATCCAGATTAATTAATACATTGAGGTGAAGCTGAATAATGAGATGTGAATT 856
QY 121 LysSerHisMetThrTyThrPArgLeuGluAsnIleAlaLysThrgluProProLysIle 140
Db 857 AAATCTCATATGACATTAAGATTAAGAACTAAGAACTAAGAACTAAGAACTAAGATT 916
QY 141 PheArgValLysProValLeuGlyLysArgMetIleGlnIleGluTrpIleLysPro 160
Db 917 TTCGGTGAACCAAGTTTGGGCAATCAACCAATGATTCAATGATGAATAAGCTT 976
QY 161 GluLeuAlaProValLysSerSerAspLeuLysTyThrLeuArgPheArgThrValAsnSer 180
Db 977 GAGTTGGCGCTGTTCATCTGATTTAAATACACATTCGATTGAGGACACTCAACAGT 1036
QY 181 ThrserTrpMetGluValAsnPhelAlaLysAsnArgLysAspLysAsnGlnThrTyAsn 200
Db 1037 ACCAGCTGATGAGTCAACTTCCTGTAAGAACCGTAAGATAAAACCAACGTAACAAC 1096
QY 201 LeuThrglyLeuGlnProPheThrglyTyValIleAlaLeuArgCysAlaValLysGlu 220
Db 1097 CTCACGGGCTCAGACCTTTTACAGATATGTCATAGCTCTGCAATGTCGGTCAAGAG 1156
QY 221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrgluGluAlaPro 240
Db 1157 TCAAGTTCTGAGATGACTGAGCAACCAAAAAATGGGAATGACTGAGGAAAGACTCCA 1216
QY 241 CysGlyLeuGlnLeuTrpArgValleuLysProAlaGluAlaAspGlyArgArgProVal 260
Db 1217 TGTGGCTGGAACTGTGGAGATCTTGAACCAAGCTGAGCGGATGGAAGAGCCAGTG 1276
QY 261 ArgLeuLeuTrpLysLeuAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyAsn 280
Db 1277 CCGTTCTTATGAGAAAGCAAGAGAGGCCCAAGTCTTAGAATAAACCTTGGCTAACAAC 1336
QY 281 lIeTrpTyTyTyProGluSerAsnThrsAsnleuThrgluThrMetAsnThrThrsGln 300
Db 1337 ATATGCTACTATCCAGAAAGCAACATACTCACAGAAACATGAACTCTTAACCCAG 1396
QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyAsnSer 320
Db 1397 CAGCTTGAACCTCATCTGGGAGCGAGAGCTTTGGGTGTCTATGATTTCTTAATATTT 1456
QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
Db 1457 CTTGGGAATCTCCAGTGGCCACCTGAGAGATTCACAGTATTCAGAAAAACATTTGAG 1516
QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
Db 1517 TGCATTAAGATCATGACAGGCTGCGTGTCTGAGACACAGCTAGTGTGAAGTGGCAAGC 1576
QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db 1577 TCTGCTCTGAGAGGTGAACCTTGGATGATGATGATGATGATGATGATGATGATGATGATG 1636


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OY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrThrTrpTrpIleGlnGlnAspLys 400
DB 1637 ACCACCCTTCTCGGAATCTGTGTCTCAGGCCACAACTGACGATCCAGCAAGTTAA 1696
OY 401 LeuLysProPheTrpCysTrpAsnIleSerValTyrProMetLeuHisAspLysValGly 420
DB 1697 TTTAAACCTTTCTGGGTATTAACATCTGTGTATTCATATGTTCATGATGACAAAGTTGAC 1756
OY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluLysProGluThr 440
DB 1757 GAGCCATATTCATCCAGGCTTATGCAAGAAAGGCGCTCCATCAAAAGTCTCTGAGAC 1816
OY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluLysProLysSer 460
DB 1817 AAGGTGGAACATTCGCTGCGCTGAAGAGCTCAGCATCACTGAAAGAGTTCCCAAGACT 1876
OY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
DB 1877 GAGAGAAAGGTATCATCTGCAACATCAACCATCTTTTACCAAGCTGAAGTGAAAAAGGA 1936
OY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
DB 1937 TTCTCCAAACAGTCATTCATCCAGCATCTTGACAGTACGGCTGAGTCCCTGAAACGAAAG 1996
OY 501 ThrSerTyrIleValGlnValIleAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520
DB 1997 ACCTTACATTTGTCAGATCATGGCCAGCACCAAGTCTGGGGAACCAACGGAGCCAGC 2056
OY 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
DB 2057 ATTAATTCAGACATTCATTCATTCAGTCTTGAGATATATCTTCACTTACCTCTGAGAT 2116
OY 541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysProAsn 560
DB 2117 GGTGAGGCGCTTATTCATTCATTCATTCAGCAGAGTGCATGAGTCTCAAAAACCCAGC 2176
OY 561 LysLeuThrIleLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
DB 2177 AATGATCTCATCTGTGTGGCCACCGTTCCCAACCTGCTGAAAGTATGATAGCCACA 2236
OY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
DB 2237 TGGCATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATGATCTGTGAAC 2296
OY 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
DB 2297 ACAGAAAGCAGGATCTTAAACCATGTTCCACCCAGTACACAGTGTGGTGAATTGACAAAG 2356
OY 621 LeuValIleAsnPheGlyAsnValIleGlnGlnIlePheThrAspGluAlaArgThrGly 640
DB 2357 TTGGTGTGACCTTGGGAGATGTTCTGCAAGAAATTTTCCACAGATGAAGCCGAAACGGGT 2416
OY 641 GlnGluLysGlnPheArgArgGlyLysGluTyrAsp 652
DB 2417 CAGGA-AAACAATTTAGGAGGGGAAAGATGGAGC 2451

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; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2903
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497)...(2482)
US-10-351-157-4

Alignment Scores:
Pred. No.: 0 Length: 2903
Score: 3451.00 Matches: 650
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.05% Indels: 1
DB: 17 Gaps: 0

US-10-006-265-2 (1-652) x US-10-351-157-4 (1-2903)
OY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
DB 497 ATGAAGCTCTCCCAAGCTTCATGATGTAACCTGGGAGATGATGAACCTGGGACATG 556
OY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
DB 557 TGAATGCTCCCTTACCTGCAATTCAGCTGGGAGCTTCCAGCTTAAGCTGAGAAC 616
OY 41 IleSerCysValIleTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 617 ATTTCTGTGTCTACTACTATAGAAATAATTTAACTGCACTTGAGATGCCAGAAAGGA 676
OY 61 ThrSerTyrTrpGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
DB 677 ACCAGTTATACCAGTACACAGTTAAGAACTTAACGTTTGAAGAAACATGATATAT 736
OY 81 CysThrThrAsnSerSerThrSerGluAsnArgLaseCysSerPhePheLeuProArg 100
DB 737 TGTACAAACCAATAGTCTACAAAGTGAATAATGTCTCTCTTTTCTCTCCAAAG 796
OY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
DB 797 ATAACGATCCAGATTAATTAATTAACATGAGGTGAAGCTGAATAATGAGATGTAATT 856
OY 121 LysSerHisMetTrpTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
DB 857 AAATCTCATATGACATCTGAGATTAGAGAACTAGCAAAACTGAAACCACTTAAGATT 916
OY 141 PheArgValLysProValIleGlyIleLysArgMetIleGlnIleGluTyrIleLysPro 160
DB 917 TTCCTGTGAAACCAAGTTTGGGATCAAAAGATGATTCAAATTGAATGATTAAGCT 976
OY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB 977 GAGTTGGCGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGAGCAGTCAACAGT 1036
OY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrThrAsn 200
DB 1037 ACCAGCTGAGAGAAAGTCAACTTCGTAAGAACCGTAAGATTAATAACCAACCGTACAC 1096
OY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB 1097 CTCACGGGGGCTGACGCTTTTACGAATATGTCTACCTGCGATGTGCGGTCAAGAG 1156

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QY 221 SerIyPheTrpSerAspTrpSerGlnGluYmeGlyWetThrGlnGlnGlnAlaPro 240
Db 1157 TCAGAGCTTCGAGTGAAGTGAAGCAAGAAAAATGGGAATGACTGAGGAAGAAGCTCA 1216
QY 241 CysGlyLeuGlnLeuTrpArgValLeuLysProAlaGlnAlaAspGlyArgArgProVal 260
Db 1217 TGTGGCTGTGAACCTGGAGAGTCTGGAAACAGCTGAGGCGGATGGAGAAAGCCAGAG 1276
QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGlnLysTrpLeuGlyTrpAsn 280
Db 1277 CGGTGTATGAGAAAGAGCAAGAGAGCCCACTCTTAAGAAACACTTGGCTTCACAC 1336
QY 281 IleTrpTrpTrpProGluSerAsnTrpAsnLeuThrGluThrMetAsnThrTrpAsnGln 300
Db 1337 ATATGTAATCATCCAGAAAGCAACACTTAACCTCAAGAAACAAATGAACAATCAACCA 1396
QY 301 GlnLeuGlnLeuLysIleuGlyGlyGluSerPheTrpValSerMetIleSerTrpAsnSer 320
Db 1397 CACCTTGAACCTGCATCTGGAGAGCGAGAGCTTTGGGTGTCTATGATTTCTTATTAATTC 1456
QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlnLysSerPheGln 340
Db 1457 CTTGGGAAGTCTCCAGTGGCCAGGAGATTCAGCTATTCAGAAATAATCATTTCCAG 1516
QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
Db 1517 TGCATTGAGGTGATGCGAGGCGCTCGGTTGCTGAGAGCACAGCTAGTGGTGAAGTGGCAA 1576
QY 361 SerAlaLeuAspValAlaThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db 1577 TCTGCTCTGACCTGGAACACTTGATGATGATGAAATGGTTCCGATGTGGAGCTCAGAGCC 1636
QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
Db 1637 ACCACCTTTCTCGGAATGTGTCTCAGGCCACGAATCGACATCCAGCAAGATTAAT 1696
QY 401 LeuLysProPheTrpCysTrpAsnIleSerValTrpProMetLeuHisAspLysValGly 420
Db 1697 TTTAAACCTTTCTGGGTATTAACATCTGTGTATCAATGTTCATGATGACAAAGTTGG 1756
QY 421 GluProTrpSerIleGlnAlaTrpAlaLysGluGlyValProSerGluGlyProGluThr 440
Db 1757 GAGCCATATTCATCCAGGCTTATGCCAAAGAGGCTTCATCAGAGAGCTCTGAGACC 1816
QY 441 LysValGlnAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
Db 1817 AAGTGGAGAACCTTGGCTGAGAGCGGTACGATCAGATGAAAGAGATTTCCAAAGAGT 1876
QY 461 GluArgLysGlyIleIleCysAsnTrpTrpIlePheTrpGlnAlaGluGlyLysGly 480
Db 1877 GAGAGAAAGGTATCATCTGCACTACACATCTTTTACCAAGCTGAAGTGAAGAAAG 1936
QY 481 PheSerLeuThrValAsnSerSerIleLeuGlnTrpGlyLeuGlnSerLeuLysArgLys 500
Db 1937 TTCTCCAAAGCACTGATTCAGACATCTTGACATAGCGGCTTGAGATCCCTGAAACCAAG 1996
QY 501 ThrSerTrpIleValGlnValMetAlaAsnThrSerAlaGlyLysThrAsnGlyThrSer 520
Db 1997 ACCTTTTACCTTTTCAAGTACAGGACGACACAGAGTGGGGAACCAAGGGAACAG 2056
QY 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db 2057 ATAAATTTCAAGCATGTGATTCAGATGCTTTGAGATTAATCTCATTAATCTTCGATT 2116
QY 541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTrpGlyLeuLysLysProAsn 560
Db 2117 GGTGAGGCGCTTCTTATTCATTAATTCAGACAGTGGCATATGCTCTCAAAAAACCAAC 2176
QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db 2177 AATTTACATCATCTGATGAGCCACCGATTCCCAACCTGTGAAAGATGATAGCAACA 2236

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QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
Db 2237 TGGCATGAGATGATGATTTCAAGGATTAAGCTAACTGAAGAGTGTGATGATCTTGAAC 2296
QY 601 ThrGlnAspArgIleLeuLysProCysSerTrpProSerAspLysLeuValIleAspLys 620
Db 2297 ACAGAAAGACAGATCTTAAACCATGTTCCACCCCAAGACAGTGGTGTGATGCAAG 2356
QY 621 LeuValAlaAsnPheGlyAsnValLeuGlnGluIlePheThrAspGlnAlaArgTrpGly 640
Db 2357 TTGGTGTGTAACCTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAACCGAAGCGGT 2416
QY 641 GlnGluLysGlnPheArgArgGlyLysGluTrpAsp 652
Db 2417 CAGGA-AAACAATTTAGAGGGGAAAGAAATGGAC 2451

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RESULT 5

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US-10-352-554-4
; Sequence 4, Application US/10352554
; Publication No. US20030224487A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Novak, Julia E.
; APPLICANT: Grose, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND
; FILE REFERENCE: 02-01
; CURRENT APPLICATION NUMBER: US/10/352,554
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/375,323
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/435,315
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2903
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497) ... (2482)
; US-10-352-554-4

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Alignment Scores:

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Pred. No.: 0 Length: 2903
Score: 3451.00 Matches: 650
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 99.05% Indels: 1
DB: 17 Gaps: 0

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US-10-006-265-2 (1-652) x US-10-352-554-4 (1-2903)

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QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetTrpThrTrpAlaLeu 20
Db 497 ATGAAGCTCTCTCCCAAGCTTCATGTTGTTAACTGGGGATGATGAGACTGGGACACTG 556
QY 21 TrpMetLeuProSerLeuLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db 557 TGGATGCTCTCCCTTCACTGCAAAATTCAGCCCTGGAGGCTCTGCCAGCTTAAGCTTGA 616
QY 41 IleSerCysValTrpTrpTrpTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db 617 ATTTCTGTGCTACTACTATGAGAAATTTAACTGCACTTGAAGTCCAGGAAAGAA 676
QY 61 ThrSerTrpThrGlnTrpThrValLysArgThrTrpAlaPheGlyLysHisAspAsn 80

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Db 677 ACCAGTATACCAAGTACACAGTTAAGAACTTACGCTTTGGAGAAAACATGATAT 736
Qy 81 CysThrThrAsnSerSerThrsSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 737 TGTACMACCAATAGATTCTACAAAGTAAATCGTCGTGCTCTTTTCTTCCATCAAGA 796
Qy 101 IleThrIleProAspAsnThrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db 797 ATAAAGATCCAGATATATATACATGAGGTGAGAGCTGAAATGAGAGATGATTAAT 856
Qy 121 LysSerHisMetThrTyTrpArgLeuGluAsnIleAlaLysThrGluProGlySile 140
Db 857 AAATCTGATATGACATACTGGAGATTAGAGAACATAGGGAATAACCAACCTAAGATT 916
Qy 141 PheArgValLysProValLeuGlyLysLysArgMetIleGlnIleGluTrpIleLysPro 160
Db 917 TTCCTGTGAAACCGATTGCGCATCAACCAATGATTCAAATTGAATGGATTAAGCCT 976
Qy 161 GluLeuAlaProValSerSerAspLeuLysTyThrIleuArgPheArgThrValAsnSer 180
Db 977 GAGTTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGACAGTCAACGT 1036
Qy 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyAsn 200
Db 1037 ACCAGCTGGATGGAAGTCAACTGCTAAGAACCTTAAGATTAATAACCAACCTAAGAC 1096
Qy 201 LeuThrGlyLeuGlnProPheThrGluTrpValIleAlaLeuArgCysAlaValLysGlu 220
Db 1097 CTCACGGGGCTGACGCTTTTACAGAAATATGTCATAGCTGCGCATGCGGTCAGAG 1156
Qy 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
Db 1157 TCAAGATTCGAGAGTGAAGTGAAGCAAAAAAGGAAATGACTGAGAGAAAGACTCA 1216
Qy 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
Db 1217 TGTGGCCTGGAAGTGTGAGAGTCTCTGAACCAAGTGAAGCGGATGAAAGAGCAAGT 1276
Qy 261 ArgLeuLeuTrpLysLysAlaArgGlyValAProValLeuGluLysFthLeuGlyTyAsn 280
Db 1277 CGGTGTATGGAAGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1336
Qy 281 IleTrpTyTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
Db 1337 ATATGTAATCAATCAAGAAAGAACACTAACCTCAAGAAACAAATGAACACTAAGCAG 1396
Qy 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyTrpAsnSer 320
Db 1397 CAGCTTGAACCTGCACTGGAGAGGAGAGAGCTTTGGGTGTCTATGATTTCTTATATCT 1456
Qy 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
Db 1457 CTTGGGAAGTCTCCAGTGGCCACCTGAGATTCAGACTAATTCAGAAATAATCAATTCAG 1516
Qy 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
Db 1517 TGCATGTGGTCAATGAGAGCGTGGCTGCTGAGAGACCGATGATGATGAGGAAAGC 1576
Qy 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db 1577 TCTCTCTACAGACGTAACACTTGAATGATTAATGATTTCCGATGTGATCAGAGCC 1636
Qy 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGluAspLys 400
Db 1637 ACCACCCCTTCTCTGGATCTGTGTCTCAGGCCACAGACTGAGACGATCCACAGATTA 1696
Qy 401 LeuLysProPheTrpCysTyTrpAsnIleSerValTyTrpMetLeuHisAspLysValGly 420
Db 1697 TTAACACCTTCTCTGTCTATACACTCTCTGTATTCAAATGTTGCAAGAACAGAGTGGC 1756
Qy 421 GluProTySerIleGlnAlaTyTrpAlaLysGluGlyValProSerGluGlyProGluThr 440

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Db 1757 GAGCATATTCATCCAGACTTATGCCAAAGAGCGTTCATCAGAGTCTGAGACC 1816
Qy 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
Db 1817 AAGGTGAGAACATGGCGGTGAAGACGGTCAAGATCAATGATGAAGAAATTCACAAAGT 1876
Qy 461 GluArgLysGlyIleIleCysAsnTyThrIlePheTyTrpGlnAlaGluGlyValLysGly 480
Db 1877 GAGAGAAAGGTATCATCTGCACTACACCATCTTTTACCAAGCTGAAGGTGAGAAAG 1936
Qy 481 PheSerLysThrValAsnSerSerIleLeuGlnTrpGlyLeuGluSerLeuLysArgLys 500
Db 1937 TTCCTCAAGACAGTCAATTCAGCATCTTGAGTACGGCTGAGAGTCCCTGAAACGAAG 1996
Qy 501 ThrSerTyTrpIleValGlnValMetAlaAsnThrSerAlaGlyTyThrAsnGlyThrSer 520
Db 1997 ACCCTTCAATGTTGTCAGTATGATGCCAGCACCGTGTGGGGAACCAAGGAGCAGC 2056
Qy 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db 2057 ATAAATTTCAAGACATTTGCTCATTCAGTGTCTTTAGATTAATCTCATTAATCTCTGATT 2116
Qy 541 GlyGlyLeuLeuLeuIleIleLeuThrValAlaTyArgLysLeuLysProAsn 560
Db 2117 GGTGAGGCTTCTTATTTCTCATTCCTGACAGTGGCATGTGCTCAAAAAACCCAAAC 2176
Qy 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db 2177 AAATGACTCATCTGTGTGGCCACCGTTCACCAACCTGCTGAAAGTATATGCCCCA 2236
Qy 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
Db 2237 TGGCATGAGATGATTTTCAGAGATTAAGTAACTGAAAGAGTCTGATCTGTGAAAC 2236
Qy 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
Db 2297 ACAGAAAGCAGAGATCTTAAACCATGTTCCACCCCAAGTGAAGATGTGATGACAAAG 2356
Qy 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
Db 2357 TTGGTGTGAACTTTGGGAAGTGTCTCAAGAAATTTTTCACAGATGAAGCCAGAACGGT 2416
Qy 641 GlnGluLysGlnPheArgArgGlyLysGluTrpAsp 652
Db 2417 CAGCA-AAACATTTAGAGAGGGAAGAAATGGAGC 2451

RESULT 6
US-10-772-531-53
; Sequence 53, Application US/10772531
; Publication NO. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kujiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2903

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; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (497)...(2482)
 ; US-10-772-531-53

Alignment Scores:

Pred. No.:	0	Length:	2903
Score:	3451.00	Matches:	650
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.69%	Mismatches:	1
Query Match:	99.05%	Indels:	1
DB:	18	Gaps:	0

US-10-006-265-2 (1-652) x US-10-772-531-53 (1-2903)

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QY      1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetThrThrThrAlaLeu 20
DB      497 ATGAAGCTCTCTCCAGCCTTCATGTGTTAACTGGGGATGATGAGACCTGGCACTG 556
QY      21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
DB      557 TGGATCTCCCTTCACCTGCAAAATTCAGCTGGCAGCTTCGCACCTAAGCCTGAGAAC 616
QY      41 LLeSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB      617 ATTTCCTGTCTACTACTACTATAGAAAATTTAACTGCACCTTGGAGCTCAGAGAAAGAA 676
QY      61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
DB      677 ACCAGTTAATACCCAGATACACAGTTAAGAGAACTTAACGCTTTGGAAGAAACATGATTAAT 736
QY      81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB      737 TGTACACCAACAATGTTCTCAAGTGAAGAACTGTGCTTCCTTTTCCCTTCCAAAG 796
QY      101 LLeThrLLeProAspAsnTyrThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
DB      797 ATACACATCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 856
QY      121 LysSerHisMetThrTyrTrpArgLeuGluAsnLLeAlaLysThrGluProLysLLe 140
DB      857 AAATCTCATATGACATACATGAGATTAGAGAACATAGCGAAACCTGAACCACTTAAGATT 916
QY      141 PheArgValLysProAlaLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
DB      917 TTCGGTGTGAACCAAGTTTGGGCATCAACGAATGATTCAAAATTAATTAATTAATTAATTAAT 976
QY      161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB      977 GAGTTGGCGCTTTTCATCTGATTTTAAATACACACTTCGATTCAGAGACAGTCAACAGT 1036
QY      181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
DB      1037 ACCAGCTGATGAGTGAAGTCAACTTCGCTAAGAACCTTAAGATTAAGAAACCAACGTTCAAC 1096
QY      201 LeuThrGlyLeuGlnProPheThrGluTyrValLLeAlaLeuArgCysAlaValLysGlu 220
DB      1097 CTCACGGGGCTGACGCTTTTACAGAAATATGATCATAGCTTCGCAATGTGGGTCAGAGAG 1156
QY      221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
DB      1157 TCAAAGTTCTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1216
QY      241 CysGlyLeuGluLeuLeuTrpArgValLLeuLysProAlaGluAlaAspGlyArgArgProVal 260
DB      1217 TGTGGCTGGAACCTGTGAGAGATCTGTGAACCAAGCTGAGGCGGATGGAAGAACCAAGTGTG 1276
QY      261 ArgLeuLeuLeuTrpLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
DB      1277 CGGTTGTATTAGAAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1336
  
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QY      281 LLeTrpTyrTyrProGlnSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
DB      1337 ATATGGTACTATCCAGAAAGCAACTAATCTCACAGAAACATGAACACTAATCAACAG 1396
QY      301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLLeSerTyrAsnSer 320
DB      1397 CAGCTTGACCTCATCTGGGAGGCGAGAGCTTTGGGTGTATGATTTCTTAATAATTTCT 1456
QY      321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
DB      1457 CTTGGAGATCTCCAGTGGCCACCTTGAGATTTCCAGCTATTCAGAAAAATCATTTCCAG 1516
QY      341 CysLLeGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSer 360
DB      1517 TCATATTGAGTATGAGGCTGCGGTGTGAGGACCAACTAGTGGTGAAGTGGCAAGC 1576
QY      361 SerAlaLeuAspValAsnThrTrpMetLLeGluTrpPheProAspValAspSerGluPro 380
DB      1577 TCTGCTCTAGAGGTGAACCTTGAGATGATTAATGATTTCCGATGTGAGCTCAGAGCCC 1636
QY      381 ThrThrLeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrLLeGlnLLeAspLys 400
DB      1637 ACCACCTTTCTCGGAGATCTGTCTCAGGCCACAGAACCTGAACATCCAGCAAGATAAA 1696
QY      401 LeuLysProPheTrpCysTyrAsnLLeSerValTyrPrometLeuHisAspLysValGly 420
DB      1697 TTAAACCTTTCTGGGTGATTAACATCTGTGTATCCAACTTGATGATGACAAAGTTGGC 1756
QY      421 GluProTyrSerLLeGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
DB      1757 GAGCATATTCCATCCAGGCTTATGCAAGAGGCGTTCATCGAAGGCTCCTGAGACC 1816
QY      441 LysValAlaAsnLLeGlyValLysThrValThrLLeThrTrpLysGluLLeProLysSer 460
DB      1817 AAGGTGGAACAATTTGGCTGTGAAGACGTACAGATCACTGAAAGAGATTTCCAGAGAT 1876
QY      461 GluArgLysGlyLLeLLeCysAsnTyrThrLLePheTyrGlnAlaGluGlyLysGly 480
DB      1877 GAGAGAAAGGTATATCATCTGCAATACACACTTTTACCAAGCTGAAGTGAAGAAAGGA 1936
QY      481 PheSerLysThrValAsnSerSerLLeLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
DB      1937 TTCTCCAGACAGTCAATTCAGACATCTTGACGTACGCGCTGAGAGCTCTGAAGCAAAAG 1996
QY      501 ThrSerTyrLLeValGlnValMetAlaAsnThrSerAlaGlyGlyThrAsnGlyThrSer 520
DB      1997 ACCTTTAATTTGTCAGGTCAATGGCCACACAGTCTGGGGGAACCAACGGACCAAG 2056
QY      521 LLeAsnPheLysThrLeuSerPheSerValPheGluLLeLLeuLLeThrSerLeuLLe 540
DB      2057 ATTAATTTCAAGACATTTGTCATTTCAAGTGTCTTGAAGATTATCTCTAATCTTCTGATTT 2116
QY      541 GlyGlyGlyLeuLeuLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLeLLe 560
DB      2117 GGTGAGGCGCTTATTTCTCATTAATCTCGACAGTGGCATATGATCTCAAAAAACCAAC 2176
QY      561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerLLeAlaThr 580
DB      2177 AATTTGATCTCATCTGTGTGGCCACCGTTCCCAACCTGCTGAAGATGATTAAGCAACA 2236
QY      581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluLysAspAspSerValAsn 600
DB      2237 TGGCATTGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGATGATGATCTGTGAAAC 2296
QY      601 ThrGluAspArgLLeLLeLysProCysSerThrProSerAspLysLeuValLLeAspLys 620
DB      2297 ACAGAAAGACAGATCTTAATAACATGTTCCACCCAGAGCAAGTAAGTGTGATTTGCAAG 2356
QY      621 LeuValValAsnPheGlyAsnValLeuGlnGluLLePheThrAspGluAlaArgThrGly 640
DB      2357 TTGGTGTGAACCTTGGGATGTCTGCAAGAAATTTTACAGATGAAGCCAGAACGGGT 2416
QY      641 GlnGluLysGlnPheArgArgLysGluTrpAsp 652
  
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Db      2417 CAGCA-AAACATTTAGGAGGGGAAAAAGATGGGAC 2451
RESULT 7
US-09-892-949-45
; Sequence 45, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Premeil, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kujioper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(2108)
; US-09-892-949-45

Alignment Scores:
Pred. No.: 0 Length: 2529
Score: 3441.00 Matches: 648
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 98.77% Indels: 1
Gaps: 0

US-10-006-265-2 (1-652) x US-09-892-949-45 (1-2529)
QY      3 LeuserProgluInProSerCyValaAsnLeuGlyMetMetTrpThrTyrAlaLeuTrpMet 22
Db      129 CTCTCTCCCGAGCCTTCATGTGTTAACTGGGGATGATGTGACCTGGGCACTGTGGATG 188
QY      23 LeuProSerLeuCyValaPheSerLeuAlaAlaLeuProAlaLysProGluAsnLeuSer 42
Db      189 CTCCCTCACTCTGCAAAATTCAGCTGGAGCTCTGCCAGCTAAACCTGAGAACTTTCC 248
QY      43 CyValaTyrTyrTyrValaLysAsnLeuThrCyThrTrpSerProGlyLysGluThrSer 62
Db      249 TGTGCTACTACTATAGGAAAAATTAACTGCACTTGGAGTCCCGAAAGAAACCACT 308
QY      63 TyrThrGlnTyrThrValaLysArgThrTyrAlaPheGlyGluLysHisAspAsnCyThr 82
Db      309 TATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATTAATTGTCA 368
QY      83 ThrAsnSerSerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgLleThr 102
Db      369 ACCAATAGTCTACAAAGTAAATGCTGCTGCTCTTTTCTTCCAAAGAAATACG 428
QY      103 IleProAspAsnTyrThrIleGluValaGluAlaGluAsnGlyAspGlyValIleLysSer 122
Db      429 ATCCCAAGTAAATTAACCATTTGAGGTGAGCTGAAAAATGAGATGCTTAATTAACT 488
QY      123 HisMetThrTyrTrpArgLeuGluAsnLeuAlaLysThrGluProProLysIlePheArg 142
Db      489 CATATGACATACTGAGATTAAGAAACATAGGAAAACTGAACCACTTAAGATTTCCGT 548

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QY      143 ValLysProValaLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
Db      549 GTGAACCAAGTTTGGGATCAAAAGATGATTCAAATTGATTAAGATTAAGCTGAGTTG 608
QY      163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValaAsnSerThrSer 182
Db      609 GCGCTGTTTATCTGATTTAAATACACACTGATTCAGAGACAGTCAACAGTCCAGC 668
QY      183 TrpMetGluValaAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
Db      669 TGGATGAAGTCAACTTGTCTAAGAACCGTTAAGATTAACAAACCTTAACTCAAG 728
QY      203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCyValaValLysGlySerLys 222
Db      729 GGGCTGCGACCTTTTACGAATATGTCATACCTCTGCGATGTGGCTCAGAGATCAAG 788
QY      223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242
Db      789 TTCTGAGTGA CTGGAGCCAAAGAAAAATGGGAATGACTGAGGAAGAGCTCCATGTGCG 848
QY      243 LeuGluLeuTrpArgValaLeuLysProAlaGluAlaAspGlyArgArgProValaArgLeu 262
Db      849 CTGGAACGTGTGAGAGTCTCTGAACCAAGCTGAGCGGATGGAAGAGCCAGTGGGTG 908
QY      263 LeuTrpLysLysAlaArgGlyAlaProValaLeuGluLysThrLeuGlyTyrAsnIleTrp 282
Db      909 TTATGAAGAGAGGCAAGAGAGCCCGACCTCTAAGAAACACTGGCTTACAACTATAGG 968
QY      283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnLeu 302
Db      969 TACTATCCAGAAACACACACTACCTCACAAGAAACATGAACACTACACAGAGCTT 1028
QY      303 GluLeuHisLeuGlyGlyGlySerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
Db      1029 GAACGTGCACTGTGGAGGCGAGGAGCTTTTGGGTGTCATGATTTCTTAAATCTCTTGGG 1088
QY      323 LysSerProValaIleThrLeuArgIleProAlaIleGlnGluLysSerPheGluCysIle 342
Db      1089 AAGTCTCCAGTGGCCACCTGAGGATTCACACTTTCAGAAAAATCATTTCAAGTGCATT 1148
QY      343 GluValMetGlnAlaCyValaAlaGluAspGlnLeuValaLysTrpGlnSerSerAla 362
Db      1149 GAGGTCATGCAAGGCTGGGTGCTGAGAGACCAAGCTAAGGTGAAGTGGCAAGCTCTGCT 1208
QY      363 LeuAspValaAsnThrTrpMetIleGluTrpPheProAspValaAspSerGluProThr 382
Db      1209 CTAAACGTGAACACCTTGATGATTAAGATGTTTCCGATGTGAGTCAAGCCCAACACC 1268
QY      383 LeuSerTrpGluSerValaSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeuLys 402
Db      1269 CTTTCTGAGAAATGTGTCTCAGGCCACGAACGTGACGATCCAGCAAGATTAATAA 1328
QY      403 ProPheTrpCyTyrAsnIleSerValTyrPheMetLeuHisAspLysValaGlyLysPro 422
Db      1329 CTTTCTGAGTCTAATCACTCTGTGTATCCATGTTGCATGACAAAGTTGGGAGGCA 1388
QY      423 TyrSerIleGlnAlaTyrAlaLysGlyValaProSerGluGlyProGluThrLysVal 442
Db      1389 TATTCCATCCAGGCTTATGCCAAAGAGGCTTCCATCAGAAAGCTCTGAGAACCAAGGTG 1448
QY      443 GluAsnIleGlyValaLysThrValaThrIleThrTrpLysGluIleProLysSerGluArg 462
Db      1449 GAGAACATGTGCGTGAAGACGCTACCATCACTGAAAGAGATTTCCACAGAGTGAAGA 1508
QY      463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
Db      1509 AAGGATTAATCTCACAATCACTACCATCTTTTACCAACACTGAAGTGAAGAAATTTCTCC 1568
QY      483 LysThrValaAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer 502
Db      1569 AAGACAGTCAATTCACACATCTTGCAATGAGGCTGAGAGTCCCTGAAGCAAAAGACCTCT 1628
QY      503 TyrIleValaGlnValMetAlaAsnThrSerAlaGlyGlyLysThrAsnGlyThrSerIleAsn 522

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Db 1629 TACATGTTGAGTCATGAGCCACACAGTGCTGGGGGAAACCAACGGACACGACATTAAT 1688
Qy 523 PhyleThreusSerPheSerValPheGluIleIleuIleThreSerIleuIleGly 542
Db 1689 TTCAGACATGTCATTCATGACGTGCTTGAGATTATCTCTTAATCTTGATTTGGGA 1748
Qy 543 GtyleuIleuIleuIleIleuThrValAlaTyrGlyLeuIleuIleProAsnIleu 562
Db 1749 GGGCTTCTTATTTCTCATTTATCCGACAGTGGCATATGTTCAAAAAACCAAAATTC 1808
Qy 563 ThreIleuCystrpProthrValProAsnProAlaGluSerIleAlaThrTrpHis 582
Db 1809 ACTCATGTGTGTGGCCACCGTTCCCAACCTGTGAAGTAGTATGACCATGGCAT 1868
Qy 583 GtyleuAspPheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 602
Db 1869 GGAAGATGATTCAAGAGTAAGCTAAACCTGAAGAGTGTGATGATCTTGAAACAGAA 1928
Qy 603 AspArgIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 622
Db 1929 GACAGATCTTAAACATTTCCACCCACGACAGCAAGTTGATGACCAAGTTGGTG 1988
Qy 623 ValAsnPheGlyAsnValIleuGluIleuIleuIleuIleuIleuIleuIleu 642
Db 1989 GTGAACCTTGGGATGTTCTGCAAGAAATTTTCACAGATGAAACCGAGGTCAGAA- 2047
Qy 643 LysGlnPheArgArgGlyIleuIleuIleuIleuIleuIleuIleuIleuIleu 652
Db 2048 AAACAATTAGAGGAGGAAAGATGGAC 2077

RESULT 8

US-10-351-157-108
; Sequence 108, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kuljber, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PaacSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(2108)
US-10-351-157-108

Alignment Scores:

Pred. No.: 0
Score: 3441.00
Percent Similarity: 99.85%
Best Local Similarity: 99.69%

Length: 2529
Matches: 648
Conservative: 1
Mismatch: 1

Query Match: 98.77% Indels: 1
DB: 17 Gaps: 0
US-10-006-265-2 (1-652) x US-10-351-157-108 (1-2529)

Qy 3 LeuSerProGlnProSerCysValAsnIleuGlyMetMetTrpThrAlaLeuTrpMet 22
Db 129 CTCCTCCCCACGCTTCATGTTAACTGGGAGATGATGAGCCTGGGACCTGGAGG 188
Qy 23 LeuProSerLeuCylysePheSerIleuAlaIleuProAlaIleuProGluAsnIleSer 42
Db 189 CTCCTCCCTGCAATTCAGCTGCGAGCTGCGACGCTGAGCTGAGAACATTTCC 248
Qy 43 CysValTyrTyrTyrArgIleuIleuIleuIleuIleuIleuIleuIleuIleu 62
Db 249 TGTGTCTACTATATGAGAAATTTAACTCTGACCTGGAGTCCAGAAAGAACACT 308
Qy 63 TyrThrGlnTyrThrValIleuIleuIleuIleuIleuIleuIleuIleuIleu 82
Db 309 TATACCACTACACAGTTAAAGAACTTACGCTTTTGGAGAAACATGATATTGTACA 368
Qy 83 ThrAsnSerThrSerGluAsnArgIleuIleuIleuIleuIleuIleuIleuIleu 102
Db 369 ACCAATAGTTTCAAGTAAGTAAGTGTGCTGCTCTTTTCTTCCAGAAATTAAG 428
Qy 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleuIleu 122
Db 429 ATCCCAAGATTAATTAATCACTGAGGTGAGAGTGAAGTGAAGTGAAGTGAAGTGA 488
Qy 123 HisMetThrTyrTrpArgLeuGluAsnIleuIleuIleuIleuIleuIleuIleu 142
Db 489 CATATGACATCTGAGATTAAGAACTAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 548
Qy 143 ValIleuProValIleuGlyIleuIleuIleuIleuIleuIleuIleuIleuIleu 162
Db 549 GTGAACCGATTTGGGATTCAGAAAGATGATTAATTAAGTGAAGTGAAGTGAAGTGA 608
Qy 163 AlaProValSerSerAspLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 182
Db 609 GGGCTGTTTCAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 668
Qy 183 TrpMetGluValAsnPheAlaIleuIleuIleuIleuIleuIleuIleuIleuIleu 202
Db 669 TCGATGGAAGTCAACTCTCTTAAGAACCTTAAGAACTTAAGAACTTAAGAACTTA 728
Qy 203 GtyleuGlnProPheThrGluIleuIleuIleuIleuIleuIleuIleuIleuIleu 222
Db 729 GGGCTGCAAGCTTTTACAGAAATGTCATAGCTCTGCGATGTCGCTCAAGAGTCAAG 788
Qy 223 PheTrpSerAspTrpSerGlnIleuIleuIleuIleuIleuIleuIleuIleuIleu 242
Db 789 TTCTGAGAGTCTGAGAGCCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTCAAGT 848
Qy 243 LeuGluLeuTrpArgValIleuIleuIleuIleuIleuIleuIleuIleuIleu 262
Db 849 CTGGAACCTGAGAGTCTGTAAGAACAGCTGAGGCGAGTGAAGAGGCACTGCGCTTG 908
Qy 263 LeuTrpIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 282
Db 909 TTATGGAAGAGCAGAGAGAGCCCAAGTCTTGAAGAAACCTTGGCTACAAACATATG 968
Qy 283 TyrTyrProGluSerAsnThrAsnIleuIleuIleuIleuIleuIleuIleuIleu 302
Db 969 TACTATCCAGAAAGCACTAACTCAGAGAAACATGAACATCACTAACAGCAGCTT 1028
Qy 303 GtyleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 322
Db 1029 GAACCTGATCTGGAGAGCGAGAGCTTTGGGTGTCTATGATTTCTTAATTTCTTGGG 1088
Qy 323 LysSerProValAlaThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 342
Db 1089 AAGTCTCCAGTGCCACCTGAGATTCAGGCTATTCAAGAAATCAATTTCAAGTCAAT 1148

QY	343	GUUValMeGAlAICyValAlaGluAaPBGlnLeuValValLytrpGlnSerIle	362
Db	1149	GAGGTCATGCAAGCCCTCGCTCTGAGAACCAAGCTAAGTGTAAAGTGGCAAGCTCGCT	1206
QY	363	LeuAaPValAaenThrTrpMetIleGluTrpPheProAaPValAaPSeGluProThrThr	382
Db	1209	CTAAGACGTGAACACTTGATGATTAAGTTGTTCCGGAATGTGAGCTCAGAGCCCAACCC	1266
QY	383	LeuSerTrpGluSerValSerGlnAlaThrAenTrpThrIleGlnGlnAaPlyLeuLyv	402
Db	1269	CTTTCCTGGGAATCTGTGCTCTCAGGCCACGAATCGAGCATCACCAAGATTAATTAA	1326
QY	403	ProphetrPyCyTyAaenIleSerValTyrrPomeIleuHlaAaPlyValGlyGluPro	422
Db	1329	CTTTCCTGGTGTAAACACTCTGTGTATCCAAAGTTGCATGACAAAGTTGGCAAGCCA	1386
QY	423	TyrSerIleGlnAlaTyrrAlaLyvGluGlyValProSerGluGlyProGluThrTyrrVal	442
Db	1389	TATTCATCTCAGGCTTATGCTCCAAABAAGCGTTCCATCAGAAAGCTCTGAGCCAAAGTG	1446
QY	443	GluAaenIleGlyValLyvThyrrValThrIleThrTrpLyvGluIleProLyvSerGluArg	462
Db	1449	GAGAACATTTGGCGGTGAAGACGGCTCAAGATCATGAGAAAGAAATCCCAAGTGAAGGA	1506
QY	463	LyvGlyIleIleCyAaenTyrrThrIlePheTyrrGlnAlaGluGlyLyvGlySer	482
Db	1509	AAGGGTATCATCTGCAACCTACACCAATCTTTTACCAAGCTGAAGGATGGAAGAAATTCCTC	1566
QY	483	LyvThrValAaenSerSerIleGluGlnTyrrGlyLeuGluSerLeuLyvArgLyvThrSer	502
Db	1569	AAGACAGTCATTCACAGCATCTTGAGAGTACGGCTCGAGTCCCTTAACGAAAGCCCTCT	1622
QY	503	TyrIleValGlnValMeAlaAaenThrSerAlaGlyIleGlyThyrrAaenGlyThrSerIleAa	522
Db	1629	TACATTTGTTCAAGTCATGCGCAGCACACAGTGTGGGGGAACCAACGGGACCATTAAT	1686
QY	523	PheLyvThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly	542
Db	1669	TTCAAGACATTTGTCATTCAGTGTCTTTAGATTATCTCATTAACCTTCTGATTTGTGGA	1748
QY	543	GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrrGlyLeuLyvLevProAaenLyvLeu	562
Db	1749	GGCCTTCTTATTTCTATTAATCTCTGACAGTGGCATATGCTTCACAAACCCCAACAAATTG	1806
QY	563	ThrIleLeuCyStrTrpProThrValProAaenProAlaGluSerSerIleAlaThrTrpHis	582
Db	1809	ACTCATCTGTGTGGCCCAACCGTTCCCAACCTGCTGAAGATGATAGTACCATAGCAT	1866
QY	583	GlyAaPaaPheLyvAaPlyLeuAaenLeuLyvGluSerAaPaaPaaPaaSerValAaenThrGlu	602
Db	1869	GGAGATGATTTCAAGGATTAAGCTTAACCTGAAGAGGTCTGATGACTCTGTGAACACAGAA	1928
QY	603	AaPaaGlyIleLeuLyvProCySerThrProSerAaPlyAaLeuValIleAaPlyLeuVal	622
Db	1929	GACAGGATCTTAAACATGTTCCACCCCAAGTCACAAAGTGATTAAGCAAGTTGCTG	1988
QY	623	ValAaenPheGlyAaenValLeuGlnGluIlePheThrAaPgluAlaArgThrGlyGlnGlu	642
Db	1989	GTGAACCTTTGGGAAGTTCTCTCAAGAAATTTTCCACAGATGAAGCAGAACGGGTACAGA	2047
QY	643	LyvGlnPheArgArgGlyLyvGluTrpAaP	652
Db	2048	AAACCAATTTAGAGGGAAGAAAGATGGAGC	2077
RESULT 9			
US-10-772-531-45			
; Sequence 45, Application US/10772531			
; Publication No. US20040142422A1			
; GENERAL INFORMATION:			
; APPLICANT: Sprecher, Cindy A.			
; APPLICANT: Preenell, Scott R.			
; APPLICANT: Geo. Zeren			
; APPLICANT: Whitmore, Theodore E.			

	:	APPLICANT:	Kuijper, Joseph L.		
	:	TITLE OF INVENTION:	CYTOKINE RECEPTOR ZCYTOR17		
	:	FILE REFERENCE:	00-42		
	:	CURRENT APPLICATION NUMBER:	US/10/772,531		
	:	CURRENT FILING DATE:	2004-02-05		
	:	PRIOR APPLICATION NUMBER:	US/09/992,949		
	:	PRIOR FILING DATE:	2001-06-26		
	:	PRIOR APPLICATION NUMBER:	US 60/214,282		
	:	PRIOR FILING DATE:	2000-06-26		
	:	PRIOR APPLICATION NUMBER:	US 60/214,955		
	:	PRIOR FILING DATE:	2000-06-29		
	:	PRIOR APPLICATION NUMBER:	US 60/267,963		
	:	PRIOR FILING DATE:	2001-08-02		
	:	NUMBER OF SEQ ID NOS:	93		
	:	SOFTWARE:	FastSeq for Windows Version 3.0		
	:	SEQ ID NO	45		
	:	LENGTH:	2529		
	:	TYPE:	DNA		
	:	ORGANISM:	Homo sapiens		
	:	FEATURE:			
	:	NAME/KEY:	CDS		
	:	LOCATION:	(162) ... (2108)		
	:	US-10-772-531-45			
		Alignment Scores:			
		Pred. No.:	0	Length:	2529
		Percent Similarity:	3441.00	Matches:	648
		Best local Similarity:	99.85%	Conservative:	1
		Query Match:	98.69%	Mismatches:	1
			Indels:	Gaps:	0
			DB:		
		US-10-006-265-2 (1-652) x US-10-772-531-45 (1-2529)			
Oy	3	LeuSerProGlnProSerCysValAsnLeuGlyMetLTrpThrTyrAlaLeuTrpMet	22		
Db	129	CTCTCCGCCAGCTTCATGTATTAACTGGGGATGATGTACCTGGCATCTGTGATG	188		
Oy	23	LeuProSerLeuCylsPheSerLeuAlaIleuProAlaIysProGluAsnIleSer	42		
Db	189	CTCCCTCACTCGCAAATTCAGCTGCAGACTGCGCAGTTAAGCTTGGAACATTTCC	248		
Oy	43	CysValIYrTYrTYrArgLyAsnLeuThrcYsrHrTPSsrProGlyLYvGLUthrSer	62		
Db	249	TGtGTcTAActATArTAgAAAAATTTAACCTGCACtttgaaGTccagaaaaggaaaccagt	308		
Oy	63	TyrThrGlntYrThrVallYeaRgThrTyrrAlaPheGlyGLULysHIIsApAsnCystr	82		
Db	309	TATAACCAGATACACAGTTTAGAGAATTAACTTCTTGGAGAAAACAATGATTATGTACA	368		
Oy	83	ThrAsnSerSerThserGluasnArGlaSerCysSerPhePheLeuProArgIleThr	102		
Db	369	ACCAATATGTTCTACACATGCAAAATGTGTCTTCCTTTTTTCTTCCACAGATAACG	428		
Oy	103	IleProASPasnTYrThrIIegLUvalGluNagiubnsngIyaSPglYvalIIelySer	122		
Db	429	ATCCAGATATAATTAADCACTTGAGGTGAAGCTGAAAATGAGATGGGTATTAATCT	488		
Oy	123	HisMetThrTYrTriPrArgLeuGluAsnIIealALysThrgLuPProPolYsIIepheaRg	142		
Db	489	CARNTACACTACGTGGAGATTAGANGAACATACGAAACTGAACCACTTAAGATTTCCGT	548		
Oy	143	ValIysProValLeuGIYILeysaRgmEtllegInileguTRPIelYsProGluLeu	162		
Db	549	GTGAAACCACTTTTGCGCATCAACAGAAATGATTCAATTTGAATGATAAGACTCGAATTG	608		
Oy	163	AlaProValSerSerAspleuLYsTYrThreuaRgPheaRgThrValJaenSerThSer	182		
Db	609	GGCGCTGTTTCACTGATTATAATAACACACTTGATTCAGGACAGCCAAGAACAGC	668		
Oy	183	TrpMetGluValasnPheAlalyseAnRglysaBplysAnglIntHYrAsnLeuThr	202		

Db 669 TGGATGGAAGTCACTTCGCTTAAGAACCGTAAAGATTAATAAACCAAGTACACCTCAAG 728
Qy 203 GYLeuGlnProPherThrGluTyrValIleAlaLeuArgCysAlaValLysGlnSerLys 222
Db 729 GGAGCTCAGGCTTTTACAGAAATATGTCATATGCTCTGGAGATCGGTCAAGGAGTCAAG 788
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGlnGlnGluAlaProCysGly 242
Db 789 TTCGTGAGTGACTGAGGCGCAAGAAAAAATGGAAATGATCGAGAGAGAGCTCATGTGGC 848
Qy 243 LeuGlnLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValAlaGlu 262
Db 849 CTGGAACTGGGAGAGTCTCGAAACCAAGCTGAGCGGATGGAAAGAGCGCAGCGGTG 908
Qy 263 LeuTrpLysLeuValaArgGlyAlaProValLeuGlnLysThrLeuGlnLysThrAsnIleTrp 282
Db 909 TTTTGAAGAGGCGAAGAGAGGCCCAAGTCTTAGAGAAACACTGGCTTCAACATATGG 968
Qy 283 TyrTrpProGlnSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
Db 969 TACTATCCAGAAAGCAACACTAATCTCAAGAAACATGAACACTAATCAACGACGCTT 1028
Qy 303 GlnLeuHisLeuGlnGlyGlnSerPheTrpValSerMetLysSerTrpAsnSerLeuGly 322
Db 1029 GAACCTCATCTGGAGAGCGAGACCTTTGGTGTCATATGATTTCTTATATCTCTTGGG 1088
Qy 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGlnLysSerPheGlnCysGly 342
Db 1089 AAGCTCTCAGATGGCCACCTGAGAGATTCAGCTATTCAGAAAAATCATTTCACTGTCAT 1148
Qy 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSerSerAla 362
Db 1149 GAGGTATGAGGCGCTGCGTTGTCGAGACCACTAGTGTGAAGTGGCAAACTCTGCT 1208
Qy 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 382
Db 1209 CTAGAGCTGAACCTTGAGATGATGAATGTTCCGATGTGCACTCAGAGCCACACACC 1268
Qy 383 LeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
Db 1269 CTTTCTGGGAATCTGTCTCAGGCCACGACCTGACGATCCAGCAAGATTAATTAATA 1328
Qy 403 ProPheTrpCysTrpAsnLysSerValTyrProMetLeuHisAspLysValGlyGluPro 422
Db 1329 CTTTCTGGGCTATTAACATCTGTGTATCCAAATGTGATGACAAAGTTGGCGAGCCA 1388
Qy 423 TyrSerIleGlnAlaTyrAlaLysGlnGlyValProSerGlnGluLysProGluThrLysVal 442
Db 1389 TATTTTCATCCAGGCTTATGCGAAAGAGCGTTCATCGAAGAGCTCTGAGACCAAGGTG 1448
Qy 443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGlnIleProLysSerGluArg 462
Db 1449 GAGAACATTTGGCTGAAGACGTCACGATCACAATGAAAGATTCCTCAAGATGAGAGA 1508
Qy 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
Db 1509 AAGGATATCATCTGCACTACACCACTTTTACCAAGCTGAAGTGAAGAAAGATTTCTCC 1568
Qy 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer 502
Db 1569 AAGACAGTCAATTCAGCATCTTGACGTACGGCTCGAAGTCCCTGAAACCAAAAGACCTCT 1628
Qy 503 TyrIleValGlnAlaMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSerIleAsn 522
Db 1629 TATATGTTCAAGTCACTGAGCAGACCAAGTCTGGGGGAAACCAAGGACCAACATTAAT 1688
Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
Db 1689 TTCAAGGCATGTGCATTCAGTGTCTTTGAGATTATCTCTTAATCTCTCGATTTGGTGA 1748
Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
Db 1749 GGCTCTTATTTCTCATTTATCTGACAGTGGCATATGTTCTCAAAAAACCAACAATTTG 1808

Qy 563 ThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrpHis 582
Db 1809 ACTCATCTGTCTTGGCCCACTTCCCAACCTTGTGAAAGATATACCAATGCGCAT 1868
Qy 583 GlyAspAspPheLysAspLysLeuAsnLeuLysGlnSerAspAspSerValAsnThrGlu 602
Db 1869 GGAGATGATTTCAAGATTAAGTAAACCTGAAGGAGTGTGATGACTGTGTGAACAGAA 1928
Qy 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db 1929 GACAGATCTTAAACCATGTTCCACCCCACTGACCAAGTTGTGATTCACAAATTGGTG 1988
Qy 623 ValAsnPheGlyAsnValLeuGlnGlnIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db 1989 GTGAACCTTGGAAATGTTTGTGCAAGAAATTTTCAACGATGAAGCCAGAACGGGTACGA 2047
Qy 643 LysGlnPheArgArgGlyLysGluTrpAsp 652
Db 2048 AAACAATTTAGAGGGGAAAGAAATGGAGC 2077

RESULT 10
US-09-972-708-5
; Sequence 5, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRL AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-5

Alignment Scores:
Pred. No.: 0 Length: 2238
Score: 3435.00 Matches: 647
Percent Similarity: 99.69% Conservative: 2
Best Local Similarity: 99.39% Mismatches: 1
Query Match: 98.59% Indels: 1
DB: 10 Gaps: 0

US-10-006-265-2 (1-652) x US-09-972-708-5 (1-2238)

Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db 1 AAGAAGCTCTCCGCCAGCTTCATGTGTAACTGGGAGATATGAGACCTGGGACACTG 60
Qy 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
Db 61 TGGATGCTCCCTTCACTCTGCAAAATTCAGCCCTGGAGAGCTCTGCCAGTAAAGCTTGAAGAC 120
Qy 41 HisSerCysValTyrTyrTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db 121 ATTTCTGTGTACTACTATAGAAAAATTTAAACCTGACCTTGAAGTCCAGAAAAAGGAA 180
Qy 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn 80
Db 181 ACCAGTTAACCAACAGTACACATTAAGAGAACTTAAGCTTTTGAAGAAAAACATGATAAT 240
Qy 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 241 TGTACAAACAATAGTTCTCAAGTGAAGAAATCGTGTCTGTCTTTTCCCTTCCAAAGA 300

QY 11ethrileproaspasntyrthrilegluvalagluasnglvnapglvalille 120
 Db 301 ATAAAGATCCCGAATATATATACCATTTAGGTGAGAACTGAAATGGAATGATGTAAAT 360
 QY 121 lysserhiametthrtprargleugluasnilealalyethrgluprobolyale 140
 Db 361 AAATCTCATATGACATCTGAGATTAAGAACATAGCGAAACTGACACTTAAGATT 420
 QY 141 pheargvallvprovalleuglyilelysarqmetileglnileglutrpillelyapro 160
 Db 421 TTCCTGTGTAACCAAGTTTGGGCATCAAAACGAATGATTCAATGAAATGATTAAGCCT 480
 QY 161 gluvalaprovalseraserasplesuerythrileuargpheargrthralanser 180
 Db 481 GAGTTGGGCGCTGTTCATCTGATTTAAATACACCTTCGATTCAGACGACGTCAACGT 540
 QY 181 thrsertprmetgluvalasnphelialysasnarqlyasaplyasnglnthrtprasn 200
 Db 541 ACCACCTGGATGGAAAGTCAACTTCCTTAAGAACCGTAAGATRAAAACCAACCGTAAC 600
 QY 201 leuthrglyleuglnprophethrglutyryvalilealaleuargcyaalavallysglu 220
 Db 601 CTCACGGGGCTGCACCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAGGAG 660
 QY 221 serlyspheprseraspthrserglngluysmetglvmetthrglulgluvalapro 240
 Db 661 TCAAAAGTTCTGAGATGACCTGAGCCAGCAAGAAATAGGAGATGACGAGAGAAACCTCCA 720
 QY 241 cyseglyleuglnleuthrpargvalleuysproalaglualaaspglvargrproval 260
 Db 721 TGTGCTCTGGAACTGTGAGAGCTCTGAACAACGCTGAGCGGATGGAAGAGCCAGTG 780
 QY 261 argleuleuthrplysalyaalarglyalaprovalleuglnlyethrleuglytyrarn 280
 Db 781 CGGTGTATATGAGAAAGCAAGAGAGAGGCCAGCTCTAGAGAAACACTTGGCTACAC 840
 QY 281 illetprtyrtyrprgluserasnthrarnleuthrgluthmetarnthrxngln 300
 Db 841 ATATGTACTATCCGAAAGCAACCTAACCTCACAGAAACATATGAACCTACTAACAG 900
 QY 301 gluleuglnleuhalaleuglyglvgluserphetrpvalisermetilesertryarnser 320
 Db 901 CAGCTTGAACGTGCACTGTGAGAGCGAGAGCTTTTGGGTCTATATATTTCTTATATCT 960
 QY 321 leuglylysserprovalalathleuarglileproalaleglnlulysserphegln 340
 Db 961 CTGGGAGAGTCTCCAGTGGCCACCTGAGGATTCAGGATTCAGAAATAATCATTTGAG 1020
 QY 341 cyseilegluvalmetglinalacyvalalagluabpgleuvalvallystprlnser 360
 Db 1021 TGCATTTGAGGTCTATGAGAGCCCTGCTGTGAGACCGCTAGGTGTAAGGTGAGAAAGC 1080
 QY 361 seralaleuaspvalasnthrtrpmetileglutrpheproaspvalaspserglupro 380
 Db 1081 CCTGCTCTAGAGCTGAACCTTGAGTGAATGATGATTTCCGAGTGTGACCTCAAGCCC 1140
 QY 381 thrthrleusertrppluservalserglnalathraantprthrileglnlnasplys 400
 Db 1141 ACCACCTTTCTCTGGAAATCTGTCTCAGGCCAGAACTGGACATCCAGAAAGATTA 1200
 QY 401 leuysrprophettrpcygltryasnliiservaltyrprometleuhalasplysvalgly 420
 Db 1201 TTTAAACCTTTCTGTGTCTATTAACATCTCTGTGTTCATATGTTCCATGACAAATTTGGC 1260
 QY 421 gluprotyrserileglnalalyzralalysgluvalaproserglulgluproglnthr 440
 Db 1261 GAGCATATTTCCATCAAGCTTATTCCTCAAAAGAGCGTTCCTCAAGAGCTTCAAGACC 1320
 QY 441 lyvalagluasnilegylvalalyethrvalthrilethrtprlysgluileprolysser 460
 Db 1321 AAGGTGAGAAACATTTGGCGTGAAGACGGTCAAGATCAATGGAAGAGATTTCCCAAGAGT 1380

QY 461 gluarglysglyileilecyasantyrthrilepheuryrglnalaglulglvlysgly 480
 Db 1381 GAGAGAAAGGATATATCTGCACTACCACTCTTTACCAAGCTGAAGGTGGAAGAGCA 1440
 QY 481 pheserlysrthvalasnserseerileleuglntrygyleuglnuserleuysarplys 500
 Db 1441 TTCTCCAGACAGCTCAATTTCCAGATCTTGCGATGCGGCTGAGATCCCTGAAACGAAAG 1500
 QY 501 thrsertyrillevalgluvalmetcalasanthseralagllythrasnglythrser 520
 Db 1501 ACCCTCTACATGTTCCAGGTCAATGCGCACACAGGTCTGGGGGAACGACGCGACAGC 1560
 QY 521 ileasnphelysrthleuserpheservalpheglnileleuilethrseryrle 540
 Db 1561 ATAAATTCAGACATTTGTCTATTCAGTCTTTGAGATTAATCTCATATCTTCTGATT 1620
 QY 541 glylygylleuileuileleuilethrvallalyrglyleuylalyproasn 560
 Db 1621 GGTGAGGCTTTCTTATCTCATTAATCTGACAGTGCATATGGTCCAAAAACCCAAC 1680
 QY 561 lybleuthrhlseuqystrpprothrvallproasnproalagluserseerillealthr 580
 Db 1681 AAATGACTCATCTGTGTGGCCACCGTTCACACCTGTGAAAGTATAGCCACA 1740
 QY 581 trphlsglyasppasphelyasplybleuasnleuylsgluseraspasprvalasn 600
 Db 1741 TGGCATGAGATGATTTTAAGATAGCTTAACCTGAAAGAGTCTGATGACTCTGTGAC 1800
 QY 601 thrgluasparglileuylsprocysserthrproserasplybleuvalilleasplys 620
 Db 1801 ACAGAAAGCAGAGCTTAAACCATGTTCCACCCCGAGTGAAGTTGTGATGACAAAG 1860
 QY 621 leuvalvalasnphleglyasnvalleuglnlulephethrappglualahrgthrly 640
 Db 1861 TTGGTGTGAACCTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAGCCAGACGGGT 1920
 QY 641 glnlulysglnpheargargglylysgluptr 651
 Db 1921 CAGGA-AAACAATTTAGAGGGGAAAGAAATGG 1952

RESULT 11
 US-10-715-667-5
 ; Sequence 5, Application US/10715667
 ; Publication No. US20040152161A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corporation
 ; APPLICANT: Cosman, David J.
 ; APPLICANT: Mosley, Bruce A.
 ; APPLICANT: Bird, Timothy A.
 ; APPLICANT: Dubose, Robert F.
 ; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
 ; FILE REFERENCE: 3160-B
 ; CURRENT APPLICATION NUMBER: US/10/715,667
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: US/09/972,708
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 2238
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-715-667-5

Alignment Scores:
 Pred. No.: 0 Length: 2238
 Score: 3435.00 Matches: 647
 Percent Similarity: 99.69% Conserves: 2
 Best Local Similarity: 99.39% Mismatches: 2
 Query Match: 98.59% Indels: 1
 DB: 18 Gaps: 0

Qy	58	GLVAspAspPheIysAspIysLeuAsnLeuIysGluSerAspAspSerValAsnThrGlu	602
Db	1878	GGAGATGATTTCAAGATATAGCTAAACCTGAAGAGCTGATGACTGTGAACACAGAA	1939
Qy	603	AspArgIleuLeuIysProCysSerThrProSerAspIysLeuValIleAspIysLeuVal	622
Db	1938	GAGAGATCTTAABAACCATGTTCCACCCCACTGACAAAGTTGTGATGACAAAGTTG	1999
Qy	623	ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu	642
Db	1998	GTAACATTTGGCAATGATCTCGACAGAAATTTTTCACAGATGAAGCAGAACCGGTCA	2050
Qy	643	LysGlnPheArgArgGlyIysGluTrp	651
Db	2057	AAACAAATTTAGAGAGGGGAAAAAGAAATGG	2083
RESULT 13			
US-10-351-157-110			
; Sequence 110, Application US/10351157			
; Publication No. US20030215838A1			
; GENERAL INFORMATION:			
; APPLICANT: Sprecher, Cindy A.			
; APPLICANT: Gao, Zeren			
; APPLICANT: Kuljper, Joseph L.			
; APPLICANT: Dasovich, Maria M.			
; APPLICANT: Grant, Francis J.			
; APPLICANT: Presnell, Scott R.			
; APPLICANT: Whitmore, Theodore E.			
; APPLICANT: Hammond, Angela K.			
; APPLICANT: No. US20030215838A1ak, Julia E.			
; APPLICANT: Grose, Jane A.			
; APPLICANT: Dillon, Stacey R.			
; TITLE OR INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS			
; FILE REFERENCE: 02-02			
; CURRENT APPLICATION NUMBER: US/10/351,157			
; CURRENT FILING DATE: 2003-01-21			
; PRIOR APPLICATION NUMBER: US 60/435,361			
; PRIOR FILING DATE: 2002-12-19			
; PRIOR APPLICATION NUMBER: US 60/389,108			
; PRIOR FILING DATE: 2002-06-14			
; PRIOR APPLICATION NUMBER: US 60/350,325			
; PRIOR FILING DATE: 2002-01-18			
; NUMBER OF SEQ ID NOS: 183			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 110			
; LENGTH: 2402			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (171) ... (2366)			
US-10-351-157-110			
Alignment Scores:			
Pred. No: 0			
Score: 3435.00			
Percent Similarity: 99.85%			
Best Local Similarity: 99.69%			
Query Match: 98.59%			
DB: 17			
Gaps: 0			
US-10-006-265-2 (1-652) x US-10-351-157-110 (1-2402)			
Qy	3	LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTPAlaLeuTrpMet	22
Db	138	CTCTCTCCCAAGCCTTCACTGTGTAACTCGGGAATGATGTGACCTGTGGCACTGTGATG	197
Qy	23	LeuProSerLeuCysIysPheSerLeuAlaLeuProAlaIysProGluAsnIleSer	42
Db	198	CTCCCTCACTTGCAAATTCAGCGCTGCGAGCTTGCACGCTAAGCTGAACAATTTCC	257
Qy	43	CysValIysTrpTrpTrpArgIysAsnLeuTrpCysThrTrpSerProGlyIysGluThrSer	62

Dh	258	TGtGTCTACATCTATAGAGAAAAATTTAACTCGACCTTGAGTCCAGAGAAAGAAACCAAGT	317
Qy	63	TyTThrGlnTyThrValIlysaqThrTyAlaPheGlyGlyIysHisaspaenCyseThr	82
Dh	318	TATACCAAGTATACACAGTTTAAGAGAACTTAGCGTTTGTGAGAAAAACATGTATTAATTGACA	377
Qy	83	ThrasnserThrserserGluamaraAlaSerCyseSerPhePheIuProaXIlleThr	102
Dh	378	ACCAATAGTCTACAGAGTAAAAATCGCGTTCGTCCTTTTCTCTTCCAGAAATACG	437
Qy	103	IlleProaspasnTyTrThrIleGluValAlaGluIuasnGlyaspGlyValIleIysSer	122
Dh	438	ATCCACATATATATATACATTGAGTGGAGAGCTGAANAATGAGATGTGTATTAATTC	497
Qy	123	HisMetThrTyTrTPaArgLeuGluasnIleAlaIysThrGluProPolysIlePheArg	142
Dh	498	CATATGACATACAGATGAGATTAAGAGACATPAGCCGAAACCTGAACCTAAGATTTCGCT	557
Qy	143	ValIysProValleuGlyIleIysArgMetIleGlnIleGluTrpIleIysProGluIleu	162
Dh	558	GTGAACCAATTTGGGCATCAACGATATTCATTAATGAATGAATPAAGCCTGAGTGG	617
Qy	163	AlaProValSerSeraspLeuIysTyThrLeuArgPheArgTrpValIasnSerThSer	182
Dh	618	CGCGCTGTTTCATCTGTATTTAAATACACCTTCGATTACAGACAGTCACACAGTACACG	677
Qy	183	TrpMetGluValaenPheAlaIysasnArgIysaspIysasnGlnThrTyraenLeuThr	202
Dh	678	TGATGTGAATGTCAACTCGCTAAGAACCGTAAGGATTAACCAACGTCACACTCAGC	737
Qy	203	GlyIuennInProPethrGluTyTrValIleAlaIeuArgCysAlaValIysGluSerIys	222
Dh	738	GGCGGTGAGCCTTTTACAGATATGTATATAGCTTCGAGTGTGGTACAGAGATCAAG	797
Qy	223	PheTrpSeraspTrpSerGlnIuIysMetGlyMetThrGlnGlnIuAlaProCyseGly	242
Dh	798	TTCTGGAGTACCTGAGCCACAGAAAAATGGAAATGACTGAGAGAAAGCTCCATGTGGC	857
Qy	243	LeuGluIuennTrpArgValleuIysProAlaGluAlaaspGlyArgArgProValArgIeu	262
Dh	858	CTGGAACTGTGAGAGTCTGAAACCGACTGAGGCGGATGGAGAGAGGCCAGTCGGTGG	917
Qy	263	LeuTrpIysIysAlaArgGlyAlaProValleuGluIysThrIleuGlyTyraenIleTrp	282
Dh	918	TTATGAGAAAGGACGACAGAGAGCCGACTGTAGAGAAACACTTGGCTACACATATGG	977
Qy	283	TyTrpTrpGluSeraspThrasnThrIleuThrGlnThreCasnThrTrasnGlnIleu	302
Dh	978	TACTATCCAGAACCACTACCTACCTACAGAAACATGACACTACTACACAGACTT	1037
Qy	303	GluIuennIleIuengIyGlyIuSerPheTrpValSerMetIleSerTyraenSerIeuGly	322
Dh	1038	GAACTGCATCTGGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCTTAAATTCCTTGGG	1097
Qy	323	LysSerProValAlaThrIleuArgIleProAlaIleGlnGluIysSerPheGlnCysIle	342
Dh	1098	AAGTCTCCAGTGGCCACCTGAGGATTCGAGCTATTAAGAAAAATCATTTCACTGACTT	1157
Qy	343	GluValMetGlnAlaCysValAlaGluaspGluIeuValIuIysTrpGluIuSerSerAla	362
Dh	1158	GAGGTCTACAGCGGCTCGTGTCTGAGAGACACGACTAGGTGAGTGGCAAGCTCTGCT	1217
Qy	363	LeuaspValAsnThrTrpMetIleGluTrpPheProaspValaspSerGluProThrThr	382
Dh	1218	CTAAGCTGAACACTTGATGATTTGATGTTCCTCGATGTGACTCAGAGCCACACACC	1277
Qy	383	LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGluaspIysIleuIys	402
Dh	1278	CTTTCCTGGGAATCTGTCTCAGGCCACCAACATGCGATCCGCAAGATTAATTAA	1337
Qy	403	ProPethrTrpCysTyraenIleSerValTyProMetIeuHisaspIysValGlyIuPro	422
Dh	1338	CTTTTCTGGGTATTAACATCTCTGTATTCACATGTGTGATGACAAAGTTGGGGAAGCA	1397


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QY 423 TysSerIleGlnAlaTyrAlaIleValProSerGluGlyProGluThrIleVal 442
DB 1398 TATTTCATCCAGGCTTATGCCAAGAGGCGTTCCATCCAGAGGTCGAGACCAAGGG 1457
QY 443 GlnAenIleGlyValIleThrValThrIleThrIlePheGlyIleProIleSerGluArg 462
DB 1458 GAGAACTATGGCGTGAAGCGGTCAAGATCAATGGAAGAGATTCGCCAGAGTGAAGA 1517
QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyIleLysGlyPheSer 482
DB 1518 AAGGTAATCATCTGCACTACACCACTTTTACCAAGCTGAAGGAGGAGAAAGATTC 1577
QY 483 LysThrValAsnSerSerIleGluGlnTyrGlyLeuGluSerLeuIleLysArgIleThrSer 502
DB 1578 AAGACAGCATTTCCAGCATCTTGAGTGGCGCTGAGAGTCCCTGAAGAGAAAGCTCT 1637
QY 503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSerIleAsn 522
DB 1638 TACATTTGTTACGTCATGATGCCAGCACAGTCTGGGGGAAACCAAGGACCAAGCATTAAT 1697
QY 523 PheIleThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
DB 1698 TTCAAGACATTTGTCATGATGCTTTGAGATTATCTCATTAATCTTCTGATGTGGA 1757
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
DB 1758 GGCCTCTTATTTCTATTAATCTGACAGGCGATATGCTCAAAAACCCCAAAATATG 1817
QY 563 ThrIleLeuCysTyrProThrValProAsnProIleGluSerSerIleAlaThrTrpHis 582
DB 1818 ACTCATCTGTGTGGCCCAAGCTTCCCAACCTGCTGAAGATGATACCAAGATGCGCAT 1877
QY 583 GlyAspAspPheIleAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu 602
DB 1878 GGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATGATCTGTGAACACAGAA 1937
QY 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
DB 1938 GACGAGATCTTAACCAAGTTCACCCCGAGTGAAGATGATGATGACAAAGTTGTGTG 1997
QY 623 ValAsnPheGlyAsnValIleGlnGlnIlePheThrAspGluAlaArgThrGlyGlnGlu 642
DB 1998 GTGAATCTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAGCCAGAACGGGTGAGA- 2056
QY 643 LysGlnPheArgArgGlyLysGluTrp 651
DB 2057 AAACAATTTAGAGGGAAGAAATGG 2083

RESULT 14
US-10-772-531-1
; Sequence 1, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Piresnell, Scott R.
; APPLICANT: Geo, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kujiiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772, 531
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892, 949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214, 282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214, 955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267, 963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2402.
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (171)...(2366)
US-10-772-531-1

Alignment Scores:
Pred. No.: 0
Score: 3435.00
Percent Similarity: 99.85%
Best Local Similarity: 99.69%
Query Match: 98.59%
DB: 18 Gaps: 0

US-10-006-265-2 (1-652) x US-10-772-531-1 (1-2402)

QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetThrTrpAlaLeuTrpMet 22
DB 138 CTCTCTCCCGAGCCTTCATGTGTAACTGGGAGATGATGTGACCTGGCCTGTGGATG 197
QY 23 LeuProSerLeuCysLysPheSerLeuAlaIleuProAlaLysProGluAsnIleSer 42
DB 198 CTCCCTCATCTGCAATTAATCACTGGAGCTCTGCACTGCACTGAGCAATTCCTCC 257
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
DB 258 TGTGTCTACTACTATTAAGAAATTTAACTGCACTTGAGATCCAGAGAAAGAAACAGT 317
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisIleAspAsnCysThr 82
DB 318 TATACCCGATCACAGTTAAGAGAACTTACCTTTTGGAGAAACATGATTAATGTACA 377
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB 378 ACCAATGTTCTACAGTAAGAAATGCTGCTGCTCTTTTCTTCCCAAGAAATACG 437
QY 103 IleProAspAsnTyrThrIleGluValGluIleGluAsnGlyAspGlyValIleLysSer 122
DB 438 ATCCAGATATTAATTAACATTTGAGAGTGAAGCTGAAATGAGATGGGTATTAATCT 497
QY 123 HisMetThrTyrTrpAspGluAsnIleAlaLysThrGluProPheIlePheArg 142
DB 498 CATATGACATACATGAGATTAAGAACATACGAAACCTGAACCACTTAAGATTTTCGT 557
QY 143 ValLysProValIleGluValIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
DB 558 GTGAACCAAGTTTGGGCAATCAACGAATGATTAATGATGATTAAGCTGTGAGTGG 617
QY 163 AlaProValSerSerAspLysLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
DB 618 GCGCTGTTTCATCTGATTTTAATTAACACTTGCATTCAGAGACATCAAGATCAAGC 677
QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnIleTyrAsnLeuThr 202
DB 678 TGGATGGAAGTCAACTTCGCTAAGAACCGTAAGATTAACCAACCAAGTCAACCTCACG 737
QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
DB 738 GGGCTGAGCCTTTTACAGAAATGATGATGCTTGGAGTGTGGCTCAAGAGATCAAG 797
QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242
DB 798 TTCTGAGTACTGACGACCAAGAAATTAAGGAATGACTGAGAGAAAGCTCCATGTGGC 857
QY 243 LeuGluLeuTrpArgValIleLysProAlaGluAlaAspGlyArgArgProValArgLeu 262
DB 858 CTGGAACGTGAGAGATCTGAAACCAAGCTGAGCGGATGGAAGAAAGCCAGTGCCTGG 917
QY 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282

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Db      918 TTATGAGAGAGGCAAGAGAGCCAGTCTCTAGAGAAACCTTGCTCAACATATGG 977
Qy      283 TTTTyrProGlnSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
Db      978 TACTATCCAGAAAGCAACACTAACCTCACAGAAACATGAACACTCTAACCGAGCTT 1037
Qy      303 GlnLeuHleuGlyGlnSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
Db      1038 GAATCTGATCTGGGAGCGGAGACCTTTGGGTCTATGATTTCTTATATTTCTTTGGG 1097
Qy      323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGlnLysSerPheGlnCysIle 342
Db      1098 AAGTCTCCAGTGGCCACCTCGAGGAATTCACGATTTCAAGAAAAATCATTTTCAGTCATT 1157
Qy      343 GluValMetGlnAlaCysValAlaGluAsnGlnLeuValValLysTrpGlnSerSerAla 362
Db      1158 GAGGTATGAGGCGCTGGCTGTGTGAGGACACACTAGTGTGAAGTGGCAAACTCTGCT 1217
Qy      363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db      1218 CTAGACGTGAACCTTGAGATTTGAATGTTTCCGATGTGACTCAGAGCCACACCACC 1277
Qy      383 LeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
Db      1278 CTTTCTCGGAATCTGTGCTCTCAGGCCACGAACTGAGCATCCAGCAAGATAATTAAAA 1337
Qy      403 ProPheTrpCysTrpAsnIleSerValTyrProMetLeuHleAspLysValGlyGluPro 422
Db      1338 CTTTCTGGTGTATACATCTGTGTATCCAAATGTGTATACAAAGTGTGGAGGCCA 1397
Qy      423 TyrSerIleGlnAlaTyrAlaLysGlnGlyValProSerGlnGlyProGluThrLysVal 442
Db      1398 TATTCATCCAGGCTTATGCCAAAGAGGCTTCCATCAGAAAGCTCTGAGACCAAGGTG 1457
Qy      443 GluAsnIleGlyValLysThrValThrIleThrLysGlnIleProLysSerGluArg 462
Db      1458 GAGAAATCTGGCTGAAAGCGGTACGATCACATGAAAGATTCACCAAGATGAGAGA 1517
Qy      463 LysGlyIleIleLysAsnTyrThrIlePheTyrGlnAlaGlnGlyGlyLysPheSer 482
Db      1518 AAGGGTATCATCTGCACATACACATCTTTTACCAAGCTGAAGGTGAAGAAAGATTTCTCC 1577
Qy      483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer 502
Db      1578 AAGACGTCAATTCACGACATCTTGACATAGCGCTGGAAGTCCCTGAAACCAAGACCTCT 1637
Qy      503 TyrIleValGlnValMetAlaAsnThrSerAlaGlyGlyLysThrAsnGlyLysSerIleAsn 522
Db      1638 TACATGTTCAGGTATGCGCACACACAGTGTGGGGGAACCAACGGGACCAACATTAAT 1697
Qy      523 PheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerLeuIleGlyGly 542
Db      1698 TTCAAGCATATGTCATTCAGTGTCTTGAGATTATCTCTCAATCTCTCGATTTGGGGA 1757
Qy      543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
Db      1758 GGGCTTCTTATTTCTATATCTGACGACGTGCAATAGGTCTCAAAAAACCAACAATTTG 1817
Qy      563 ThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrpHis 582
Db      1818 ACTCATCTGTGTGGCCACCGTTCACCAACCTGTGTAAGTAGTATAGCCATGGCAT 1877
Qy      583 GlyAspAspPheLysAspLysLeuAsnLeuLysGlnSerAspAspSerValAsnThrGln 602
Db      1878 GAGGATGATTTCAAGATTAAGCTAAACCTTAAGAGAGCTGATGATCTTGGAACACAGAA 1937
Qy      603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db      1938 GACAGATCTTAAACCATATTTCAACCCCAAGTGAACAGTGGTGAATGCAAGTTGGGTG 1997
Qy      623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGlnAlaArgThrGlnGln 642

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Db      1998 GTGAACCTTGGAGATGTTCTCGACAGAAATTTTCAAGATGAAGCCAGAA CGGCTCAGA - 2056
Qy      643 LysGlnPheArgArgGlyLysGluTrp 651
Db      2057 AAACAAATTTAGAGGGGAAAGAAATGG 2083

RESULT 15
US-09-972-708-3
; Sequence 3. Application US//09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-3

Alignment Scores:
Pred. No.: 0 Length: 2480
Score: 3435.00 Matches: 647
Percent Similarity: 99.69% Conservative: 2
Best Local Similarity: 99.39% Mismatches: 2
Query Match: 98.59% Indels: 1
DB: Gaps: 0

US-10-006-265-2 (1-652) x US-09-972-708-3 (1-2480)
Qy      1 MetLysLeuSerProGlnProSerCysValAsnLeuGluMetMetTrpThrTrpAlaLeu 20
Db      132 ATGAGCTCTCTCCACGCTTCATGTGTAACTGGGGATATATGGAGCTGGGCACTG 191
Qy      21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGlnAsn 40
Db      192 TGGATCTCTCTTCACTCTGCAAAATTCAGCCCTGGAGCTCTCCAGCTAAGCTGGAAC 251
Qy      41 IleSerCysValTyrTyrTyrAlaLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db      252 ATTTCTGTGTCTACTATAGTAAATTTTAACTGCATCTGGAGTCCAGGAAAGGAA 311
Qy      61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlnLysHisAspAsn 80
Db      312 ACCAGTTAAACCCAGTACACAGTTAAAGAACTTACGCTTTTGGAGAAAAACATGATTAAT 371
Qy      81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db      372 TGTACAAACCAATAGTTCTTCAAGTGAAATCTGTCTGCTCTTTTCTTCCATCAAGA 431
Qy      101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db      432 ATTAAGATCCCAAGATTAATATACATTTGAGTGAAGGTGAAGAAATGAGATGATTAAT 491
Qy      121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
Db      492 AAATTCATATGACATACATACGAGATTTAGAGAACATAGCAAAACCTGAACACCTTAAGATT 551
Qy      141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
Db      552 TTCCGTGTAACCAAGTTTGGCATCAACAAATGATTTCAAAATTCAAATGATTAAGCTT 611
Qy      161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180

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Db 612 GAGTGGCCGCTTTCATCTGATTTAAATACACACTTCGATCAGGACAGTCAACAGT 671
 Qy 181 ThSerTrpMetGluValAsnPheAlaIysAsnArgIleAspIleAsnGlnThrTyrAsn 200
 Db 672 ACCAGCTGGAGGAGGAGTCACTGCTGTAAGAACCTTAAGATTAACCAACGTAACAC 731
 Qy 201 LeuThrGlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValIleGlu 220
 Db 732 CTCACGGGGCTGCACGCTTTTACAGAAATATGTCATAGCTTCGCGATGTCGGTCAAGAG 791
 Qy 221 SerIysPheTrpSerAspTrpSerGlnIleIleuIleuMetGlyMetThrGluGluGluAlaPro 240
 Db 792 TCAAGTCTCGAGAGTGAAGTGAAGCAAGAAAGAAATGATGATGAGGAAAGAAAGTCTCA 851
 Qy 241 CysGlyLeuGluLeuTrpArgValIleuIleuProAlaGluAlaAspGlyIleArgTrpVal 260
 Db 852 TGTGGCTCGAAGCTGTGAGAGTCTGAAACACGCTGAGGCGGAGGAGGAAAGGCGACAGT 911
 Qy 261 ArgLeuLeuTrpIleuValIleuArgValIleuProValLeuGluIleuThrLeuGlyTyrAsn 280
 Db 912 CGGTGTTATGAGAAAGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 971
 Qy 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGlnThrMetAsnThrThrAsnGln 300
 Db 972 ATATGTAATCTATCCAGAAAGCAACCTAACCTCAAGAAACATGAACTACTAACAG 1031
 Qy 301 GlnLeuGluLeuAlaLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320
 Db 1032 CAGCTTGAACTGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1091
 Qy 321 LeuGlyIleuSerProValAlaThrIleuArgIleProAlaIleGlnIleuIleuSerPheGln 340
 Db 1092 CTGAGGAGCTCCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1151
 Qy 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValIleTrpGlnSer 360
 Db 1152 TGCAATTGAGGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1211
 Qy 361 SerIleuLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db 1212 CTGCTCTAGACGTGAACACTTGATGATGAATGGTTCCGATGTGACTCAGAGGCC 1271
 Qy 381 ThrThrIleuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspIle 400
 Db 1272 ACCACCTTCTCTGAGAACTGTGTCTAGGCGCAGAACTGAGCATCCAGAAATTA 1331
 Qy 401 LeuIleuProPheTrpCysTyrAsnIleSerValTyrProMetLeuIleAspIleValGly 420
 Db 1332 TTTAAACCTTCTGAGTATTAACATCTCTGTATCCAAATGTTGATGACAAAGTTGGC 1391
 Qy 421 GluProTyrSerIleGlnAlaTyrAlaIleGluGlyValProSerGluGlyProGluThr 440
 Db 1392 GAGCATATTCATCCAGGCTTATGCCAAAGAGGCGTTCCATCAGAAAGTCTGAGACC 1451
 Qy 441 LysValGluAsnIleGlyValIleValThrValThrIleThrTrpIleuGluIleProIleSer 460
 Db 1452 AAGGTGAGAACATTTGGCGTGAAGCGGTCAAGATCACATGAAAGAGATTCACAGAGT 1511
 Qy 461 GluArgIleGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyIleGly 480
 Db 1512 GAGAGAAAGGATATCATCTGCACTACACATCTTTTACCAAGCTGAAGGTGAAAGGA 1571
 Qy 481 PheSerIleThrValAsnSerSerIleuGlnTyrGlyLeuGluSerLeuIleuArgIle 500
 Db 1572 TTTCCCAAGACAGTCAATTCAGCATCTTGACATGAGGCTGAGTCCCTGAAACGAAG 1631
 Qy 501 ThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGlyIleThrAsnGlyThrSer 520
 Db 1632 ACCTCTTACATGTTTCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1691
 Qy 521 IleAsnPheIleThrLeuSerPheSerValPheGluIleIleuIleThrSerLeuIle 540
 Db 1692 ATAAATTTCAAGACATTTGTCTATTCAGTGTCTTTGAGATTATCTCATTAATCTCTGATT 1751

Qy 541 GlyGlyGlyLeuLeuIleLeuIleIleuThrValAlaTyrGlyLeuIleuIleuProAsn 560
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 Qy 561 LysLeuThrIleLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
 Db 1812 AAATTGACTCATCTGTGTGGCCACCGCTTCCAACTGCTGAAGATGATAGCCCA 1871
 Qy 581 TrpHisGlyAspAspPheIleAspIleuAsnLeuIleuIleuIleuIleuIleuIleu 600
 Db 1872 TGGCATGAGATGATTTCAAGATTAAGCTAACTGAAGAGTCTGATGACTCTGTGAAC 1931
 Qy 601 ThrGluAspArgIleIleuIleuProCysSerThrProSerAspIleuValIleAspIle 620
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 Qy 621 LeuValIleAsnPheGlyAsnValLeuGlnIleIlePheThrAspGluAlaArgThrGly 640
 Db 1992 TTGGTGTGAATCTTGGGAATGTTCTGCAGAAATTTTCAAGATGAAGCCAGAACGGGT 2051
 Qy 641 GlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 651
 Db 2052 CAGGA-AAACATTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2083

Search completed: February 23, 2005, 20:17:05
 Job time : 1084.05 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:54:07, Search time 5993.32 Seconds
(without alignments)
1140.927 Million cell updates/sec

Title: US-10-006-265-2

Perfect score: 3484
Sequence: 1 MKLSPQSCVLMGMWTAL.....FTDEARTGQKQFRGKEMD 652

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn2_1/USPRO.spool/US10006265/runat_18022005_094658_22193/app_query.fasta_1.2069
-DB=BS1 -QFWT=fastcap -SUFFIX=rest -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=pct -NORM=ext -HEPSTRIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10006265@cgn2_1_7723@runat_18022005_094658_22193 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESOURCE -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_hic:
5: gb_est3:
6: gb_est4:
7: gb_est5:
8: gb_est6:
9: gb_gse1:
9: gb_gse2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	709.5	20.4	2232 3	AK030512 Mus muscu
2	655.5	18.8	5264 3	BC071555 Homo sapi
3	647.5	18.6	3055 3	AY101038 Rattus no
4	526	15.1	663 2	BB617934 BB617934
5	470.5	13.5	653 5	BU455838 BU455838
6	468.5	13.4	637 7	CF174021 CF174021
7	464.5	13.3	2804 3	AK089305 Mus muscu
8	459.5	13.2	2592 9	AY412152 Homo sapi
9	423.5	12.2	2792 3	BC040954 Homo sapi

10	397	11.4	651 7	CF915066
11	395.5	11.4	2535 9	AY412154 Mus muscu
12	389	11.2	1931 3	CR610771 full-length
13	355	10.2	1512 3	BC020454 Mus muscu
14	347	10.0	592 6	CA561173 K0283D09-CA560924
15	342	9.8	479 6	CA560924 K0279C07-BU271003
16	326	9.4	828 5	BU271003 603508092
17	325.5	9.3	851 5	BU460273 603368742
18	320.5	9.2	825 6	CB518939 UI-M-GH0-AV412153
19	320.5	9.2	2591 9	AY412153 Pan trogl
20	315.5	9.1	776 7	CF747542 UI-M-HB0-CR634184
21	306	8.8	715 7	CR634184 UI-M-HB0-BX380515
22	305.5	8.8	1131 5	BX380515 BX380515
23	304	8.7	1659 3	CR611411 full-length
24	302	8.7	546 6	CA535774 K0202F08-CA559989
25	297	8.5	553 6	CA559989 K0266C03-BU288431
26	296.5	8.5	763 5	BU288431 603607401
27	294.5	8.5	628 6	CB427282 602850 MA
28	294	8.4	697 7	CN529323 UI-M-HB0-AO022781
29	291	8.4	459 8	AO022781 HS-2180-A
30	291	8.4	642 6	CB512958 B6A1T9D54
31	286	8.2	751 5	BQ770280 UI-M-F10-BX359249
32	286	8.2	1097 5	BX359249 BX359249
33	283	8.1	1577 3	CR612729 full-length
34	282	8.1	761 5	BU460413 603369157
35	279	8.0	669 5	BU322304 603854025
36	278	8.0	721 7	CN454854 UI-M-HNO-BQ185371
37	277	8.0	709 5	BQ185371 UI-M-EU1-AG138991
38	275.5	7.9	612 9	AG138991 Pan trogl
39	275.5	7.9	1073 5	BX382126 BX382126
40	270	7.7	518 6	CA561193 K0283F09-CA559290
41	270	7.7	523 6	CA559290 K0256G09-CD350375
42	270	7.7	698 6	CD350375 UI-M-F10-CF780723
43	268.5	7.7	887 4	CF780723 AGENCIOFT
44	268	7.7	587 7	BG921322 602824173
45	266.5	7.6	699 6	CB168262 HSF603268

ALIGNMENTS

RESULT 1	AK030512	LOCUS	AK030512	2232 bp	mRNA	linear	HTC 03-APR-2004
DEFINITION	Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:530424C19 product:hypothetical protein, full insert sequence.						
ACCESSION	AK030512						
VERSION	AK030512.1 GI:26326508						
KEYWORDS	HTC; CAP trapper.						
SOURCE	Mus musculus (house mouse)						
ORGANISM	Mus musculus						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
AUTHORS	Carninci, P. and Hayashizaki, Y.						
TITLE	High-efficiency full-length cDNA cloning						
JOURNALS	Meth. Enzymol. 303, 19-44 (1999)						
MEDLINE	99279253						
PUBMED	10349636						
REFERENCE	2						
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.						
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes						
JOURNALS	Genome Res. 10 (10), 1617-1630 (2000)						
MEDLINE	20499374						
PUBMED	11042159						
REFERENCE	3						
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitesu, T., Tashiro, H., Itoh, M., Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,						

TITLE
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
20530913
11076861

REFERENCE
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
REFERENCE
AUTHORS
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS
6
(bases 1 to 2322)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Kahira, S., Takeuchi, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teikoku-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES
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REFLVENIPHSKGEV"

ORIGIN

Alignment Scores:

Pred. No.: 1,156-64 Length: 2232
Score: 709.50 Matches: 141
Percent Similarity: 79.81% Conservative: 25
Best Local Similarity: 67.79% Mismatches: 39
Query Match: 20.36% Indels: 3
DB: 3 Gaps: 2

US-10-006-265-2 (1-652) x AK030512 (1-2232)

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Qy	454	TrypGluIleProIleSerSerGluArgIleIleCysAspThrThrIlePheTyr	473
Db	272	TGGAGGAGATTCTTAAAGTCTTGAATGATATTTACAAATTAACCTGATTTTC	331
Qy	474	GlnAlaGluGlyGlySerIlePheSerIleThrValAsnSerSerIleGluIleTyrGly	493
Db	332	CAAGCTGAAGGTGGAAGAAAGAACTTCAAGACTGTTAACTTCATGCGCTGAGTGAC	391
Qy	494	LeuGluSerIleuValArgIleThrSerTyrIleValGlnValMetAlaAsnThrSerAla	513
Db	392	CTGGAGTCTCTCAACGAGGACCTCTTAACTGTTGGTATGCGCCAGCAGAGCT	451
Qy	514	GlyGlyThrAsnGlyThrSerIleAsnPheIleThrLeuSerPheSerValPheGluIle	533
Db	452	GGAGGTACCAAGGGGTGAGATTAATCTTCAAGACATTTCAATCATGTGTGAAAT	511
Qy	534	IleLeuIleThrSerIleuIleGlyGlyLeuLeuIleLeuIleIleLeuThrValAla	553
Db	512	GTCCCTTCAACATCTTACTGATGAGAGGCTTTCTTCTTCACTTACATCAAAAGAGACT	571
Qy	554	TyrGlyLeuIleuValProAsnIleuThrIleuValIleuValIleuValIleuValIleuVal	573
Db	572	TTTGGCTTCAAGACCAACCGGTGACTCCCTGTGTGTCGATGTTCCCAACCT	631
Qy	574	AlaGluSerSerIleAlaThrIleIleGlyAspAspPheIleAspIleuAsnIleuVal	593
Db	632	GCTGAAGATGATTTTACCCATGCTCGAGATGTTTCAAG--AAGTCAATATGAAG	688
Qy	594	GluSerAspSerValAsnThrGluAspArgIleLeuIleProCysSerThrProSer	613
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Qy	614	AspIleuValIleAspIleuValIleAsnIleuValIleAsnIleuValIleuValIleuVal	633
Db	749	GAT-----CTCATTTGACAAAGCTGTGATGAACTTTGAGAAATTTCTGGAATTTTG	802
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RESULT 2			
BC071555		5264 bp	mRNA linear
LOCUS			HTC 02-JUN-2004
DEFINITION			Homo sapiens cDNA clone IMAGE:4374041, containing frame-shift
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
1	(bases 1 to 5264)		
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,			
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schley, G.D.,			
Altechul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K.,			
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F.,			
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,			
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,			

Scheetz, T.E., Brownstein, M.J., Uedini, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mollay, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wotley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hally, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Rodriguez, A.C., Grimwood, J., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalka, U., Smalins, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Maizumi, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT

NIH-MGC Project URL: <http://mgs.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palcovite, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.sbcg.stanford.edu>
Contact: (Dickson, Mark) mdickpaxil@stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 167 Row: a Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28610146
This clone has the following problem: frame shifted.

FEATURES

location/Qualifiers
1..5264
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ORIGIN

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Pred. No.: 3.17e-58 Length: 5264
Score: 655.50 Matches: 175
Percent Similarity: 46.75% Conservative: 113
Best Local Similarity: 28.41% Mismatches: 261
Query Match: 18.81% Indels: 68
DB: 3 Gaps: 16

US-10-006-265-2 (1-652) x BC071555 (1-5264)

QY 35 ProAlaLysProGluAenILeserCyValTyrTyrArGlyAsnLeuThrCyThr 54
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QY 55 TTPserProGlyLysGluThrSerTyr--ThrGlnTyrThrValLys-----Arg 70
DB 581 TGGGATGGTGGAGGAAACACACTTGAGACAAACCTTAAATCTGAATGGGCA 640

QY 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCySerThrAsn 84
DB 641 AACACCAAGTTTGGCGATTCGAAAGCAAAAGTAGACACCCCACTGATGACCTGTAT 700
QY 85 SerSerThrSerGluAenArGlyAlaSerCySerPhePheLysProArgIleThrIlePro 104
DB 701 TATTTCTACT-----GTGATTTTGTTC----- 721
QY 105 AsparnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
DB 722 --AACATTGAAGCTGGTGAAGAGCAAGATCCCTTGGGAAGTTTACATCATGATAT 778
QY 124 MetThrTyrTPArGLeuGluAenIleAlaLysThrGluProProLysIlePheArgVal 143
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QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTyrIleLysProGluLeuAla 163
DB 836 ATCAACTCAGAGAACTGCTAGATATCTTAAATTTGACATGAGCAACCAAGTATTAAG 895
QY 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrTyr 183
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QY 223 PheTTPserAspTPserGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
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QY 242 GlyLeuGluLeuTPArGValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
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DB 1604 GCAAGAGCAAAATGCTATTTGATTAACAGTATCTCCAGTATATGATGAGACCAAGAGC 1663
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RESULT 3
LOCUS      AY310138              3055 bp      mRNA      linear      HTC 07-JUL-2003
DEFINITION Rattus norvegicus Acl1055 mRNA, complete cds.
ACCESSION  AY310138
VERSION     AY310138.1 GI:32264598
KEYWORDS   HTC.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
REFERENCE  1 (bases 1 to 3055)
AUTHORS    Xu,C.S., Li,W.O., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.O.,
            Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
            Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
            Liver regeneration after PH
            Unpublished
            2 (bases 1 to 3055)
TITLE      JOURNAL
AUTHORS    Xu,C.S., Li,W.O., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.O.,
            Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
            Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
            Direct Submision
            Submitted (29-MAY-2003) Henan Bioengineering Key Lab, Henan Normal
            University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
            China
FEATURES
Source      1..3055
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QSCSQPMSPDVSHFERSQVPSGSEBDPVRKKQOQVSDHISEPVSQRRRLPQESV
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ORIGIN
Alignment Scores:
Pred. No.:          9,53e-58          Length:          3055
Score:             647.64             Matches:          185
Percent Similarity: 45.64%             Conservative:    108
Best Local Similarity: 28.82%           Mismatches:      276
Query Match:       18,58%              Indels:          74
DB:                3                  Gaps:            22

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 290 AsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeuGluLeuIleGlyGly 309
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560 AsnLysLeuThrIleLeuCySeryTrpProThrValProAsnProAlaGluSerSerIleAla 579
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 1955 CAGTGTACACTCACACCCCCCAAGGACCAATTTAACTCCAAAGATCAGATGACTCA 2014
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 DEFINITION BB617934 RIKEN full-length enriched, adult male pituitary gland Mus
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 ACCESSION BB617934
 VERSION BB617934.1 GI:15396442
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 663)
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
 Hara,A., Hizemoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,O.,
 Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
 Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
 Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T.,
 Sugabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
 Takeda,Y., Tanaka,T., Toyo,T., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 TITLE JOURNAL
 COMMENT Unpublished (2001)
 CONTACT: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujisake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Matsubara,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
 and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
 Sugahara,Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shingawa,A.,
 Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,


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RESULT 6
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DEFINITION      Musculus cDNA clone N1A:B0932D09 IMAGE:30475340 5', mRNA sequence.
ACCESSION      CF174021
VERSION      CF174021.1 GI:33283570
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 637)
AUTHORS      Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
TITLE      Construction of long-transcript enriched cDNA libraries from
method      submicrogram amounts of total RNAs by a universal PCR amplification
Genome Res. 11 (9), 1553-1558 (2001)
JOURNAL      MEDLINE
PUBMED      11544199
COMMENT      Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@isaun.grc.nia.nih.gov
Plate: B0932 row: D column: 09
Seq primer: M13 Reverse
High quality sequence stop: 637
POLYA-NO.

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FEATURES
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/note="Vector: pCMV-SPORT6 (Invitrogen), Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://isun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 148 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen): 5'-GGACTAGTCTAGATCGGACGCGCCCTTTTCTTTT-3', treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker Lb-Sal4, purified by phenol/chloroform, and separated from free linker by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
ORIGIN
Alignment Scores:
Pred. No.:      1.58e-39      Length:      637
Score:      468.50      Matches:      96
Percent Similarity:      63.59%      Conservative:      21
Best Local Similarity:      52.17%      Mismatches:      54
Query Match:      13.45%      Indels:      13
DB:      7      Gaps:      4
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Db      119 CCTCTGGGTGGAACGCTGGAATATATGTGACCTTGACATGTCGCGCATCTTCTTCCTC 178
Oy      27 CysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCybValTyrTyr 46
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Oy      67 ThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCybThrThrAsnSerSer 86
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Oy      145 ProValLeuGlyIleLysArgMetIleGlnIleGluTTPIleLysPProGluLeuAlaPro 164
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QY 185 GluValAsnPhe 188
 Db 626 GAAGTCATATTT 637

RESULT 7
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 LOCUS AK089305
 DEFINITION Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone: F730003J03 Product: colony stimulating factor 3 receptor (granulocyte), full insert sequence.

ACCESSION AK089305.1 GI:26105194
 VERSION AK089305.1
 KEYWORDS HTCC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Taahito, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 MEDLINE 11076861

REFERENCE
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE 11076861

REFERENCE
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Aikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, K., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Kahira, S., Takekida, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
 JOURNAL
 Direct Submission
 Submitted (16-Apr-2002) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-research@riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
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 putative"

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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
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 /db_xref="taxon:10090"
 /clone="F730003J03"
 /cell_type="B6-derived CD11 +ve dendritic cells"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /note="colony stimulating factor 3 receptor (granulocyte) (MGD|MGJ:1339755, GB|NM_007782, evidence: BLASTN, 99%, match=2783)
 putative"

ORIGIN
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 Best Local Similarity: 26.688 Mismatches: 251
 Query Match: 13.33% Indels: 95
 DB: 3 Gaps: 26

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 Db 571 CCGCCAGCCCTCAAACTATCTGCTGCATGCACCTCACCACCAACAGCTGCTGC 630
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QY 54 ThrTpsrProGlyLybgluThrSerYr---ThrGlnYrThrValLybArgThrYr 72
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 Db 631 CAGTGGAGCCAGGCTCTGAGACCACTGCCACCACTGCTATCTCTAAAG----- 681
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QY 73 AlaphglYgluLybHisAspAnCyThrThrAsnSerSerThr----- 87
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 Db 682 AGCTTCAGAGAGCCGCCACAC---TCTACGTACCAAGGAGACATCCCGATTTGTG 738
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QY 88 ---SerGluAsnArgLAserCysSerPhePheLeuProArgIleThrIleProAspAn 106
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 Db 739 GCAAGAGAAGAGCAGAACTGCTCCATCCCGCAAAACTGCTCTGTACACAGTAT 798
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QY 107 TyrThrIleGluValGluAlaGluengLyAspGlyValIleLySerHisThrYr 126
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QY 127 TrpArgLeuGluAsnIleAlaLybThrGluProPolyIle-----PheArgValLy 144
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QY 145 ProValIleu-----GlyIleLybArgMetIleGlnIleGluThrIleLy 159
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Db      919 CCTGATGATGCTCTCACCAAGCTGCTGCTGTGCTGAGCTGAGGACCATGAGGCC 978
Qy      160 ProGUleuAlaProValSerSerAspLeuGlyTyrThrLeuArgPheArgThrValAsn 179
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Qy      180 SerThrSerTrpMetGluValAsnPheAlaValAsnArgGlyAspValAsnGlnThrTyr 199
Db      1039 -----TGGACTCTGTGTGTCCACCTGCTTCCAGCAGAGACAG-----TTT 1080
Qy      200 AsnLeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValAs 219
Db      1081 GAGCTCTGGGGCTCATCAGGCCCGACAGCTTACCCCTACAGATGCGATGCG---ATTCGC 1137
Qy      220 GluSer-----LysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGlnGlu 237
Db      1138 TCATCTCTGCTGATCTGTGAGCTTGGAGCCCTGAGGCCCGGCTGACCTGAGGCTTACCATG 1197
Qy      238 GluAlaPro---CysGlyLeuGlnLeuThrParGValLeuLysProAlaGluAlaAspGly 256
Db      1198 AAGGCCCCACCATCAGACTGACACGCTGTCTGAAAGAACATGAT---CCAGGG 1254
Qy      257 ArgArgProValArgLeuLeuTrpLysAlaArgGlyAlaProValLeuGlu----- 274
Db      1255 ACAGTAGAGTGTGAGCTGTCTGAAAGCCA-----ACGCCCTGACAGAAACAGAGT 1305
Qy      275 ---LysThrLeuGlyTyrAsnIle---TrpTyrTyrProGluSerAsnThrAsnLeuThr 292
Db      1306 GGAAGATCCAGGGGTACTCTGTCTGAGATTCCACAGATCATCAAGGACAGACATA 1365
Qy      293 GluThrMetAsnThrThrAsnGlnGlnLeuGluIleAlaGlyLysSerPheTrp 312
Db      1366 CACCTTGCAACACACGACGACTGCTGTATCTTCTCTGCTGCTGACGAGGCCAGAAC 1425
Qy      313 ValSerMetIleSerTyrAsnSerLeuGlyLysSerProValAlaThrLeuArgIlePro 332
Db      1426 GTGACCTGTGTGGCTTACAAAGACAGGAGCCTTCCACTACCTACAGTG----- 1476
Qy      333 AlaIleGlnGluLysSerPheGlnCysIleGluValMetGlnAlaCysValAlaGluAsp 352
Db      1477 GTTTCTCGAGAAC-----GAAAGT 1497
Qy      353 GlnLeuValValLysTrpGlnSerSerAlaLeuAspValAsnThrTrpMetIleGluTrp 372
Db      1498 CCACTGTGACCGGACCTCATGCTGAGCCCAAGACCTTACACCATCTGGTGGATCTGG 1557
Qy      373 ---PheProAspValAspSerGluProThrThrLeuSerTrpGluSerValSerGlnAla 391
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Qy      398 ---GlnAspLysLeuLysProPheTrpCysTyrTrpAsnIleSerValTyrProMetLeuHis 416
Db      1678 TTAAAGCAACATTAATCTCTTACAGCTTACAGAAATTAACATGAGCTCCCTGACCCA 1737
Qy      417 AspLysValGlyLysProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGlu 436
Db      1738 GGCATCGTGGGACCTCTGTAATGTCTACACCTTCCGTGAGAGAGAGAGCTTCTTCAT 1797
Qy      437 GlyProGluThrLysValGluAsnIleGlyValLysThrValIleThrTyrLysGlu 456
Db      1798 GCTCCAGGCTGCACTTAACAGCATGTTGGCAACCTGGGACAGCTGGAGTGG----- 1851
Qy      457 IleProLysSerGluLysGlyIleIle-----CysAsnTyrThrIlePheTyrGln 474
Db      1852 GTACTTGAAGCCCTTACGCTGGAGTGAATACCTTACACCTACACCATCTTCTGGGCC 1911
Qy      475 AlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeu 494
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Qy      495 GluSerLeuLysArgLysThrSerTyrIleValGlnValMetAlaAsnThrSerAlaGly 514
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Qy      535 LeuIleThrSerLeuIleGlyGlyLeuLeuLeuIleIleLeuThrValAlaTyr 554
Db      2092 CTG-----GGCATACTTGTCTTGTAGTACTTGTCCACTACCTGT 2130
Qy      555 GlyLeuLysLysProAsnLysLeuThrHisLeuLys----- 566
Db      2131 -----GTAGTACCTGCTGTGCTGCAAAACCAAGAGAAAGACTTCC 2172
Qy      567 ---TrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
Db      2173 TTCTGTCAATGTGTCCAGACCCAGCCACAGTACCTGAGCTCTGTG 2220

RESULT 8
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LOCUS      2592 bp DNA linear GSS 16-DEC-2003
DEFINITION Homo sapiens CSF3R gene, VIRUTAL TRANSCRIPT, partial sequence,
ACCESSION AY412152
VERSION    AY412152.1 GI:39768117
KEYWORDS   GSS.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 2592)
            Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
            This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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Score:          459.50      Matches:      165
Percent Similarity: 39.68%      Conservative: 81
Best local Similarity: 16.61%      Mismatches: 279
Query Match:    13.19%      Indels:      95
Db:              9      Gaps:      25

US-10-006-265-2 (1-652) x AY412152 (1-2592)
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Db      1339 GGAAAGAAATGGAGAGCCAGGGGTTTCTGCTGAAGAGAAC--ATCAGGCCCTTTCA 1395
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Db      1396 GCCTTATGAGATATGCTACTCTCTTGTACAGAGACACCATGGACCTCCCAAGATGT 1455
Qy      425 eGlnAlaTyraIaLysGluGlyValProSerGluGlyProGluThrIyValGluAsn1 445
Db      1456 CTATGCTACTCTCAAGAAATGGCTCCCTCCAGCCGAGAGCTGCATTAAGACAT 1515
Qy      445 eGlyValIyThrValThrIleThrIleThrIleProIySerGluArgIyGly1 465
Db      1516 TGCAAGACCTGGGCAACAGCTGGAGTGGCTGCTGAGCCCTGAGCTGGGAGAGGCC 1575
Qy      465 etIeCyAsnTyThrIlePheTyrgIlnaIaGluGlyIyGlyPheSerIyThrVa 485
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Qy      505 IglValMetAlaAsnThrSerIaGlyIyThrAnGlyThrSerIleAsnPhelyTh 525
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Db      1816 GCTCACCTGCTCTGTGGAACTGCTGCTGCTGTGGAGCCCAAGAGAAATCCCT 1875
Qy      565 uCySTPProThrValIProAsnProAlaGluSerSerIleAlaThrTP-----561
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Qy      582 ----HisGlyAspAspPhelys-----AspIyIleuAs 591
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ACCESSION CP915066
VERSION    CP915066.1 GI:38186268
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 651)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)

JOURNAL    MEDLINE
PUBMED     11544199
COMMENT    Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@nigun.grc.nia.nih.gov
Plate: B0973 Row: F Column: 04
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FEATURES
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/note="Vector: PCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
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Research Program, NIH (http://jgun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). (PMID: 11544199)). Total
RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an oligo(dT)
primer (Invitrogen:
5'-pACACTAGTTCTAGATCGCAGCGCGCCGCTTTTCTTTT-3'1,
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker lI-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of PCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.5 kb. The library was
constructed by Yulan Piao."

ORIGIN
Alignment Scores:
Pred. No.:      8,66e-32      Length:      651
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Percent Similarity: 64.90%      Conservative: 19
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DB:              7          Gaps:      3

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Qy      46 TyrTyAlaGluAsnIleuThrCyThrTyPseProGlyIyGluIySerTyThrIyGln 65
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Qy      66 TyrThValIyAlaGlyThrTyAlaPheGlyIyIyHISAspAsnCyThrThrAsnSer 85
Db      409 TACATGTGACTTGTGACTTATCTCTATGAAA-----AGC 444
Qy      86 SerThrSerGluAsnArgAlaSerCySerPhePheIeuProArgIleThrIle----- 103
Db      445 AATTATATGAGACATCTACAGAGGCTCATATTCTTTCCCGCTGTGCATGATGCC 504
Qy      104 ProAspAsnTyThrIleGluValaGluIaGluAsnGlyIyArgGlyValIleIySerHis 123
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Qy 124 MetThyTyrPArgLeuGluAsnIleAlaLysThrGluProProlyIlePheArgVal 143
 Db 565 ATCAATATGGCATTTATCTCCATAGAAAACGAAACCATTAATTTAAGTGG 624
 Qy 144 LysProValLeuGlyIleLysArgMetIleGln 154
 Db 625 AATCCAATT-----TGTAATAGAAATGTTCCAG 651

RESULT 11
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 LOCUS Mus musculus CSF3R gene, VIRUTAL TRANSCRIPT, partial sequence,
 DEFINITION AY412154
 ACCESSION AY412154
 VERSION AY412154.1 GI:39768119
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2535)
 REFERENCE Clark,A.G., Gnanowskri,S., Nielson,R., Thomas,P., Kejarival,A.,
 AUTHORS Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene ctions
 TITLE Science 302 (5652), 1960-1963 (2003)
 JOURNAL
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 2535)
 AUTHORS Clark,A.G., Gnanowskri,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sminsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submision
 TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 JOURNAL Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
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 Best Local Simlarity: 25.33% Mismatches: 228
 Query Match: 11.35% Indels: 140
 DB: 9 Gaps: 24

US-10-006-265-2 (1-652) x AY412154 (1-2535)

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 Qy 127 TrpArgLeuGluAsnIleAlaLysThrGluProProlyIle-----PheArgVal 144
 Db 658 CTCGACCCCATGATGTTGTGAATTTGAGCTCCCATGCTCGACAGCCCTGACATTGGC 717

145 ProValLeu-----GlyIleLysArgMetIleGlnIleGluTrpIleLys 159
 Db 718 CCGATGATGATGCTTCACACCACTGCTGCTGTGCTGAGCTGGAAGCCATGGAAGCCC 777

160 ProGluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsn 179
 Qy 778 AGTGAGTACATGAAACAGAGAGTGAAATTGCTGATCACGCCACAGCTCAAGACCCAAC 837

180 SerThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyr 199
 Db 838 -----TGACTCTGGTGTTCACCTGCTTCCTGCTTCAGCAAGACAG-----TTT 879

200 AsnLeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLys 219
 Db 880 GAGCTCTGGGGCTTCATCAGAGCCCAAGTCTACACCTCAGATGATGCATGC---ATTGCG 936

220 GluSer-----LysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 237
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238 GluLysProCysGlyLeuGluLeuTrpArgValLeuLys-----ProAlaGluAlaAsp--- 255
 Db 973 -----GGCTTGACCTGAGGCTTACCTAGAGGGTCCCCACCTGACACTGG 1020

256 -----GlyArgArgProValArgLeuLeuTrp 264
 Db 1021 ACACGTGTGTGCAGAGAAGCAATGATCCAGGAGACAGTG-AGTGTGACTGTTCGG 1079

265 LysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrpTyrTyr 284
 Db 1080 AAGCAGAGAC----- 1088

285 ProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGlnGluLeu 304
 Qy 1089 -----ATACACCTTGGCAACACAGCAGCTCAGCTGATCTTC 1127

305 HisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGlyLysSer 324
 Db 1128 CTCCTGCCCTCAGAGGCCCAAGAGTGAACCTTGCTGCTTCAACAAGGAGGACCTCT 1187

325 ProValAlaThrLeuArgGlieProAlaIleGlnGluLysSerPheGlnCysIleGluVal 344
 Qy 1188 TCACCTACTACAGTGT-TTTCTCGA----- 1213

345 MetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAlaLeuAsp 364
 Db 1214 GAACGAAGGTGCCAGCT-----GTGACCGAGCTCCATGCGCAGGCCCAAGAC 1261

365 ValAsnThrTrpMetIleGluTrp---PheProAspValAspSerGluProThrThrLeu 383
 Db 1262 CTTAACACCATCTGGAGAACTGGGAAGCCCGACCTTGCTGCTAGGGCTATCTCAT 1321

384 SerTrpGluSerValSerGlnAlaThrAsn-----TrpThrIleGln--- 397
 Db 1322 GAGTGGGAATGAGCTTCTCCAGCTACATAACAGCTATTAAGTCTGATGATGAACCT 1381

398 -----GlnAspLysLeuLysProPheTrpCysTyrAsn 408
 Db 1382 AACGGAAATCATCTGAATTTCTGTAAAGCAACAATAATCCCTTTCAGCTCTACAGA 1441

409 IleSerValTyrProMetLeuHisAspLysValGlyGluProTyrSerIleGlnAlaTyr 428
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[illegible]

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Score:	43.72%	Conservative: 65
Percent Similarity:	29.15%	Mismatch: 180
Best Local Similarity:	11.17%	Indels: 71
Query Match:	3	Gaps: 19
DB:		
US-10-006-265-2 (1-652) x CRE10771 (1-1931)		
QY	199 TyrAenLeuThrglyLeuGlnProPheThrglyTyValIleAlaLeuAryCyS--Ala 217	
Db	27 TATGAGCTCTCGGGGCTCTCCACCAAGGCGCTACACCTCAGATCAGATGCTGATCCG 86	
QY	218 VallysGluSerLyPheThrSerAspTrpSerGlnGlnLylMetGlyMetThrGlnGlu 237	
Db	87 TGGCCCTGCTGGCCACTGAGCAGCAGCAGACCCGACCTGAGCTGAGATACCGAA 146	
QY	238 GluAlaPro--CysGlyLeuGlnLeuTrp-----ArgValLeuLysProAlaGlu 253	
Db	147 CGGGCCCCCACTGCTCAGACTGAGCAGCATGCTGGCGGAGAGGAGCAGCTGAGACCCC 200	
QY	254 AlaAspGlyAraGArgProValAraGluLeuTrpLysAlaAraGlyAlaProValLeu 273	
Db	201 -----AGGACAGTGCAGCTGTTCTGGAGCCA-----GTGCCCTGGAG 239	
QY	274 Glu-----LysThrLeuGlyTyraSniIeTrpTyTyProGluSerAsnThrAn 290	
Db	240 GAAGACAGCGGACGGATCCAGGTTATGTTGTTCTGGAGACCTCAGACCGAGCTGG 299	
QY	291 --LeuThrGlnThrMetAsnThrThraSngInGlnLeuGlnLeuHisLeuGlyGln 309	
Db	300 GCCATCTGCCCTCTGCAACACACAGAGCTCAGCTGACCTTCCACTGCTTACAGA 359	
QY	310 SerPheTrpValSerMetIleSerTyraSniSerLeuGlyLysSer-----ProVal 326	
Db	360 GCCCAGAGAGTGGCCCTTGCGCTATAAATCAGCCGGAGCCTCTGCTCCACTCCGGT 419	
QY	327 -----AlaThrLeuAraGlyLeuProAlaIleGlnGlnLylSerPheGlnIleGluVal 344	
Db	420 GTCTTCTAGAAAGCAGAGGCCACCTCTGACACAGCTCCAT----- 461	
QY	345 MetGlnAlaCyValAlaGluAsp-----GlnLeuValValLysTrpLysSerSerAla 362	
Db	462 -----GCCATGCGCCGAGACCCCTCAGACCTCTGGGTAGCGTGGAGACCCCC 509	
QY	363 LeuAspValAsnThrTrp-----MetIleGlnTrpPhe-----ProAsp 375	
Db	510 -----AATCATGGCCTCAGGCGTATGATGAGTGGGGCCTGGAGCCCCCCACAG 560	
QY	376 ValAspSerGluProThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThr 395	
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QY	396 IleGlnGlnAspLysLeuLysProPheTrpCysTyraSniSerValLysProMetLeu 415	
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QY	416 HisAspLysValGlyGluProTySerIleGlnAlaTyraLysGlnLylValProSer 435	
Db	678 CAGGACACACATAGGAGCCCTCCAGCATGTCTATGCTACTCTCAAGAAATGGCTCCCTC 737	
QY	436 GluGlyProGlnThrLysValGlnAsnIleGlyValLysThrValThrIleThrTrpLys 455	
Db	738 CATGCCCCAGAGCTCACTAAAGCACAATTGGCAGACACTGGGACACAGCTGGAGTGGGTG 797	
QY	456 GluIleProLysSerGluAraGlyLeuIleIleCysAsnTyThrIlePheTyraGlnAla 475	
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[illegible]

RESULT 13					
BC020454					
LOCUS					
DEFINITION	BC020454	1512 bp	mRNA	linear	HTC 19-NOV-2003
	Mus musculus interleukin 6 signal transducer,		mRNA		
	IMAGE:3598166).				

VERSION	BC020454.1	GI:18045025
KEYWORDS	HTC.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS
Strauberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
1 (bases 1 to 1512)
Euryarchaeota, Metazoa; Chordata; Crustacea; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE	JOURNAL
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
Klausner, R.D., Collins, F.S., Wagner, L., Shenmer, C.M., Schuster, G.D., Altschuler, S.F., Zeeberg, B., Butcove, K.H., Schaefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Useldi, T.B., Tasanly, T., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abraham, R.D., Mullen, S.J., Bosak, S.A., Mcwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Woley, K.C., Hale, S.C., Garcia, A.M., Gay, L.J., Hultky, S.W., Vittal, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Keltman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shcherbo, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Buttefield, Y.S., Krzywinski, M.I., Skalka, U., Smilins, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	

MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (baaes 1 to 1512)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian

REMARK
COMMENT

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNI)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Louisseged, H., Kowik, C.R., Speed, A.J., Martin, R.G., Muzny, D.M., Nanaevli, A.N., Gibbs, R.A.

clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 16 Row: k Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gt: 6754337
This clone has the following problem: no polyA-tail.

FEATURES
Source

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/_clone="IMAGE:359816"
/_tissue_type="Mammary tumor, C3(1)-Tag model, Infiltrating
ductal carcinoma, 5 month old virgin mouse."
/_clone_1b="NCI CGAP_Mam6"
/_lab_host="DH10B"
/_note="Vector: pCMV-SPORT6"

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ORIGIN

Alignment Scores:	
Pred. No.:	1,18e-26
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Best Local Similarity:	29.61%
Query Match:	10.19%
DB:	3
Length:	1512
Matches:	90
Conservative:	63
Mismatches:	133
Indels:	18
Gaps:	11

US-10-006-265-2 (1-652) x BC020454 (1-1512)

[illegible]

Db	Accession	Source	Organism	Reference Authors	Title	Journal Comment
Db	949	TTAAAGCTATCATGGGCTTCAGGCGCTGGCGCGCTCTT	---	TTAGATCTTAAAGTCTGAC	1005	
Qy	173	LeuAargPhearqThrValaIasnSerThrSerTrpMetGluValaIasnPhalaIaAsnArg	192			
Db	1006	ATCCAAATATAGGACCAAGAATGCTCTCAACTTGATTCAGAGTCCCTCTT	---	GAAGATACA	1062	
Qy	193	LyasAspLybsAsnGlnThrTyraAsnLeuThrGlyLeuGlnProPheThrGlnTyrrValIle	212			
Db	1063	ATGTCCTCTCGAACCTTCCTTCACGTGCGAGGACCTCAAGCCTTTTACAGAAATATGTGTTT	1122			
Qy	213	AlaLeuArgCysAlaValaIlyeGluSer	---	LyPheTrpSerAspTrpSerGlnGlu	230	
Db	1123	AGGATCCCG	---	TCATTAAAGCAACGTGGAGGCGCTACTGAGTGACTGGAGTGAAGAG	1179	
Qy	231	LyseMetGlyMetThrGlnGluGlnAlaProCys	---	GlyLeuGluLeuTrpArgValleu	249	
Db	1180	GCTAGTGGGACCATATGAGAGACAGACATCCAAACCAACAAGTTCTGTATATAGACA	1239			
Qy	250	LyseProAlaGluAlaAspGlyArgArgProValArgLeuLeuTrpLybAlaArgGly	269			
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Qy	270	AlaProValleuGlnGlyLybThrLeuGlyTYrraAsnIleTrpTYrrTyProGluSerAsnThr	289			
Db	1300	TCTTAAGCCCAATGGGAAAATTTGGATTATGAAGT	---	ATTCTTAAGCAAGTCAAG	1353	
Qy	290	AsnLeuThrGlnThrMetAsnThrThraSngInGlnLeuGlnIleuGlnGlyGlyGlu	309			
Db	1354	TCACTGTCACAAAAGCTACACAGTCACGTGCGACAGAGCGTGAACCGTGAATCTCACCAAGTAC	1413			
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Qy	330	ArgIleProAla	333			
Db	1474	ACCATCCCCAGC	1485			
RESULT 14						
LOCUS	CA561173	592 bp	mRNA	linear	EST 19-NOV-2002	
DEFINITION	K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus musculus cDNA clone NIA:K0283D09 IMAGE:30052652 5', mRNA sequence.					
ACCESSION	CA561173					
VERSION	CA561173.1	GI:25105828				
KEYWORDS	EST.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	EumayrPot; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.					
AUTHORS	1 (bases 1 to 592) Piao, Y., Karpiul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A., Martin, P., Alba, K., Tanaka, T. and Ko, M.S.H.					
TITLE	Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (Long)					
JOURNAL	Unpublished (2001)					
COMMENT	Other ESTs: K0283D09-3 Contact: Dawood B. Dudekula Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdhaa@gsun.grc.nia.nih.gov Plate: K0283 row: D column: 09 Seq primer: M13 Reverse High quality sequence stop: 592 POLYA=No.					
FEATURES						
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/cb xref="taxon:10090"
/clone="NIA:K0283D09 IMAGE:30052652"
/tissue_type="Unfertilized Egg"
/lab host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library
(long)"
/notes="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). (PMID: 11544193)). Total RNAs were
extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen:
5'-pGACCTAGTCTTGAATCGCAGCGCCGCTTTTCTTTTCTTTT-3'),
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
lone-linker l1-sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-5. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Yulan Piao (NIA)."
```

ORIGIN

Alignment Scores:

Score:	1.86e-26	Length:	592
Percent Similarity:	347.00	Matches:	67
Best local Similarity:	65.89%	Conservative:	18
Query Match:	51.94%	Mismatches:	34
	9.96%	Indels:	10
DB:	6	Gaps:	2

US-10-006-265-2 (1-652) x CA561173 (1-592)

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QY      6  GlnProSerCysValaIaenLeuGlYmeMetTrrThrTrrAlaLeuTrrMetLeuProSer 25
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QY      66  TyrThrValIysaRgThrTrrAlaPheGlyGluIaenIshIsaPheancysTrrThraAnsSer 85
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Db      409 TACATTTGACTTGGATCTTACTCTCTTAAGAAAA-----AGC 444
QY      86  SerThrSerGluIaenATGAlaSerCysSerPhePheLeuProAlaIaenIle----- 103
          ::|||
Db      445 AATATATGTGACAAATGTTACAGAGGCTTCAATATCTTTTCCCGTTCGTGCAATGCC 504
QY      104  ProAspAntYrThrIleGluValaGluAlaGluIaenGlyIaenGlyValIleIysSerHis 123
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Db      505 CCAGACATCTCGAGTGTGGAAGTACAAAGCTCAAAATGAGATGTAAAGTTAAATCTGAC 564
QY      124  MetThrTrrTrrPargLeuGluIaenIle 132
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RESULT 15

LOCUS	CA560924	479 bp	mRNA	linear	EST 19-NOV-2002
DEFINITION	K0279C07-5N NIA Mouse Unfertilized Egg cDNA Library (Long)	Mus			

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8	1292	95.1	2903	6	AX365201	Sequence	AX365201
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12	1282	94.4	1299	9	AX499340	Sequence	AX499340
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16	1282	94.4	2445	6	AX362331	Sequence	AX362331
17	1282	94.4	2445	6	AX454786	Sequence	AX454786
18	1282	94.4	2445	6	AX491264	Sequence	AX491264
19	1282	94.4	2445	9	AX358740	Sequence	AX358740
20	1282	94.4	2529	6	AX365193	Sequence	AX365193
21	1282	94.4	2529	9	AX499339	Sequence	AX499339
22	1282	94.4	2776	6	BD178876	Sequence	BD178876
23	1282	94.4	2858	6	BD178875	Sequence	BD178875
24	1282	94.4	2870	6	BD178874	Sequence	BD178874
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39	588.5	43.3	3590	6	BD178877	Sequence	BD178877
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ALIGNMENTS

RESULT 1

BD091865

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD091865

Novel hemopoietin receptor protein, NR10.

2440 bp

DNA

linear

PAT 27-AUG-2005

BD091865

BD091865.1 GI:22637476

WO 0075314-A/2.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2440)

Maeda, M. and Yaguchi, N.

Novel hemopoietin receptor protein, NR10

Patent: WO 0075314-A 2 14-DEC-2000;

CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC., MASATSUGU

MAEDA, NORIKO YAGUCHI

OS Homo sapiens (human)

PN WO 0075314-A/2

PD 14-DEC-2000

PF 01-JUN-2000 WO 2000UD003556

PR 02-JUN-1999 JP 99P 155797.30-JUL-1999 JP 99P 217797 PI

PC C12N15/12, C12N5/10, C07K14/715, C07K16/28, C12P21/02, G01N33/53, G01N33/56

CC

FT CDS

Key

Location/Qualifiers

(523). (1278).

FEATURES
source

Location/Qualifiers
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ORIGIN

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Pred. No.: 8.12e-127 Length: 2440
Score: 1358.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-006-265-4 (1-252) x BD091865 (1-2440)

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QY 181 ThrSerTyPheGlyValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyAsn 200
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QY 201 LeuThrGlyLeuGlnProPheThrGluTyTrpValIleAlaLeuArgCysAlaValLysGlu 220
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QY 241 LeuLeuProAlaIleProValLeuSerThrLeuVal 252
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RESULT 2 AX365169 1476 bp DNA linear PAT 15-FEB-2002
LOCUS AX365169
DEFINITION Sequence 21 from Patent WO0200721.

ACCESSION AX365169
VERSION AX365169.1 GI:18696927
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuiper, J.L.
and Maurer, M.F.
TITLE Cytokine receptor zcytor17
JOURNAL Patent: WO 0200721-A 21 03-JAN-2002;
ZymoGenetics, Inc. (US)

FEATURES
source

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ORIGIN

Alignment Scores:

Pred. No.: 1.42e-125 Length: 1476
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Query Match: 98.90% Indels: 0
DB: Gaps: 0

US-10-006-265-4 (1-252) x AX365169 (1-1476)

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DB 129 CTCTCTCCCACTTCATAGTGTAACTGGGAGATGATGACCTGGGCACTGGAGATG 188
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DB 189 CTCCTCTCACTGCAAAATTCAGCTGCGAGCTCTGCCAGCTAAGCTGAACAATTCC 248
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QY 63 TyTrpGlnTyTrpValLysArgThrTyAlaPheGlyGluLysHisAspAsnGlyThr 82
DB 309 TATACCACTACACAGTTTAAGAACTTAACGCTTTTGGAGAAAACATGATTAATGTACA 368
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DB 369 ACCAATAGTCTTACAAAGTGAATGCTGCTCTGTGCTCTTTTCTTCTTCCAAAGATAAG 428
QY 103 IleProAspAsnTyTrpIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
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QY 123 HisMetThrTyTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
DB 489 CATATGACATACTGAGATTAAGAAACATAGCAAAACGAAACCACTTAAGATTTTCCGT 548
QY 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
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Qy 203 GLYLEUGINPPOPHETHRGUITYRVALILEALALEUA9GYSBALAVALLYGLUSERYS 222
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Qy 223 PHEITPSEAPITPSESGINGULYSEWETGLYMETHTRGUGLUGLUGLYLYSELEUEN 242
Db 789 TTTCGAGTGACTGAGGCAAGAAAATGGGAATGACTGAGAGAAAGGCAAGCTACTC 848
Qy 243 PROALALEPROVALLEUSERITHLEUVAL 252
Db 849 CCTGCGATTCCCGTCTGCTGCTGCTG 878

RESULT 3
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LOCUS AF106913 1761 bp mRNA linear PRI 01-DEC-2001
DEFINITION Homo sapiens CRJ3 protein (CRJ3) mRNA, complete cds.
ACCESSION AF106913
VERSION AF106913.1 GI:17221662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Zhang, W., Man, T., He, L., Yuan, Z. and Cao, X.
TITLE A novel soluble type I cytokine receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1761)
AUTHORS Zhang, W., Man, T., He, L., Yuan, Z. and Cao, X.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-1998) Department of Immunology, Shanghai
Brilliance Biotechnology Institute & Second Military Medical
University, 800 Xiangyin Road, Shanghai 200433, P.R.China
FEATURES
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ORIGIN
Alignment Scores: 2.47e-120 Length: 1761
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 9 Gaps: 0

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Qy 21 TTPMETLEUPROSELEUCYELYPHESELEUALALEUPROALALEPROGLUN 40
Db 174 TGGATGCTCCCTTACCTGCAATTCAAGCTTGCAAGCTTGCCAGCTGAGCAAG 233
Qy 41 ILESECYVALITYRYTYRARGLYASMLEUTHRCYTHRTTPSEPROGLYLYSGLU 60
Db 234 ATTTCGTGTGCTACTACTATAGAAAATTAACTGCACTTGAGAGTCCAGAAAGGA 293
Qy 61 THISERTYTHRGUITYRTHVALYARGTHYRZALAPHEGLYGLYVHIAEPAN 80
Db 294 ACCAGTTATACCGATACACAGTTAGAGGACCTTAAGCTTTTGGAGAAAACATGATAT 353
Qy 81 CYETHRTHASERSETHERSERGLUASNAHGLASERCYSESPHELEUPROARG 100
Db 354 TGTACACCAATAGTCTTACAGTAAGTAATGTCTGTCTCTTTTCTTCCACAGA 413
Qy 101 ILETHRILEPROAPASNTYRTHRILEGLUVALGLUAGLUANGLYASGLYVALILE 120
Db 414 ATTAAGATCCAGATTAATTATACATTGAGGTGAGAGTGAATAATGGAGATGTAT 473
Qy 121 LYSSETHSWETHRYTRTPARGLEUGLUNLLEALALYTHRGUPTROLYSILE 140
Db 474 AAATCTCATATGACATCTGAGATTAGAGAACATAGGAAACCTAACCACTTAAGATT 533
Qy 141 PHEARGVALYSPROVALLEUGLYILEYASRGMETILEGNIILEGUTPILLYSEPRO 160
Db 534 TTCGTGTGAACCAAGTTTGGGCAACAGATGATTCAATTAATGATTAAGATCT 593
Qy 161 GLULEUALPROVALISERSEASPLEULYERYTHREUARGPHEARGTHVALASNER 180
Db 594 GAGTTGGGCGCTGTTTATCATCGATTAAATACACACTGATTACAGACGTCACAGT 653
Qy 181 THISERTYMETGLVALASNPALALYASNAHGLYASAPPLYSAENGINTHTYTHASN 200
Db 654 ACCAGCTGAGTAGAAGCACTTCGCTTAAGAACCGTAAGATGATAAAACCAAACTTACAA 713
Qy 201 LEUTHRGYLEUGINPPOPHETHRGUITYRVALILEALALEUA9GYSBALAVALLYGLU 220
Db 714 CTCACGGGCGCTGCAAGCTTTTACAGAAATGTCATAGCTTCGCAATGCGGCTCAAGAG 773
Qy 221 SERLYSPHERTPSEAPITPSESGINGULYSEWETGLYMETHTRGUGLUGLU 238
Db 774 TCAGATTCTGAGTGACTGAGGCAAGAAAATGGGAATGACTGAGAAAGA 827

RESULT 4
BD091877 2119 bp DNA linear PAT 27-AUG-2002
LOCUS BD091877
DEFINITION Novel hemopoietin receptor protein, NR10.
ACCESSION BD091877
VERSION BD091877.1 GI:22637488
KEYWORDS WO 0075314-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2119)
Maeda, M. and Yaguchi, N.
TITLE Novel hemopoietin receptor protein, NR10
JOURNAL Patent: WO 0075314-A 14 14-DEC-2000;
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU
MAEDA, NORIO YAGUCHI
COMMENT
OS Homo sapiens (human)
PN WO 0075314-A/14
PD 14-DEC-2000
PF 01-JUN-2000 WO 2000JP003556
PR 02-JUN-1999 JP 99P 155797,30-JUL-1999 JP 99P 217797 P1

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Qy 221 SerlyspHetTPSerAspTTPSerGlnGluYbMetGlyMetThrGlnGlnGlu 238
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LOCUS Sequence 68 from Patent WO0200721.
DEFINITION AX365216
ACCESSION AX365216.1 GI:18696970
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
1
Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kujiper, J.L., and Maurer, M.F.
Cytokine receptor zcytor17
Patent: WO 0200721-A 68 03-JAN-2002;
JOURNAL ZymoGenetics, Inc. (US)
FEATURES
Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 3,43e-120 Length: 2295
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
Gaps: 0
DB: 6

US-10-006-265-4 (1-252) x AX365216 (1-2295)

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Qy 41 lIeserCyValIyTyrTyrTyrGlyAbnleuThrCySthTTPSerProGlyIyIyGlu 60
Db 121 ATTTCCTGTCTCTACTATAGAAATTTAACTCTGACCTTGAGATGCCAGAAAGGAA 180
Qy 61 ThreSerTyrThnGlnIyTyrThValYbArghThrTyrAlaPheGlyGlyIyIyIyAspAsn 80

Db 181 ACCAGTTATACCCAGTACAGAGTTAAGGAACTTAACGCTTTTGGAGAAAAATGATATAT 240
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Qy 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaIeUArgCyAlaIyValIyGlu 220
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Qy 221 SerlyspHetTPSerAspTTPSerGlnGluYbMetGlyMetThrGlnGlnGlu 238
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LOCUS Sequence 3 from Patent WO0229060.
DEFINITION AX467333
ACCESSION AX467333.1 GI:21900584
VERSION
KEYWORDS
SOURCE
ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
Cosman, D.J., Mosley, B.A., Bird, T.A., Dubose, R.F. and Wiley, S.R.
Hematopoietin receptors hprt1 and hprt2
Patent: WO 0229060-A 3 11-Apr-2002;
JOURNAL Immunex Corporation (US)
FEATURES
Location/Qualifiers
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Alignment Scores:
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
Gaps: 0
DB: 6

US-10-006-265-4 (1-252) x AX467333 (1-2480)

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Qy 21 TrpMetLeuProSerLeuCyAlbYbSerLeuAlaIaIeUProAlaIaYbProGluAsn 40

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Db 252 ATTTCCGTGTCACACTATAGAAAATTTAACTGCACCTTGAGTCCAGGAAAGGAA 311
Qy 61 ThSerTyrrThrgIntyrrThrVal1yysargThrrTyrrAlpheGlyGluysrHisaapen 80
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Qy 81 CyserrThrrasnSerThrrSerGluasnArgAlSerCysSerPhePheLeuProArg 100
Db 372 TGTACACACCAATAGTCTCAAGTGAATAATCGCTTCGCTCTTTTCTCCCAAG 431
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Qy 121 LysSerHisMetThrrTyrrTrpAcgLeuGluasn11eAlalyThrrGluProPolysile 140
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Qy 221 SerTyrrPheThrrSerAspTrpSerGlnGluLysMetGlyMetThrrGluGluGlu 238
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RESULT 8
LOCUS AX365201 2903 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 53 from Patent WO0200721.
ACCESSION AX365201
VERSION AX365201.1 GI:18696955
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
Bakayota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Krijger,J.L.
and Maurer,M.F.
Patent: WO 0200721-A 53 03-JAN-2002;
Cytokine receptor ZCYFOR17
ZymoGenetics, Inc. (US)
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ORIGIN
Alignment Scores:
Pred. No.: 4,6e-120 Length: 2903
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
Gaps: 0
DB: 6

US-10-006-265-4 (1-252) x AX365201 (1-2903)
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Db 497 ATGAGCTCTCTCCCAAGCTTCATGTTTAACTGGGAGATGATGAGCTGGGCACCTG 556
Qy 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlalyProGluasn 40
Db 557 TGGATGCTCCCTTCACACTCGCAAAATTCAGCCTGGCAGCTCTCCAGCTAAGCTAGAAG 616
Qy 41 11eSerCysVal1yrrTyrrArglysaenLeuThCyserrThrSerProGlylysglu 60
Db 612 ATTTCCGTGTCACACTATAGAAAATTTAACTGCACCTGAGTTCAGAGTCAAGAAAGAA 676
Qy 61 ThSerTyrrThrgIntyrrThrVal1yysargThrrTyrrAlpheGlyGluysrHisaapen 80
Db 672 ACCAGTATACCAATATATATACCATTTGAGGTGAAAGCTGAAATGAGATGATGATAT 736
Qy 81 CyserrThrrasnSerThrrSerGluasnArgAlalySerCysSerPhePheLeuProArg 100
Db 732 TGTACACCAAAATAGTTCTTACAGTGAATAATCGTCTCTCTTTTCTCCCAAG 796
Qy 101 11eThrr11eProaspentTyrrThr11eGluVal1Glu1yasnGlyysarglyVal111e 120
Db 797 ATACAGATCCAGATATATATACCATTTGAGGTGAAAGCTGAAATGAGATGATGATAT 856
Qy 121 LysSerHisMetThrrTyrrTrpAcgLeuGluasn11eAlalyThrrGluProPolysile 140
Db 857 AATCTCATATGACATCTGAGATTTAGAGACATAGCGAAACTGAACTCAAGCTTAAGATT 916
Qy 141 PheArgVal1yysProVal1leugly11eLysArgMet11eGln11eGluTrp11eLysPro 160
Db 917 TTCGGTGGAAACAGTTTGGGCATCAACGAATGATTTCAATGATGATTAAGCTTAAGCTT 976
Qy 161 GluLeuAlaProVal1SerSerAspLeuysTyrrThrLeuArgPheArgThrrVal1asnSer 180
Db 977 GAGTTGGCGCTTTTCATCTGATTTAAATACACCTTCGATTCAGAGTCAAGCAAGCT 1036
Qy 181 ThSerTyrrMetGluVal1asnPheAlalyAsnArgLysAspLysasnGlnThrrTyrrasn 200
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Qy 201 LeuThrglyLeuGlnProPheThrglyTyrrVal111eAlalyLeuArgCysAlaVal1yysGlu 220
Db 1097 CTCACGGGCGTGCAGCTTTTACAGAAATGTCATAGCTCTGCAGTGTGGCGTCAAGAG 1156
Qy 221 SerTyrrPheThrrSerAspTrpSerGlnGluLysMetGlyMetThrrGluGluGlu 238
Db 1157 TCAAGTTCTGAGTAGTGCAGGCCAAGAAAATGGGAATGACTGAGGAAGAA 1210

RESULT 9
LOCUS AY499342 2903 bp mRNA linear PRI 10-JUL-2004
DEFINITION Homo sapiens Interleukin 31RA splice variant x4 (IL31BA) mRNA,

```

complete cds, alternatively spliced.

ACCESSION
AY499342
VERSION
AY499342.1 GI:46276462

KEYWORDS
SOURCE

ORGANISM
Homo sapiens (human)

REFERENCE
1 (bases 1 to 2903)
Dillon, S.R., Sprecher, C., Hammond, A., Bilborough, J.,
Rosenfeld-Franklin, M., Presnell, S.R., Haugen, H.S., Maurer, M.,
Harder, B., Johnson, J., Bort, S., Mudri, S., Kuijper, J.,
Bukowski, T., Shea, P., Dong, D.L., Dasovich, M., Grant, F.J.,
Lockwood, L., Levin, S.D., Leciel, C., Maggie, K., Day, H., Topouzis, S.,
Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parrish-Novak, J. and
Gross, J.A.
Interleukin 31, a cytokine produced by activated T cells, induces
dermatitis in mice

TITLE
JOURNAL
Natl. Immunol. 5 (7), 752-760 (2004)

REFERENCE
2 (bases 1 to 2903)
Dillon, S.R., Sprecher, C., Hammond, A., Rosenfeld-Franklin, M.,
Presnell, S.R., Haugen, H., Bilborough, J., Maurer, M., Harder, B.,
Johnson, J., Bort, S., Mudri, S., Kuijper, J., Bukowski, T.,
Dong, D., Dasovich, M., Lockwood, L., Levin, S., Leciel, C., Maggie, K.,
Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parrish-Novak, J. and
Gross, J.A.
Direct Submision
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA

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ORIGIN
Alignment Scores:
Pred. No.: 4.6e-120 Length: 2903
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: Gaps: 0

US-10-006-265-4 (1-252) x AY499342 (1-2903)

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DB 497 ATGAAGCTCTCTCCACAGCTTCACTGATGTTAACTGGGAGATGATGAGACCTGGACATG 556

QY 21 TrpMetLeuProSerLeuGlyPheSerLeuAlaAlaLeuProAlaGlyProGln 40

DB 557 TGGATGCTCCCTTCACTCTGCAAAATTCAGCTGGAGCTTCCGACCTAAGCTTAGAAC 616

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QY 61 ThSerTyrTrpGlnTyrTyrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn 80

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RESULT 10

LOCUS BD091864 2969 bp DNA linear PAT 27-AUG-2002

DEFINITION Novel hemopoietin receptor protein, NR10.

ACCESSION BD091864.1 GI:22637475

VERSION BD091864.1 A/1.

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2969)
Maeda, M. and Yaguchi, N.
Novel hemopoietin receptor protein, NR10
Patent: WO 0075314-A 1 14-DEC-2000;

AUTHORS CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, MASATSUGU

JOURNAL MAEDA, NORIKO YAGUCHI

COMMENT OS Homo sapiens (human)

PN WO 0075314-A/1

PD 14-DEC-2000

PR 01-JUN-2000 WO 2000JP003556

PC 02-JUN-1999 JP 99P 155797, 30-JUL-1999 JP 99P 217797 PT

PC MASATSUGU MAEDA, NORIKO YAGUCHI

PC G12N15/12, C12N5/10, C07K14/715, C07K16/28, C12P21/02, G01N33/53,

PC G01N33/566

CC FH Key Location/Qualifiers

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ORIGIN

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.14%	Indels:	0
DB:	6	Gaps:	0

US-10-006-265-4 (1-252) x BD091864 (1-2969)

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 LOCUS AX365165 Sequence 17 from Patent WO0200721.
 DEFINITION AX365165
 ACCESSION AX365165 GI:18696923
 VERSION
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 Sprechet,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kujiper,J.L.
 and Maurer,M.F.
 Cytokine receptor zcytor17
 TITLE Patent: WO 0200721-A 17 03-JAN-2002;
 JOURNAL ZymoGenetics, Inc. (US)

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ORIGIN

Alignment Scores:

Pred. No.:	1.73e-119	Length:	1299
Score:	1282.00	Matches:	236
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.40%	Indels:	0
DB:	6	Gaps:	0

US-10-006-265-4 (1-252) x AX365165 (1-1299)

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 QY 43 CysValTyrrTyrrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluTrpSer 62
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 QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
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LOCUS AY499340 1299 bp mRNA linear PRI 10-JUL-2004
DEFINITION Homo sapiens interleukin 31RA splice variant x2 (IL31RA) mRNA,
complete cds, alternatively spliced.
ACCESSION AY499340
VERSION AY499340.1 GI:46276458
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1299)
AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Bilborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J.L.,
Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., Leciel,C., Waggle,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
Interleukin 31, a cytokine produced by activated T cells, induces
dermatitis in mice
Nat. Immunol. 5 (7), 752-760 (2004)
15184896
2 (bases 1 to 1299)
AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M.,
Presnell,S.R., Haugen,H., Bilborough,J., Maurer,M., Harder,B.,
Johnston,J., Bort,S., Mudri,S., Kuijper,J., Bukowski,T., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., Leciel,C., Waggle,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.
Direct Submission
Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA
LOCATION/Qualifiers
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162. 1136
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Pred. No.: 1,73e-119 Length: 1299
Score: 1282.00 Matches: 236
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.40% Indels: 0
Gaps: 0
US-10-006-265-4 (1-252) x AY499340 (1-1299)
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QY 23 LeuProSerLeuCysIysPheSerLeuAlaIleuProAlaIysProGluAsnIleSer 42
Db 189 CTCCCTCACTCTGAAATTAAGCCTGGACCTTCGACGCTTAAGCTGAAGCAATTTCC 248
QY 43 CysValTyrTyrTyrArgIysAsnLeuThrCysThrTPSerProGluIlyGluThrSer 62
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QY 223 PheTTPSerAspTPSerGlnGluIlyMetGluIlyMetThrGluGluGlu 238
Db 789 TTCTGAGTGAAGTGAAGCAAGAAAAATGGAATGAGTGAAGAA 836
RESULT 13
LOCUS AY499341 2393 bp mRNA linear PRI 10-JUL-2004
DEFINITION Homo sapiens interleukin 31RA splice variant x3 (IL31RA) mRNA,
complete cds, alternatively spliced.
ACCESSION AY499341
VERSION AY499341.1 GI:46276460
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2393)
AUTHORS Dillon,S.R., Sprecher,C., Hammond,A., Bilborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kuijper,J.L.,

Alignment Scores:

Bukowski, T., Shea, P., Dong, D.L., Dasovich, M., Grant, F.J., Lockwood, L., Levin, S.D., Leciel, C., Maggile, K., Day, H., Topouzis, S., Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parish-Novak, J. and Gross, J.A. Interleukin 31, a cytokine produced by activated T cells, induces dermatitis in mice Nat. Immunol. 5 (7), 752-760 (2004)

JOURNAL PUBMED 15184896

AUTHORS Dillon, S.R., Sprenger, C., Hammond, A., Rosenfeld-Franklin, M., Presnell, S.R., Haugen, H., Bilborough, J., Maurer, M., Harder, B., Johnston, J., Bort, S., Mudri, S., Kujiiper, J., Bukowski, T., Shea, P., Dong, D., Dasovich, M., Lockwood, L., Levin, S., Leciel, C., Maggile, K., Kramer, J., Kuestner, R., Chen, Z., Foster, D., Parish-Novak, J. and Gross, J.A.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA

FEATURES

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ORIGIN

Alignment Scores:

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Query Match:	94.40%	Indels:	0
DB:	9	Gaps:	0

US-10-006-265-4 (1-252) x AY499341 (1-2393)

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DB 369 ACCAATAGTTCATCAAGTAAATCGTGTGTCTCTTTTTCCTTCAAGAAATACG 428

QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleIysSer 122

DB 429 ATCCAGATTAATTAATTCATGAGTGGAGCTGAAAATGGAGATGTATTAATCT 488

QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaIysThrGluProProIysIlePheArg 142

DB 489 CATATGACATCTCGAGATTAGAGAAACATGGGAAAACATGAACCTAAGATTTCCG 548

QY 143 ValIysProValIeuGlyIleIysArgMetIleGlnIleGluTrpIleIysProGluLeu 162

DB 549 GTGAAACCACTTTGGCATCAACGAAATGATTCAAATTGAATGATTAAGCTGAGT 608

QY 163 AlaProValSerSerAspLeuIysTyrThrLeuArgPheArgThrValAsnSerThrSer 182

DB 609 GGCGCTGTTTCATCTGATTTAAATACACACTTCATTCAGACAGTCAACGATCACG 668

QY 183 TrpMetGluValAsnPheAlaIysAsnArgIysAspIysAsnGlnThrTyrAsnLeuThr 202

DB 669 TGGATGGAAGTCAACTGCTTAAGAACCTTAAGATTAATAACCAACCTACACTCAG 728

QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIysGluSerIys 222

DB 729 GGGCTGCACCTTTTACAAATATGTCATGCTGCGAGTGGCGGTCAAGAGTCAAG 788

QY 223 PheTrpSerAspTrpSerGlnGluIysMetGlyMetThrGluGluGlu 238

DB 789 TTCTGGAGTACTCGAGCCAAAGAAAATGGAAATGACTGAGGAAGAA 836

RESULT 14

AX365149 2402 bp DNA linear PAT 15-FEB-2002

LOCUS Sequence 1 from Patent WO0200721.

AX365149

AX365149.1 GI:18696908

DEFINITION

AX365149.1 GI:18696908

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kujiiper, J.T. and Maurer, M.F. Cytokine receptor zcytor17 Patent: WO 0200721-A.1 03-JAN-2002; ZymoGenetics, Inc. (US)

TITLE

JOURNAL

FEATURES

source

1. .2402 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 171. .2369 /note="unnamed protein product" /codon_start=1 /protein_id="CAD23785.1" /db_xref="GI:18696909" /translation="MMMTWALMLPSLCKFSLAALPAKRENISCVYVYKNTCTWSP GKEISTQYTVKRTYAFGEKDNCTTNSTSENRASSCFELPRITIPDNYTIEVAENNDGYIKSHMTWRLENIAKTEPKI RKPVYIGIKRMIOIEMIKPELAVSDLDKYTLRPTVNSVSMWVFAKRNKDKNTY NLTGLOPTEVYVALACVAKESKESMSDOEKMEFEAPCLZELWRLKPAEDGR RPRILMKARAGAPVLEKTLGNITRYPPSNTNLTNTMTNQLHLAGESFVMS IYNSLGKSPVATLRIPAIQESFOCIEMVACVADOLVKNQSSALVNWTWMEF PVDSEPTLMSWSVSQATNWTIQDQKLPFCWYNTLSPMLDKGEPYSIOAYKE GYPSBEPETKVENIGVKTATITWKEIPKSEKICINYSIPYQABGKSFSGNSI LQYGLSKRTSYIYQWASTAGGNTGNSIFKTLSPVEFIIITSLIGGLIIL IITVAYGLKKPKLTHLCMPYVNPABESSIAWHDPPKDKINLSPDSVSDPRL LRPCTSPDKLVIDKLVNPNVAVLQEIFTDEARTGQENNDGKNGVTCPPRPDCL GSKFELPVSPEIIPKRSQYLRSRMPEGRPEAKQLFSGOSLVVDHLCEGAPNPY LKNSVYARBFVLSEKLPBHTKEV"

CDS

TMHGDPDFDKLNLKESDSDSVNTEDRILKPCSTPSDKLVIDKLNVFNGVLQBIETDEA
RTGQENNLGKNGYVTCPEPRDCEPLGSPFELPVSPRIIPPKSKYLSRMBEGTRPE
AKEQILFSGQSLVPDHLCEBGAHPNYLKNSTVBARFLVSEKLPETHKGEV"

ORIGIN

Alignment Scores:

Pred. No.:	3,71e-119	Length:	2402
Score:	1282.00	Matches:	236
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.40%	Indels:	0
DB:	6	Gaps:	0

US-10-006-265-4 (1-252) x AX365149 (1-2402)

QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTyrThrAlaLeuTyrMet 22
DB 138 CTCTCTCCCAAGCCCTTCAATGTTTAACTGGGGAATGATGTGACCTGGGCACTGTGGATG 197
QY 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
DB 198 CTCCTTCACTCTGCAAAATTCAGCTGGCAGCTCTGCCAGCTTACCTGAGAACATTTCC 257
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTyrPheProGlyLysGluThrSer 62
DB 258 TGTGTCTACTACTATAGAAAATTTAACTGTGACCTGGAGTCCAGAAAGAAACCACT 317
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyLysLysPheAsnCysThr 82
DB 318 TATACCCAGTACACAGTTAAGAACTTAACGCTTTTGGAGAAAACATGATATTGTACA 377
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB 378 ACCAATAGTCTTACAGTAAATGCTGCTGCTCTCTTTTCTTCCCAAGAAATACG 437
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB 438 ATCCAGATTAATTAAACATTGAGGTGAGAGTGAATGAGATGGTAAATTAATCT 497
QY 123 HisMetThrTyrTyrPheGluAsnIleAlaLysThrGluProLysIlePheArg 142
DB 498 CATATGACATCTGAGAGATTAGAAACATAGCGAAACCTGAACCTTAAGATTTTCCGT 557
QY 143 ValLysProValIleGluLysArgMetIleGlnIleGluTrrIleLysProGluLeu 162
DB 558 GTGAAACAGATTGGGCAATCAACGAATGATCAAAATTTGAATGATTAAGCTTAGTTCG 617
QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
DB 618 GCGCTGTTCATCTGATTTAAATTAACACCTTCGATTCAGGACAGTCAACGATCCACG 677
QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
DB 678 TGGATGGAAAGTCACTTCGTAAAGAACGTAAAGATTAACCAACCTAACCTCCACG 737
QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
DB 738 GGGCTGCGCTTTTACAGAAATATGTCATAGCTCTGCAATGCGGTTAAGAGATCAAG 797
QY 223 PheTyrSerAspTyrPheSerGlnGlyLysMetGlyMetThrGluGlu 238
DB 798 TTTCTGAGTGACTGAGACCAAGAAAATGGGAATGATGAGAGAA 845
RESULT 15
LOCUS AX358838 2445 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 91 from Patent WO0193983.
ACCESSION AX358838
VERSION AX358838.1 GI:18675320
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Carnivora; Homini; Homidae; Homo.
Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gunney, A.W., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same

TITLE

JOURNAL

Patent: WO 0193983-A 91 13-DEC-2001;

FEATURES

source

Location/Qualifiers
1..2445
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

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Score:	1282.00	Matches:	236
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	94.40%	Indels:	0
DB:	6	Gaps:	0

US-10-006-265-4 (1-252) x AX358838 (1-2445)

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DB 256 CTCTCTCCCAAGCCCTTCAATGTTTAACTGGGGAATGATGTGACCTGGGCACTGTGGATG 315
QY 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
DB 316 CTCCTTCACTCTGCAAAATTCAGCTGGCAGCTCTGCCAGCTTACCTGAGAACATTTCC 375
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTyrPheProGlyLysGluThrSer 62
DB 376 TGTGTCTACTACTATAGAAAATTTAACTGTGACCTGGAGTCCAGAAAGAAACCACT 435
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyLysLysPheAsnCysThr 82
DB 436 TATACCCAGTACACAGTTAAGAACTTAACGCTTTTGGAGAAAACATGATATTGTACA 495
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB 496 ACCAATAGTCTTACAGTAAATGCTGCTGCTCTCTTTTCTTCCCAAGAAATACG 555
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB 556 ATCCAGATTAATTAAACATTGAGGTGAGAGTGAATGAGATGGTAAATTAATCT 615
QY 123 HisMetThrTyrTyrPheGluAsnIleAlaLysThrGluProLysIlePheArg 142
DB 616 CATATGACATCTGAGAGATTAGAAACATAGCGAAACCTGAACCTTAAGATTTTCCGT 675
QY 143 ValLysProValIleGluLysArgMetIleGlnIleGluTrrIleLysProGluLeu 162
DB 676 GTGAAACAGATTGGGCAATCAACGAATGATCAAAATTTGAATGATTAAGCTTAGTTCG 735
QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
DB 736 GCGCTGTTCATCTGATTTAAATTAACACCTTCGATTCAGGACAGTCAACGATCCACG 795
QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
DB 796 TGGATGGAAAGTCACTTCGTAAAGAACGTAAAGATTAACCAACCTAACCTCCACG 855
QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
DB 856 GGGCTGCGCTTTTACAGAAATATGTCATAGCTCTGCAATGCGGTTAAGAGATCAAG 915
QY 223 PheTyrSerAspTyrPheSerGlnGlyLysMetGlyMetThrGluGlu 238
DB 916 TTTCTGAGTGACTGAGACCAAGAAAATGGGAATGATGAGAGAA 963

Search completed: February 23, 2005, 15:24:16
Job time : 3193.89 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 05:20:17 ; Search time 372.207 Seconds
(without alignments)
4007.918 Million cell updates/sec

Title: US-10-006-265-4
Perfect score: 1358
Sequence: 1 MKLSPPQSCVNLGMMWTAL.....GMTBECKTLPAIPVLSLTV 252

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
N Geneseq_16Dec04:*
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2: geneseqn1980s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1358	100.0	2440	4 AAC92338	AAC92338 Human hae
2	1343	98.9	1476	6 ABA93784	ABA93784 Human zcy
3	1343	98.9	1476	11 ADL26677	ADL26677 Human zcy
4	1292	95.1	2119	4 AAC92350	AAC92350 Human hae
5	1292	95.1	2295	6 ABA93821	ABA93821 Human zcy

6	1292	95.1	2295	10 ADD68179	ADD68179 Human zcy
7	1292	95.1	2295	11 ADL26602	ADL26602 Human zcy
8	1292	95.1	2480	6 AAD38772	AA38772 Human hae
9	1292	95.1	2903	6 ABA93808	ABA93808 Human zcy
10	1292	95.1	2903	10 ADD68146	ADD68146 Human zcy
11	1292	95.1	2903	11 ADL26569	ADL26569 Human zcy
12	1292	95.1	2969	4 AAC92337	AAC92337 Human hae
13	1282	94.4	1299	6 ABA93781	ABA93781 zcyox17
14	1282	94.4	1299	11 ADL26675	ADL26675 Human zcy
15	1282	94.4	2386	6 ABA93767	ABA93767 Human zcy
16	1282	94.4	2402	11 ADL26673	ADL26673 Human zcy
17	1282	94.4	2445	6 ABK33581	ABK33581 CDNA enco
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22	1282	94.4	2445	9 ACB68542	ACB68542 Human ang
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24	1282	94.4	2445	9 ACB68542	ACB68542 Human ang
25	1282	94.4	2445	9 ACB68542	ACB68542 Human ang
26	1282	94.4	2445	9 ACB68542	ACB68542 Human ang
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35	1282	94.4	2445	10 ADB87806	ADB87806 Human PRO
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ALIGNMENTS

RESULT 1
ID AAC92338 standard; CDNA; 2440 BP.
AC AAC92338;
DT 26-MAR-2001 (first entry)
DE Human haemopoietin receptor protein NR10.2 encoding cDNA SEQ ID NO.3.
KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KW immunoregulation; haematopoietic cell regulation; transmembrane;
KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW metal allergy; pollen allergy; se.
OS Homo sapiens.
PN WO200075314-A1.
PD 14-DEC-2000.
PF 01-JUN-2000; 2000WO-JP003556.
PR 02-JUN-1999; 99JP-00155797.
PR 30-JUL-1999; 99JP-00217797.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX Maeda M, Yaguchi N.
PI

```

XX WPI; 2001-061720/07.
DR P-PSDB; AAB51243.
XX Hematopoietic receptor protein NR10 for screening potential ligands for
PT treatment of immune and hematopoietic disorders such as autoimmune
PT diseases and allergies.
XX Claim 1; Fig 6-7; 127pp; Japanese.
XX
CC The present sequence encodes a human haemopoietic receptor protein
CC (NR10), specifically designated NR10.2. NR10 occurs as a transmembrane
CC protein and a soluble protein. NR10 is a haemopoietic receptor molecule
CC which participates in immunoregulation and haematopoietic cell regulation
CC in vivo, and is useful in searching for haematopoietic factors capable of
CC binding to the receptor. NR10 can be used for the identification of
CC substances for the treatment and prevention of immune and haematopoietic
CC disorders including autoimmune diseases and allergies such as metal and
CC pollen allergy
XX
SQ Sequence 2440 BP; 738 A; 508 C; 524 G; 670 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,48e-141 Length: 2440
Score: 1358.00 Matches: 252
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-006-265-4 (1-252) x AAC92338 (1-2440)
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Db 523 ATAAAGCTCTCTCCCAAGCCTTATGTTGTTAACTGGGGATGATGAGACCTGGACCTG 582
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
Db 583 TGGATGCTGCCCTCACCTGCAAAATTCAGCTGGAGCTTGCCAGCTAAAGCTGAGAAC 642
QY 41 LLeSerCysValLysTrpTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
Db 643 ATTTCTGTGCTACTACTATAGAAAAAATTTAACTGCACTTGAGTCCAGAGAAAGAA 702
QY 61 ThrSerTrpThrGlnTrpThrValLysArgThrTrpAlaPheGlyGlyLysAsn 80
Db 703 ACCAGTTATACCAATGACAGATTAGAGAACTTACGCTTCCGAGAAAAACATGATAAAT 762
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 763 TGTACAAACCAATGTTCTCAACATGAAATCGTGCTTCGTCCTTTTCTTCCAAAG 822
QY 101 LLeThrLLeProAspPheTrpThrLLeGluValGluAlaGluAsnGlyLysGlyVal 120
Db 823 ATACACATCCCAATATATATACCATGAGTGAAGCTGAAAATGAGATGAGTGTAAAT 882
QY 121 LysSerHisMetThrTrpTrpArgLysGluAsnLLeAlaLysThrGluProProLys 140
Db 883 AATTCATATGACATACATGAGAAATTAAGAAACATGCGAAATCGAACCACTTAAGATT 942
QY 141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
Db 943 TTCGGTGTAAACCAAGTTTGGGATCAACGAATGATTAATTAATTAATTAATTAAGCTT 1002
QY 161 GluLeuAlaProValSerSerAspLysLysTrpThrLeuArgPheArgThrValAsnSer 180
Db 1003 GAGTTGGCGCTTTTCATCTGATTTAAATACACACTTGATTCAGAGCAACAGT 1062
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnTrpTrpAsn 200
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Db 1183 TCAAAATTTCTGAGATGATCTGAGAGCCAGAAAAAATGGGATATGATGAGAAAGGCAAG 1242
QY 241 LeuLeuProAlaLLeProValLeuSerThrLeuVal 252
Db 1243 CTACTCCCTGCGATTCCTCCCTGCTACTCTGCTG 1278

RESULT 2
ABA93784
ID ABA93784 standard; cDNA; 1476 BP.
XX
XX ABA93784;
AC
XX 01-MAY-2002 (first entry)
DT
XX
XX Human zcytor17 soluble form encoding cDNA SEQ ID NO:21.
DE
XX
XX Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
XX antiinflammatory; antiviral; antineumatic; antiarthritic; cyostatic;
XX muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
XX infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200200721-A2.
PN
XX
XX 03-JAN-2002.
PD
XX
XX 26-JUN-2001; 2001WO-US020484.
PF
XX
XX 26-JUN-2000; 2000US-0214282P.
PR 29-JUN-2000; 2000US-0214955P.
PR 08-FEB-2001; 2001US-0267963P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX
XX Sprechter CA, Preenell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer MF;
XX
XX WPI; 2002-090519/12.
DR P-PSDB; ABB05733.
XX
XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders.
XX
XX Example 2; Page 178-180; 235pp; English.
PS
XX
XX The present invention describes a cytokine receptor designated zcytor17.
XX Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,
XX antihematic, antiarthritic and muscular activities. The zcytor17
XX proteins are useful for treating and diagnosing lymphoid, immune,
XX inflammatory, splenic, blood or bone disorders. Agonists or anti-
XX zcytor17 antibodies are useful in stimulating cell-mediated immunity and
XX for stimulating lymphocyte proliferation, such as in the treatment of
XX infections involving immunosuppression, including certain viral
XX infections. They are also useful for inducing cytotoxicity and for
XX treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
XX treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
XX sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
XX pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
XX chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
XX ABA93843 and ABB05730 to ABB05745 represent sequences used in the
XX exemplification of the present invention
XX
XX Sequence 1476 BP; 414 A; 326 C; 338 G; 398 T; 0 U; 0 Other;
SQ

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Alignment Scores:

Pred. No.:	5 68e-140	Length:	1476
Score:	1343.00	Matches:	249
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Best Local Similarity:	99.60%	Mismatches:	1
Query Match:	98.90%	Indels:	0
DB:	6	Gaps:	0

US-10-006-265-4 (1-252) x ABA93784 (1-1476)

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Qy      23 LeuProSerLeuCyGlyePheSerLeuAlaIaLeuProAlaIaLeuProGluAsnIleSer 42
Db      189 CTCCCTCACTCTGCAAAATTCAGCTGGCAGCTTCGACGTAACCTGAGAACCTTTCC 248
Qy      43 CyValITyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 62
Db      249 TGTGTCTCTACTATAGAAATTTAACTGCACTTGGAGTTCAGAAAGAAACCACT 308
Qy      63 TyTrhGlnTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 82
Db      309 TATACCCAGTACACAGTTAAGAACTTACGCTTTGGAGAAACATGATATTGTACA 368
Qy      83 ThrAnSerSerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThr 102
Db      369 ACCAATAGTTCTACACAGAAATGCTGCTCTTTTTCCTTCCAAAGATAACG 428
Qy      103 IleProAspAsnTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 122
Db      429 ATCCAGATTAATATACCATGAGGTGAAGCTGAAATGGAGATGGTAAATTAATCT 488
Qy      123 HisMetThyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 142
Db      489 CATATGACATATCTGAGATTTAGAGAACATAGCAAAATCGAACCTTAAGCTTCCGT 548
Qy      143 ValIaLeuProValIaLeuGlyIleIleArgMetIleGlnIleGluTrpIleLeuProGluLeu 162
Db      549 GTGAAACACAGTTTGGCATCAACGAATGATTCAAATGGAATGAAGCTGACGTG 608
Qy      163 AlaProValSerSerAspLeuLeuTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 182
Db      609 GCGCTGTTTATCTGATTTAAATACACACTTCATTCAGACGTAACAGTACCAAGC 668
Qy      183 TrpMetGluValaIaenPheAlaIeAsnArgIleAspLeuAsnGlnThrTyTrhAsnLeuThr 202
Db      669 TGGATGGAGATCACTTCGTAAGAACCTTAAGATTAAGAACCAACCTTACACTCAG 728
Qy      203 GlyLeuGlnProPheThrGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 222
Db      729 GGGCTGCGACCTTTTACAGAAATATGTCATGCTGCGATGCGGTCAAGAGCAAG 788
Qy      223 PheTrpSerAspTrpSerGlnGluGlyMetGlyMetThrGluGluGluGlyLeuLeu 242
Db      789 TTCGGAGTGACTGAGCCAAAGAAAAATGGAAATGACTGAGAGAAAGCAAGCTACTC 848
Qy      243 ProAlaIleProValIleuSerThrLeuVal 252
Db      849 CCTCGANTCCCGTCTCTGCTCTGTGTG 878

```

RESULT 3
ADL26677
ID ADL26677 standard; CDNA; 1476 BP.
XX
AC ADL26677;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human cytokine receptor zcytor17 DNA seqid 114.
XX
KM antiInflammatory; antiJicer; dermatological; antiAllergic; antiPsoriatic;

KM antibacterial; immunosuppressive; cell proliferation inhibitor;
KM immune response inhibitor; inflammatory response inhibitor;
KM multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
KM cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
KM zcytor17lg-induced proliferation; zcytor17lg-induced differentiation;
KM hematopoietic progenitor cell; zcytor17lg-induced inflammation;
KM inflammatory disease; inflammatory bowel disease; ulcerative colitis;
KM Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
KM septicemia; toxic shock syndrome; zcytor17; human; gene; ss.
KM
OS Homo sapiens.
XX
XX US2003215838-A1.
XX
XX
PD 20-NOV-2003.
XX
XX 21-JAN-2003; 2003US-00351157.
XX
XX 18-JAN-2002; 2002US-0350325P.
PR 14-JUN-2002; 2002US-0389108P.
PR 19-DEC-2002; 2002US-0435361P.
XX
XX (SPRE/) SPRECHER C A.
PA (GAOZ/) GAO Z.
PA (KUIJ/) KUIJPER J L.
PA (DASO/) DASOVICH M M.
PA (GRAN/) GRANT F J.
PA (PRES/) PRESNELL S R.
PA (WHIT/) WHITMORE T E.
PA (HAMM/) HAMMOND A K.
PA (NOVA/) NOVAK J E.
PA (GROS/) GROSS J A.
PA (DILL/) DILLON S R.
XX
PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ;
PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
XX WPI; 2003-876545/81.
DR P-PSDB; ADL26678.
XX
XX Novel multimeric or heterodimeric cytokine receptors useful for treating
PT chronic inflammatory disease such as inflammatory bowel disease,
PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
PT septicemia.
XX
XX
PS Disclosure; SEQ ID NO 114; 205pp; English.
XX
XX The invention describes an isolated multimeric or heterodimeric cytokine
CC receptor (I) having at least one polypeptide having 90 percent sequence
CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
CC acid sequence, given in specification, or at least one polypeptide
CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
CC and producing an antibody to (I) and a cytokine-binding domain of a class
CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
CC binding domain of a class I cytokine receptor and a vehicle is useful
CC for: reducing hematopoietic cells and hematopoietic progenitor cells in
CC a mammal; inhibiting zcytor17lg-induced proliferation or differentiation
CC of hematopoietic cells and hematopoietic progenitor cells; reducing
CC zcytor17lg-induced inflammation; treating a mammal afflicted with an
CC inflammatory disease in which zcytor17lg plays a role. The disease is a
CC chronic inflammatory disease such as inflammatory bowel disease,
CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
CC psoriasis. The disease is acute inflammatory disease such as
CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
CC An immune response inhibiting composition is useful for inhibiting an
CC immune response in a mammal exposed to an antigen or pathogen. An
CC inflammatory response inhibiting composition is useful for suppressing an
CC inflammatory response in a mammal with inflammation. An antibody that
CC specifically binds to (I) is useful for detecting the presence of a
CC multimeric or heterodimeric cytokine receptor in a biological sample.
CC This sequence encodes a human zcytor17 cytokine receptor that can be used
CC in a comparison with other zcytor17 receptors.

Oy		101	IleThrlIleProAspAenYrThrIIeGluValGluAlaGluAenGIyaSgIlyValIIe	120
Db		311	ATAACATCCCGAGTAAATTATACCATTTGAAGTGGAAGCTGAAAATGGAGATGGTAAATT	370
Oy		121	LvBSerHisMeChTrYrTrTPAcGLeuGluValnIIalAlayThrGIuPcPolysEIIe	140
Db		371	AATTCATATGCAATACGTGAGATTAGAGAACATATGCCGAAAACTGAAACCACTTAAGATT	430
Oy		141	PheArgValIysProValLeuGIylIeLysArgMeCIlegIIileGluTrPIleLysPro	160
Db		431	TTCGGGTGAACAACCAATTTGGGCATCAAACGAATGATTCAAATTGAATGATTAAGCCT	490
Oy		161	GluLeuLeuIleProValSerSerAspLeuLysYrThrIleuArgPheArgThrValAsnSer	180
Db		491	GAGTTGGCCGCTGTTCATCTGATTAAAAATACACTTGATTCAAGACAGTCAACAGT	550
Oy		181	ThrSetTrpMetGluValasnPheAlalyAsnArgLyAspIlyAsnEngInThrYrAsn	200
Db		551	ACCAGCTGGATGGAAAGTCAACTTCGGCTAAGAACCGTAAGGATTAAAAACCAAGGTCAAC	610
Oy		201	LeuThrGlyLeuGlnProPheThrGluYrValIIalAleuArgCySAIValILysGlu	220
Db		611	CTCACGGGGCTGCAGCCTTTTACAGAATATGTCAATAGCTCTGGCAGTGTGGGTCAAGAG	670
Oy		221	SerLysPheTrpSerAspTrpSergIngluLYsmetGlymerThrGlugluGlu	238
Db		671	TCAAAGTTCTGGAGTGACTGCAGCCAAAGAAAAATGGGAATGACTGAGGAAGA	724
RESULT 5				
ID	ABA93821	standard; cDNA; 2295 BP.		
XX AC	ABA93821;			
DT	01-MAY-2002	(first entry)		
XX DE	Human zcytor17-Fc4 fusion polynucleotide SEQ ID NO:68.			
KM KM	ZCYTOR17; chromosome 5; SGL1; cytokine receptor; immunomodulatory;			
KW KW	antiinflammatory; antiviral; antirheumatic; antiarthritic; cytosolic;			
KM KM	mucular; lymphoid; immune; inflammatory; splenic; blood; bone;			
KM KM	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;			
XX XX	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;			
OS OS	Inflammatory disease; pancreatitis; inflammatory bowel disease; ss.			
XX OS	Homo sapiens.			
XX PN	Synthetic.			
XX XX	WO200200721-A2.			
PD PD	03-JAN-2002.			
XX PF	26-JUN-2001; 2001WO-US020484.			
XX PR	26-JUN-2000; 2000US-0214282P.			
XX PR	29-JUN-2000; 2000US-0214955P.			
XX PR	08-FEB-2001; 2001US-0267963P.			
PA PA	(ZYMO) ZYMOGENETICS INC.			
XX PI	Spriecher CA, Preenell SR, Gao Z, Whitmore TE, Kuilper JL;			
XX PI	Mauer MF;			
DR DR	WFI; 2002-090519/12.			
XX XX	P-PsDB; ABB05743.			
PT PT	Isolated polynucleotide encoding a cytokine receptor zcytor17 which is			
XX XX	useful for treating and diagnosing lymphoid, immune, inflammatory,			
PS PS	splenic, blood or bone disorders.			
CC CC	Example 11; Page 216-221, 235pp; English.			
The present invention describes a cytokine receptor designated zcytor17.				

CC	Zcyclo17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC	antithematic, antidiarrhetic and muscular activities. The zcyclo17
CC	proteins are useful for treating and diagnosing lymphoid, immune,
CC	inflammatory, splenic, blood or bone disorders. Agonists or anti-
CC	-zcyclo17 antibodies are useful in stimulating cell-mediated immunity and
CC	for stimulating lymphocyte proliferation, such as in the treatment of
CC	infections involving immunosuppression, including certain viral
CC	infections. They are also useful for inducing cytotoxicity and for
CC	treating leukopenias. Antagonist of zcyclo17 polypeptides are useful for
CC	treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC	sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC	pancreatitis, and inflammatory bowel disease. Zcyclo17 was mapped to
CC	chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC	ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC	exemplification of the present invention
XX	
SQ	Sequence 2295 BP; 659 A; 578 C; 565 G; 493 T; 0 U; 0 Other:
Alignment Scores:	
Pred. No.:	5.6e-134 Length: 2295
Score:	1292.00 Matches: 238
Percent Similarity:	100.00% Conservatave: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	95.14% Indels: 0
DB:	Gaps: 0
US-10-006-265-4 (1-252) x ABA93821 (1-2295)	
QY	1 MetLysLeuSerProGlnPProSeCYsValaIasnLeuGIyMeMetTrpThTPalaleu 20
Db	1 ATGAAGCTCTCCTCCCCAGCGTTTCAGTGTAAACCTGGGATGATGGAGACTGGCACTG 60
QY	21 TrpMetLeuPProSerLeuCYslsPheserLeuaAlalaLeuProhlaIylsPProGIuAsn 40
Db	61 TGGATGCCTCCCTCACTCGCAAATTACGCTGGAGAGCTTGCACTGCACTTAAGCCTTGAGAAC 120
QY	41 IleserCYsValTYrTYrTYraGLysasneLuthrCYethTrPserProGIyLySglu 60
Db	121 ATTTCCTGTGTTACTACTCATATGAAAAATTTAACCCTGCACCTTGACCTCAGAAAAGAA 180
QY	61 ThrseryTYrhGINtyrThrvallysarGthrTYralaphedGIyLIulsHisaaPaan 80
Db	181 ACCAGATTATCCCACTACAACAGTTAAAGAACTTACGCTTTGGAGAAAACATGATTAAT 240
QY	81 CyethTrThraenSerSerThserCIusanaagIaserCYsSerPhephelauPcoay 100
Db	241 TGTAACAACCAATAGTCTCAACAAGTAAATCGTGTCTGCTCTTTTCTTCCAAGA 300
QY	101 IleThrIIleProaspAsnTYrThrllegluVAlgluAlaSnaglYasnglyValIile 120
Db	301 ATAACGATCCCAATTAATTAATTCATTGAGGTGGAAAGCTGAAAAYGSAAGTAGGTAAATT 360
QY	121 LysSerHIsmeCThrTYrTrPargLeugIubaniIealalySThrgIuProProIySile 140
Db	361 AAATCTCATATGACATACCTGAGATTAAGAAACATATAGCAAAACCACTTAAGATT 420
QY	141 PhearGvalIySProvalleuGIyIleybarGmetIlegInIegiUTrpIlelySPro 160
Db	421 TTCCCTGTGAAAACCAAGTTTGGGCACTCAAAACCAAGATTCCAATTGMAAGGATAAGGCCCT 480
QY	161 GlueuenaIaProvalSerSeraspLeuLYsTYrrhrIreUaygPheArghThVaIaanSer 180
Db	481 GAGTTGGGGCCCTGTTTCAATTCGATTTAATAATACACCTTCGATTCAAGCACGTCAACGT 540
QY	181 ThsSerTrPmetGlIuValaIasnPhealIalYsaBaNGlySaSpLySaBnglInThTYraAn 200
Db	541 ACCAGCTGATGGAAGTCAACTGCTTAAGAACCGTAAGGATTAATAAACCAACAGTCAAC 600
QY	201 LeuthrgIyleuGInProPheThrgIufurValIleaIaleuaygCyalaVallySglu 220
Db	601 CTCACGGGGCTGACGCTTTTACGAAATATGTCAATAGCTCTCGATGTGCGGTCAAGAG 660
QY	221 SerIysPheTrPserAAsnTrSergInglYlysMetGIyMeTThSGIngluInglu 238

Db 661 TCAAGTCTCGAGTGAAGCCCAAGAAAATGGAATGACTGAGGAAGA 714

RESULT 6

ADD68179

XX ADD68179;

DT 15-JAN-2004 (first entry)

XX Human zcytor17-Fc4 fusion cDNA SEQ ID NO:38.

XX se; gene; human; zcytor17; antiinflammatory; dermatological;
 KW immunosuppressive; antimicrobial; vaccine; inflammatory disease;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;
 KW toxic shock syndrome; infectious disease.

XX Chimeric.

XX Homo sapiens.

XX Key

FT CDS Location/Qualifiers

XX MO2003060090-A2.

XX 24-JUL-2003.

XX 21-JAN-2003; 2003WO-US001984.

XX 18-JAN-2002; 2002US-0350325P.

XX 25-APR-2002; 2002US-0375323P.

XX 19-DEC-2002; 2002US-0435315P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sprecher CA, Kuiper JL, Dasovich MM, Grant FU, Hammond AK;

XX Novak UE, Gross JA, Dillon SR;

XX WPI; 2003-618179/58.

XX P-PDB; ADD68180.

XX Example 8; SEQ ID NO 38; 372pp; English.

CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A
 CC polypeptide of the invention has antiinflammatory, dermatological,
 CC immunosuppressive, and antimicrobial activity, and may have a use in a
 CC vaccine. The polypeptide is useful for treating inflammatory diseases,
 CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
 CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic
 CC shock syndrome or infectious diseases. The present sequence is used in
 CC the exemplification of the invention.

XX Sequence 2295 BP; 659 A; 578 C; 565 G; 493 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 5.6e-134

XX Score: 1292.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 95.14%

XX DB: 10 Gaps: 0

XX US-10-006-265-4 (1-252) x ADD68179 (1-2295)

QY 1 MethylaseuserPrognProSerCysValAsnLeuGlyMetMetTrpThrPalaleu 20

Db 1 ATGAAGTCTCTCCCGAGCTTCATGCTTTAACTCGGGGATGATGGACCTGGGCACACTG 60

QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40

Db 61 TGAATGCTCCCTTCACTCGCAAAATTCAGCTGGAGCTTCGCCAGCTTAAGCTGAGAAC 120

QY 41 IleSerCysValTyrTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60

Db 121 ATTTCTGTGTCTACTACTATAGAAAAATTTAACTGTGACTTGGAGTCCAGAAAAAGAA 180

QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAspAsn 80

Db 181 ACCAGTTATACCCAGTACACAGTTAAGAACTTACGCTTTGGAGAAAAACATGTAAT 240

QY 81 CysThrThrAsnSerSerThrSerGluAsnAsgAlaSerCysSerPhePheLeuProArg 100

Db 241 TGTACAAACCAATAGTTCTACAAAGTAAATCGTCTCGTCTTTTCCCTCCACAGA 300

QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120

Db 301 ATTAGCATCCAGAT 360

QY 121 LysSerHisMetThrTyrTyrArgLeuGluAsnIleAlaLysThrGluProProLysIle 140

Db 361 AATCTCATATGACATGAGATGAGATGAGAACATAGCAAACTGAACCATTAAGATT 420

QY 141 PheArgValLysProValLeuGlyTyrLysArgMetIleGlnIleGluTrpIleLysPro 160

Db 421 TTCCGGTGAACCAAGTTTGGGCAATCAAAACCAATGATTCAATATGAAATGAAGTAAAGCT 480

QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrIleArgPheArgThrValAsnSer 180

Db 481 GAGTTGGCGCCGTTCATCTGATTTAAATATACACATTCGATTCAGAGCAAGTCAACAT 540

QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200

Db 541 ACCAGCTGATGAGATCAACTTCCTTAAGAACCCGTAAAGATAAACCAACCATTAAGAAC 600

QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220

Db 601 CTCACGGGGCTGACGCTTTTACAGAAATGTGATAGCTCTCGATGTGCGGTCAAGAG 660

QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238

Db 661 TCAAGTCTCGAGTGAAGCCCAAGAAAATGGAATGACTGAGGAAGA 714

RESULT 7

ADL26602

XX ADL26602 standard; DNA; 2295 BP.

XX AC ADL26602;

XX 20-MAY-2004 (first entry)

XX Human zcytor17-Fc4 fusion protein DNA.

XX antiinflammatory; antiinfect; dermatological; antiallergic; antipsoriatic;
 KW antibacterial; immunosuppressive; cell proliferation inhibitor;
 KW immune response inhibitor; inflammatory response inhibitor;
 KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KW cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
 KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
 KW hematopoietic progenitor cell; zcytor17lig-induced inflammation;
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 KW septicemia; toxic shock syndrome; zcytor17lig; zcytor17; Fc4;
 KW fusion protein; gene; ds.

XX Homo sapiens.

OS Synthetic.

XX US2003215838-A1.

XX 20-NOV-2003.
 PD 21-JAN-2003; 2003US-00351157.
 XX 18-JAN-2002; 2002US-0350325P.
 XX 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUIJ/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNELL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX Sprecher CA, Gao Z, Kuiper JL, Dasovich MM, Grant FJ,
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
 DR WPI; 2003-876545/81.
 XX P-PSDB; ADL26603.
 PT Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.
 XX
 PS Example 8; SEQ ID NO 38; 205pp; English.
 CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing hematopoietic cells and hematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor17lig-induced proliferation or differentiation
 CC of hematopoietic cells and hematopoietic progenitor cells; reducing
 CC zcytor17lig-induced inflammation; treating a mammal afflicted with an
 CC inflammatory disease in which zcytor17lig plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC psoriasis. The disease is acute inflammatory disease such as
 CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
 CC An immune response inhibiting composition is useful for inhibiting an
 CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (I) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a soluble human zcytor17-human Fc4 (not defined)
 CC fusion protein.
 XX
 SO Sequence 2295 BP; 659 A; 578 C; 565 G; 493 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5.6e-134 Length: 2295
 Score: 1292.00 Matches: 238
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.14% Indels: 0
 DB: 11 Gaps: 0

QY 1 MetlyseuserPrognProSerCyValaenleuglymetMetTrpThrPalaLeu 20
 DB 1 ATGAAGCTCTCTCCCAACCTTCACTGAGGAGATGATGAGACCTGGGCACTG 60
 QY 21 TrpMetLeuProSerLeuCyValaPheSerLeuAlaAlaLeuProAlaLeuProGlu 40
 DB 61 TGGATGCTCCCTCACTCTGCAAAATTCAGCTGGAGCTGCCAGCTAAGCTGAGAAC 120
 QY 41 IlleSerCyValaTyrrTyrrTyrrTyrrTyrrTyrrTyrrTyrrTyrrTyrrTyrr 60
 DB 121 ATTCTCTGTGTCTACTATAGAAAATTTAACTGCACTGGAGTGGAGGAAAGGAA 180
 QY 61 ThierTyrrGlnTyrrTyrrTyrrTyrrTyrrTyrrTyrrTyrrTyrrTyrrTyrr 80
 DB 181 ACCAGTTATACCACTACACAGTTAAGAACTTACGTTTGGAGAAAACATGATAT 240
 QY 81 CysThrThrAenSerSerThSerGluAenAlaSerCySerPhePheLeuProArg 100
 DB 241 TGTACAAACCAATAGTTCATCAAGTGAATAATCGTCTGCTCTTTTCTTCCAAGA 300
 QY 101 IlleThrIleProAapAenTyrrThrIleGluValaGluAlaGluAenGlyValIle 120
 DB 301 ATACGATCCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
 QY 121 LysSerHisMetThrTyrrTyrrArgLeuGluAenIleAlaTyrrGluProProLysIle 140
 DB 361 AATCTCTATGACATCTAGAGATTAGAACTTAGCAAACTGAACCACTTAAGATT 420
 QY 141 PheArgValaIleProValaLeuGlyIleValaArgMetIleGlnIleGluTrpIleLysPro 160
 DB 421 TTCGGTGGAAACCAAGTTTGGCATCAACGAATGATTCAAATGATGATTAAGCT 480
 QY 161 GluLeuAlaProValaSerSerAapLeuTyrrTyrrLeuArgPheArgThrValaAenSer 180
 DB 481 GAGTTGGCGCTGTTTCACTGATTAATTAATTAATTAATTAATTAATTAATTAAT 540
 QY 181 ThierTrpMetGluValaAenPheAlaLysAenArgLysAenArgLysAenArgLys 200
 DB 541 ACCAGCTGATGAGATGACATCTTACAGAAATGATGATGATGATGATGATGATGAT 600
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrrValIleAlaLeuArgCyValaValaIleGlu 220
 DB 601 CTCACGGGGGCGCAGCCTTTTACAGAAATGATGATGATGATGATGATGATGATGAT 660
 QY 221 SerLysPheTrpSerAapTrpSerGluLysMetGlyMetThrGluGlu 238
 DB 661 TCAAAGTTCTGAGTGACTGAGCAAGCAAAATGGAATGACTGAGAAAGAA 714
 RESULT 8
 AAD38772
 ID AAD38772 standard; cDNA; 2480 BP.
 XX
 AC AAD38772;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Human haematopoietin receptor 1 (HPR1) cDNA.
 XX
 KW Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
 KW pancytopenia; leukopenia; anaemia; thrombocytopaenia; osteoporosis;
 KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
 KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
 KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 KW osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;
 KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 KW ischaemic disease; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT	CDS	132..2369
FT		/*tag= a
FT		/product= "Human HPR1 protein"
FT		/transl_except= (pos:1680..1682, aa:Asn)
FT		/note= "This region is specifically claimed as SEQ ID NO:
FT		5 in claim 6 of the specification"
FT		191..227
FT		/*tag= b
FT		228..236
FT		/*tag= c
FT		/product= "Human mature HPR1 protein"
FT		replace(278, g)
FT		/*tag= d
FT		replace(633, g)
FT		/*tag= e
FT		replace(691, g)
FT		/*tag= f
FT		replace(1212, g)
FT		/*tag= g
FT		replace(1216, g)
FT		/*tag= h
FT		replace(1660, g)
FT		/*tag= i
FT		replace(1680, g)
FT		/*tag= j
FT		replace(2166, g)
FT		/*tag= k
PN	MO200229060-A2.	
XX	11-APR-2002.	
XX	05-OCT-2001; 2001WO-US031634.	
XX	06-OCT-2000; 2000US-0238706P.	
PR	13-OCT-2000; 2000US-024076P.	
PR	20-FEB-2001; 2001US-0270282P.	
PA	(IMMV) IMMUNEX CORP.	
PI	Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;	
DR	WPI; 2002-330172/36.	
XX	P-PSDB; AAE24024.	
XX	Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,	
XX	useful for treating cell proliferation, metabolic, and reproductive	
XX	hormone related conditions.	
XX	Claim 6; Page 83-84; 136pp; English.	
PS	The present invention relates to human and murine hematopoietin receptor	
CC	polypeptides HPR1 and HPR2. Sequences of the invention are useful for	
CC	treating cell proliferation conditions e.g., pancytopenia, leukopenia,	
CC	anemia, thrombocytopenia, neurodegenerative disorders and osteoporosis	
CC	resulting from a lack of bone-forming cells. They are also useful for	
CC	treating cell proliferation conditions such as leukaemia and tumour	
CC	metastasis, osteoporosis resulting from an excess of bone-resorbing	
CC	cells. HPR sequences are also useful for treating medical conditions and	
CC	diseases such as cell proliferation, metabolic and reproductive hormone	
CC	related conditions. They are useful for treating various haematologic and	
CC	oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal	
CC	carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,	
CC	cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including	
CC	cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,	
CC	barcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),	
CC	squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia	
CC	of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-	
CC	dysplastic syndromes (including refractory anaemia, refractory anaemia	
CC	with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-	
CC	penic purpura (TTP), sickle cell vasoocclusive crisis, myelofibrosis/	
CC	myeloid metaplasia, osteoclast disorders that lead to bone loss such as	
CC	osteoporosis including post-menopausal osteoporosis, peridontitis	

CC resulting in tooth loosening or loss, prosthesis loosening after joint
CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,
CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
CC amyotonia gravis, chronic neuronal degeneration, stroke including
CC cerebral ischaemic diseases, HPRI and HPRI2 polypeptides are also useful
CC for treating various other disorders such as osteoporosis, obesity, is
CC deficient mammary development and infertility. The present sequence is
CC human HPRI CDNA

XX
SQ Sequence 2480 BP; 722 A; 558 C; 600 G; 600 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6, 28e-134 Length: 2480
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conserves: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 6 Gaps: 0

DS-10-006-265-4 (1-252) x AAD38772 (1-2480)

QY	1	MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTPThTTPAlaLeu	20
Db	132	ATPAAGCTCTCTCCAGCTTCACAGTGTAACTGGGGAAAGATGTGACCTGGGCACTG	191
QY	21	TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn	40
Db	192	TGGATGCTCCCTTCACTGCGAATTCAGACCTGGCAGCTTGCCAGCTTAACCTGAGAAC	251
QY	41	ILlSerCysValTyTyrTyrTrpArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu	60
Db	252	ATTTCCTGGTCTACTACTATATGGAAAAATTTAACTGCACTTGGAAGTCAGGAAAGAA	311
QY	61	ThSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn	80
Db	312	ACCAAGTTAATCCAGTACACATTTAAGAACTTAACGCTTTTGGAGAAAAACAGATAT	371
QY	81	CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArg	100
Db	372	TGTACAACCAATAGTTCTTCAAGATGAATAATCGTGCTTGCTCTTTTTCCTTCCAAG	431
QY	101	ILlSerILlProAspAsnTyrThrILlGluValGluAlaGluAsnGlyAspGlyValILl	120
Db	432	ATACAGATCCCAAGATATATATACATTAAGGTGAAGCTGAATAATGAGATGGTAAAT	491
QY	121	LysSerHisMetThrTyrTrpArgLeuGluAsnILlAlaLysThrGluProProLysILl	140
Db	492	AAATTCATATGACATCTCGAGATTAAAGAACATAGGAAATCTGAACCACTTAAGATT	551
QY	141	PheArgValLysProValLeuGlyLysLysArgMetILlGlnILlGluTrpILlLysPro	160
Db	552	TTCCGGTGAATAACAGTTTTGGGCATCAACCAATGATTCAAAATGGATGATTAAACCT	611
QY	161	GluLeuAlaProValSerSerAspLeuLysTyrThrILlLeuArgPheArgThrValAsnSer	180
Db	612	GAGTGGCGCTGTTTCATCTGATTTAAATAACACTTCGATTCAGGACAGCTAACAGT	671
QY	181	ThSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn	200
Db	672	ACCAAGCTGAGTGAATCAACTTCGCTAAGAACGTTAAGATTAATAAACCAACCTAAC	731
QY	201	LeuThrGlyLysLeuGlnProPheThrGluTyrValILlAlaLeuArgCysAlaValLysGlu	220
Db	732	CTCACCGGGGTGAGCGCTTTTACAAATAATGTCAATAGCTTCGCATGTGCGGTCAAGAG	791
QY	221	SetLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetCtnrgLugLuglu	238
Db	792	TCAAAAGTCTGAGTGACTGGAGCCAGAAAAATGGAGATGACTGAGGAAGAA	845
RESULT_9			
ABA93808			

ID ABA93808 standard; cDNA: 2903 BP.
 AC ABA93808;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human zcytor17 cDNA sequence SEQ ID NO:53.
 XX
 KM Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KM antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
 KM muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KM infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KM autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KM inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO20020721-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001WO-US020484.
 XX
 PR 26-JUN-2000; 2000US-0214282P.
 PR 29-JUN-2000; 2000US-0214955P.
 PR 08-FEB-2001; 2001US-0257963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL,
 PI Meurer MF,
 PI
 XX WPI; 2002-090519/12.
 DR P-PSDB; ABB05741.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 PT
 XX Example 1; Page 199-203; 235pp; English.
 PS
 XX The present invention describes a cytokine receptor designated zcytor17.
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytoprotic,
 CC antineumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral
 CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention
 CC
 XX Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 7.91e-134 Length: 2903
 Score: 1292.00 Matches: 238
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.14% Indels: 0
 DB: 6 Gaps: 0
 US-10-006-265-4 (1-252) x ABA93808 (1-2903)
 QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetCTTPTThTPAlaLeu 20
 Db 497 ATGAAGCTCTCTCCCGACGCTTCACTGTGTTAACTGGGGAGATGATGGAAGCTGCGCACTG 556

QY 21 TrpMetLeuProSerLeuGlyLeuPheSerLeuAlaAlaLeuProAlaLeuProGluAsn 40
 Db 557 TGGATGCTCCCTTACTGCTGAATTAATCAAGCTGGACACTGCGACCTTAACCTGAGAAC 616
 QY 41 IleSerCysValTyrTyrTyrArgLeuAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 Db 617 ATTTCTGTGTCTACTACTATAGAAAAATTTTAACCTGCACTTGAGATGCCAGAAAGGAA 676
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
 Db 677 ACCAGTTATACCCGACTACAGATTAAAGAACTTACCTTTGGAGAAAAACAATGATAT 736
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProArg 100
 Db 737 TGTACCAACCAATAGTTCTACAGTGAATAATCGCTTCGTCTTTTTCCTTCCAGA 796
 QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyLysGlyValIle 120
 Db 797 ATTAACGATCCCAATATTAATTAATCAATTGAGGTGAAAGCTGAAATGAGATGTAAT 856
 QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
 Db 857 AAATCTCATATGACATACGAGATTAGAGAACATAGCAAAACCTGAACCACTTAAGATT 916
 QY 141 PheArgValLysProValIleLeuGlyIleLysArgMetIleGlnIleGluTTPIleLysPro 160
 Db 917 TTCGGTGTGAACCAAGTTTGGGCATCAACGAATGATTCMAATGATGATTAAGCT 976
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db 977 GAGTTGGCGCTGTTTATCTGATTTAAATATACACACTTCGATTCAGACAGTAAAGT 1036
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 Db 1037 ACCAGCTGATGAGAACTCACTTCGTAAAGAACCGTAAGATTAACCAACCTAACAC 1096
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
 Db 1097 CTCACGGGGCTGCAGCTTTTACAGAAATATGTCATTAAGCTTCGCATGTGCGGTAAGAG 1156
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
 Db 1157 TCMAAGTTCTGAGACTGACGAGCCAGCAAAAAATGGGAATGACTGAGAAAGA 1210
 RESULT 10
 ID ADD68146 standard; cDNA: 2903 BP.
 AC ADD68146;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human zcytor17 cDNA SEQ ID NO:4.
 XX
 KM ss; gene; human; zcytor17; antiinflammatory; dermatological;
 KM immunosuppressive; antimicrobial; vaccine; inflammatory disease;
 KM inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KM atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;
 KM toxic shock syndrome; infectious disease.
 XX
 OS Homo sapiens.
 XX
 PN Key Location/Qualifiers
 FH CDS 497..2485
 FT /*tag= a
 FT /product= "zcytor17"
 XX
 EN MO2003060090-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 21-JAN-2003; 2003WO-US001984.


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XX 18-JAN-2002; 2002US-0350325P.
PR 25-APR-2002; 2002US-0375323P.
PR 19-DEC-2002; 2002US-0435315P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
PI Sprecher CA, Kuiper JL, Dasovich MM, Grant FJ, Hammond AK;
PI Novak JE, Gross JA, Dillon SR;
XX
XX MPI: 2003-618179/58.
DR P-PSDB; AD68147.
XX
XX New zcytor17 ligand polypeptides, useful for treating inflammatory
PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.
XX
XX Example 3; SEQ ID NO 4; 372pp; English.
XX
XX The invention relates to a novel isolated zcytor17 ligand polypeptide. A
CC polypeptide of the invention has antiinflammatory, dermatological,
CC immunosuppressive, and antimicrobial activity, and may have a use in a
CC vaccine. The polypeptide is useful for treating inflammatory diseases,
CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic
CC shock syndrome or infectious diseases. The present sequence is used in
CC the exemplification of the invention.
XX
XX Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 7.91e-134 Length: 2903
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: Gaps: 0
US-10-006-265-4 (1-252) x AD68146 (1-2903)
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetThrPthTAlaLeu 20
DB 497 ATGAACTCTCTCCAGCCTTATGTAACTGGGATGATGAGACCTGGGACATG 556
QY 21 TrpMetLeuProSerLeuSerCysLysPheSerLeuAlaLeuProAlaLysProGlu 40
DB 557 TGGATCTCTCTTCACTGCAAAATTCAGCCTGGAGCTCTGCCAGTTAGCTGGAAC 616
QY 41 LeSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTTrpSerProGlyGlu 60
DB 617 ATTCTGTGTCTACTACTATAGAAAATTAACTGCACTTGAGTCCAGAAAAGAA 676
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysHisAlaPhe 80
DB 677 ACCAGTTAAACCCAGTACAGATTAAGAAACATTAAGCTTTGAGAAAACATGATAAT 736
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 737 TGTACAACCAATAGTCTTACAACTGAAATCGTCTTGTCTTTTCTTCCACAAG 796
QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
DB 797 ATAAACATCCCAATATATATACATTGAGGTGGAAGCTGAAAATGGAAGATGATTAAT 856
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProPheLysIle 140
DB 857 AAATTCATATGACATACATGAGATTAAGAAACATACGAAACCTAAAGATT 916
QY 141 PheArgValLysProValLeuGlyLysArgMetIleGlnIleGluTrpIleLysPro 160
DB 917 TTCGGTGTGAACCAAGTTTGGGCATCAACGAAATGATTAATTAATGATTAAGCCT 976
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180

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DB 977 GAGTTGGCGCCTGTTCACTGATTTAAATACACACTTCGATTCAGGACACTCAACGT 1036
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
DB 1037 ACCAGCTGATGAAATGATCACTTCGTTAGAACCTGTAAGATTAACCAACGATCAAC 1096
QY 201 LeuThrGlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB 1097 CTCACGGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTCGATATGCGGTCAAGAG 1156
QY 221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGluGlu 238
DB 1157 TCAAAAGTTCTGAGTACGACTGAGCCAGAAAATAATGGAAATGATGAGAGAGAA 1210
RESULT 11
ADL26569
ID ADL26569 standard; cDNA; 2903 BP.
XX
XX ADL26569;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Human cytokine receptor zcytor17 DNA seqid 4.
DE
XX
XX antiinflammatory; antiulcer; dermatological; antiallergic; antipsoriatic;
XX antibacterial; immunosuppressive; cell proliferation inhibitor;
XX immune response inhibitor; inflammatory response inhibitor;
XX multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
XX cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
XX zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
XX hematopoietic progenitor cell; zcytor17lig-induced inflammation;
XX inflammatory disease; inflammatory bowel disease; ulcerative colitis;
XX Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
XX septicemia; toxic shock syndrome; zcytor17; human; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX US2003215838-A1.
PN
XX
XX 20-NOV-2003.
PD
XX
XX 21-JAN-2003; 2003US-00351157.
PF
XX
XX 18-JAN-2002; 2002US-0350325P.
PR 14-JUN-2002; 2002US-0389108P.
PR 19-DEC-2002; 2002US-0435361P.
XX
XX (SPRE/) SPRECHER C A.
PA (GAOZ/) GAO Z.
PA (KUJ/) KUIJPER J L.
PA (DASO/) DASOVICH M M.
PA (GRAN/) GRANT F J.
PA (PRES/) PRESNELL S R.
PA (WHIT/) WHITMORE T E.
PA (HAMM/) HAMMOND A K.
PA (NOVA/) NOVAK J E.
PA (GROS/) GROSS J A.
PA (DILL/) DILLON S R.
XX
XX Sprecher CA, Gao Z, Kuiper JL, Dasovich MM, Grant FJ;
PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
XX
XX MPI: 2003-876545/81.
DR P-PSDB; ADL26570.
XX
XX Novel multimeric or heterodimeric cytokine receptors useful for treating
PT chronic inflammatory disease such as inflammatory bowel disease,
PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
PT septicemia.
XX
XX Example 3; SEQ ID NO 4; 205pp; English.
XX

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CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing haematopoietic cells and hematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor1719-induced proliferation or differentiation
 CC of hematopoietic cells and hematopoietic progenitor cells; reducing
 CC zcytor1719-induced inflammation; treating a mammal afflicted with an
 CC inflammatory disease in which zcytor1719 plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC psoriasis. The disease is acute inflammatory disease such as
 CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
 CC An immune response inhibiting composition is useful for inhibiting an
 CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (I) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a human zcytor17 cytokine receptor.
 XX

Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7,91e-134	Length:	2903
Score:	1292.00	Matches:	238
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.14%	Indels:	0
DB:	11	Gaps:	0

US-10-006-265-4 (1-252) x ADL26569 (1-2903)

QY 1 MellyleuSerProGlnProSerCysValAlaLeuGluMetMetTrpThrTyrPalaLeu 20
 DB 497 ATGAAAGCTCTCTCCCGACCTTCATGTGTAACTGGGGAGATGTGACCTGGGACATG 556
 QY 21 TrpMetLeuProSerLeuCysAlaPheSerLeuAlaLeuProAlaValProGluAsn 40
 DB 557 TGAATGCTCCCTTACTCTGAAATTAAGCTGCACTCCAGCTCAAGCTCGAAGAAC 616
 QY 41 IlSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 DB 617 ATTTCCGTGTCTACTACTATAGAAAATTTAACTGCACTTGAGATCCAGAAAGAA 676
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysAspAsn 80
 DB 677 ACCAGTATATCCCGTACAGACAGTTAAGAACTTAACCTTTTGAGAAAACATGATAT 736
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 DB 737 TGTACAACCAATACATCTTACAGAGAAATGAGCTTGCTCTTTTCTTCCAGA 796
 QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 DB 797 ATAAAGATCCCAAGTAATTAATACATTTGAGGTGAACGTAAATGAGATGGTGAAT 856
 QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProIleValIle 140
 DB 857 AAATCTCATATGACATACGAGATTAGAGAACTATACGAAACCAACCACTTAAGATT 916
 QY 141 PheArgValLysProValLleGluLysArgMetIleGlnIleGluTyrPileLysPro 160
 DB 917 TTCGATGAAACCAAGTTTGGGATCAACGAATGATATCAATTAATGATTAACCT 976
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 DB 977 GAGTTGGCGGCTGTTTCATGATTTAAATATACACATTCGATTCAAGACAGTCAACAGT 1036

QY 181 ThrSerTrpMetGluValaAlaPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 DB 1037 ACCAGCTGAGTGAAGTCAACTTCTGACAGAACCTGAAGATTAACCAACCAAGTACAC 1096
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
 DB 1097 CTCACGGGGCTGCAGCCTTTTACAGATATGTCTATACTCTCGCATGTGGGCTCAAGAG 1156
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetClyMetThrGluGluGlu 238
 DB 1157 TCAAGTCTCGAGTGTGACTGAGCCAGCAAGAAAATGGCAATGACTGAGAAAGAA 1210

RESULT 12

ID AAC92337 standard; cDNA; 2969 BP.
 XX AAC92337;
 AC AAC92337;
 DT 26-MAR-2001 (first entry)
 XX
 DE Human haemopoietin receptor protein NR10.1 encoding cDNA SEQ ID NO:1.
 XX
 KW Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
 KW immunoregulation; haematopoietic cell regulation; transmembrane;
 KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
 KW metal allergy; pollen allergy; ss.
 XX
 XX Homo sapiens.
 OS
 XX MO200075314-Al.
 XX
 PD 14-DEC-2000.
 XX
 PF 01-JUN-2000; 2000MO-JP003556.
 XX
 PR 02-JUN-1999; 99JP-00155797.
 PR 30-JUL-1999; 99JP-00217797.
 XX
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 PI
 PI Maeda M, Yaguchi N;
 XX
 XX WPI, 2001-061720/07.
 DR
 DR P-PSDB; AAB51242.
 XX
 PT Hematopoietin receptor protein NR10 for screening potential ligands for
 PT treatment of immune and hematopoietic disorders such as autoimmune
 PT diseases and allergies.
 XX
 PS Claim 1, Fig 3-5, 127pp; Japanese.
 XX
 CC The present sequence encodes a human haemopoietin receptor protein
 CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
 CC which participates in immunoregulation and haematopoietic cell regulation
 CC in vivo, and is useful in searching for haematopoietic factors capable of
 CC binding to the receptor. NR10 can be used for the identification of
 CC substances for the treatment and prevention of immune and haematopoietic
 CC disorders including autoimmune diseases and allergies such as metal and
 CC pollen allergy.
 XX
 SQ Sequence 2969 BP; 939 A; 618 C; 662 G; 750 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.17e-134	Length:	2969
Score:	1292.00	Matches:	238
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.14%	Indels:	0
DB:	4	Gaps:	0

US-10-006-265-4 (1-252) x AAC92337 (1-2969)

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QY      1 MetIyLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
DB      523 ATGAAGCTCTCTCCAGACCTTCATGTTAACTGGGATGATGGACCTGGGACACTG 582
QY      21 TrpMetLeuProSerLeuCysIysPheSerLeuAlaLeuProAlaIysProGluAsn 40
DB      583 TGGATGCTCCCTCACTCGAAATTCACGCTGGCAGCTCTGCACTGAAGCTCGTGAAC 642
QY      41 IIsSerCysValTyTrpTyTrpArgIysAsnLeuThrCysThrTrpSerProGlyIysGlu 60
DB      643 ATTTCCTGCTCACTACATAGAAAAATTAACTGCACTTGGAGTCGAGAAAGGAA 702
QY      61 ThrSerTyTrpGlnTyTrpValIysAsnTrpTyTrpAlaPheGlyGluIysHisAspAsn 80
DB      703 ACCAGTTAAACCCAGACACAGTTAAGAACTTAAAGCTTTGGAGAAAACATGATTAAT 762
QY      81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB      763 TGTACAAACCAATAGTCTCAAGTGAATAATCGTCTCTTTTCCCTCCAAAG 822
QY      101 IleThrIleProAspAsnTyTrpIleGluValGluAlaGluAsnGlyAsnGlyValIle 120
DB      823 ATTAACCATCCAGATATATATACATTGAGGTGGAAAGCTGAATAATGAGATGGTGAAT 882
QY      121 LysSerHisMetThrTyTrpArgLeuGluAsnIleAlaIysThrGluProProIysIle 140
DB      883 AATATCATATGACATCACTGAGATTAAGAACTTAAAGCAAACTGAACCACTAAGATT 942
QY      141 PheArgValIysProValIleGlyIleIysArgMetIleGlnIleGluTrpIleIysPro 160
DB      943 TTCCCGTGAAACCAAGTTTGGGCATCAACCAATGATTTCAATTAATGATTAAGTAA 1002
QY      161 GluLeuAlaProValSerSerAspLeuIysTyTrpThrLeuArgPheArgThrValAsnSer 180
DB      1003 GAGTTGGCCCTGTTTCATCTGATTTAAATACACTTCGATTCAGACAGCAACAGT 1062
QY      181 ThrSerTrpMetGluValAsnPheAlaIysAsnArgIysAspIysAsnGlnThrTyTrpAsn 200
DB      1063 ACCAGCTGATGGAATCAACTTCGCTAAGAACCGTAAGATTAATAACCAACGTCATC 1122
QY      201 LeuThrGlyLeuGlnProPheThrGluTyValIleAlaLeuArgCysAlaValIysGlu 220
DB      1123 CTCACGGGGCTGACGCTTTTACAGAAATGTCAATGCTCTGCGATGTGCGGTCAAGAG 1182
QY      221 SerIysPheTrpSerAspTrpSerGlnIlyIysMetGlyMetThrGluGluGlu 238
DB      1183 TCAAAGTCTGGAGTGAAGTGAACCAAAAAATGGGAATGACTGAGAGAAAGA 1236

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RESULT 13
ABA93781
ID      ABA93781 standard; cDNA; 1299 BP.
AC      ABA93781;
XX
XX
XX      01-MAY-2002 (first entry)
DE      Zcytor17 soluble form truncated in the fibronectin domain cDNA SEQ.17.
XX
XX      Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
XX      antiinflammatory; antiviral; antirheumatic; antiarthritic; cyostatic;
XX      muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;
XX      infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
XX      autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX      inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX
XX      Homo sapiens.
XX
XX      MO200200721-A2.
XX
XX      03-JUN-2002.
XX
XX      26-JUN-2001; 2001WO-US020484.
XX

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XX      26-JUN-2000; 2000US-0214282P.
PR      29-JUN-2000; 2000US-0214955P.
PR      08-FEB-2001; 2001US-0267963P.
XX
XX      (ZYMO ) ZYMOGENETICS INC.
PA
XX      Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kujiiper JL;
PI      Maurer MF;
PI      MPI; 2002-090519/12.
XX      P-PSDB; ABB05732.
XX
XX      Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
XX      useful for treating and diagnosing lymphoid, immune, inflammatory,
XX      spleenic, blood or bone disorders.
XX
XX      Example 2; Page 174-176; 235pp; English.
XX
XX      The present invention describes a cytokine receptor designated zcytor17.
XX      Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,
XX      antirheumatic, antirheumatic and muscular activities. The zcytor17
XX      proteins are useful for treating and diagnosing lymphoid, immune,
XX      inflammatory, spleenic, blood or bone disorders. Agonists or anti-
XX      zcytor17 antibodies are useful in stimulating cell-mediated immunity and
XX      for stimulating lymphocyte proliferation, such as in the treatment of
XX      infections involving immunosuppression, including certain viral
XX      infections. They are also useful for inducing cytotoxicity and for
XX      treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
XX      treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
XX      sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
XX      pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
XX      chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
XX      ABA93843 and ABB05730 to ABB05745 represent sequences used in the
XX      exemplification of the present invention
XX
XX      Sequence 1299 BP; 402 A; 276 C; 306 G; 315 T; 0 U; 0 Other;
XX
XX      Alignment Scores:
XX      Pred. No.: 3,2e-133 Length: 1299
XX      Score: 1282.00 Matches: 236
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 94.40% Indels: 0
XX      DB: 6 Gaps: 0
XX
XX      US-10-006-265-4 (1-252) x ABA93781 (1-1299)
QY      3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
DB      129 CTCTCTCCAGACCTTCAATGTTAACTGGGATGATGGACCTGGGCACTGGAGATG 188
QY      23 LeuProSerLeuCysIysPheSerLeuAlaLeuProAlaIysProGluAsnIIsSer 42
DB      189 CTCCTCTCACTCGCAATTCAGCTGGCAAGCTGCAAGCTGAACCTGAGAACTTTCC 248
QY      43 CysValTyTrpTyTrpArgIysAsnLeuThrCysThrTrpSerProGlyIysGluThrSer 62
DB      249 TGTGCTTACTACTATAGAAAAATTAACTGACCTGGAGTCGAGAAAGAAACCACT 308
QY      63 TyTrpGlnTyTrpValIysArgThrTyTrpAlaPheGlyGluIysHisAspAsnTyTrp 82
DB      309 TATACCAAGTACACAGTTAAGAACTTAAAGCTTTTGGAGAAAACATGATTAATGTA 368
QY      83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB      369 ACCAATAGTCTTACCAAGTGAATAATCGTCTCTCTTTTCCCTCCAGAAATACG 428
QY      103 IleProAspAsnTyTrpIleGluValGluAlaGluAsnGlyAsnGlyValIleIysSer 122
DB      429 ATCCAGATTAATTAATCACTTGAAGTGAAGCTGAATAATGAGATGGTGAATTAATCT 488
QY      123 HisMetThrTyTrpArgLeuGluAsnIleAlaIysThrGluProProIysIlePheArg 142

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Db 489 CATATGATATCTGAGATTAGAGAACTAGGAAACCTAGAACCTTAGATTTCCTG 548
 Qy 143 VallysPVoallLeuglyllyeayrWecilleglllgluTPlllyeProgluLeu 162
 Db 549 GTGAACCAAGTTTGGGCATCAACGAATGATTCAAATGGAATGAATGAACCTGAGTTG 608
 Qy 163 AlaProValSerSerAspLeuLylefThrThleuAagPheArgThnValAanSerThSer 182
 Db 609 GCGGCTGTTTCACTGATTATAAATACACACTTCATTACAGACGTCAACAGTACCAAGC 668
 Qy 183 TrpMetGluValaenPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
 Db 669 TGGATGGAAAGTCAACTGCTGTAAGAACCTTAAGATAAAACCAACTACACTCAAGC 728
 Qy 203 GlyLeuGlnProPheThrGluTyrVallealeuAayGysalaleVallyeGluSerLys 222
 Db 729 GGGCTGCGAGCTTTTACAGAAATATGTCAATGCTGCGATGTGCGGTCAAGAGTCAAG 788
 Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
 Db 789 TTCTGAGTGACTGAGCCAAAGAAAAATGGGAATGACTGAGGAAGAA 836
 RESULT 14
 ADL26675 ID ADL26675 standard; cDNA; 1299 BP.
 AC ADL26675;
 XX 20-MAY-2004 (first entry)
 DT
 XX Human cytokine receptor zcytor17 DNA seqid 112.
 DE
 XX antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;
 KW antibacterial; immunosuppressive; cell proliferation response inhibitor;
 KW immune response inhibitor; inflammatory response inhibitor;
 KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KW cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
 KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
 KW hematopoietic progenitor cell; zcytor17lig-induced inflammation;
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 KW septicemia; toxic shock syndrome; zcytor17; human; gene; se.
 KM
 XX
 OS Homo sapiens.
 XX
 PN US2003215838-A1.
 XX
 PD 20-NOV-2003.
 XX
 PF 21-JAN-2003; 2003US-00351157.
 XX
 PR 18-JAN-2002; 2002US-0350325P.
 PR 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 PA (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUIJ/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNELL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
 XX WPI: 2003-876545/81.
 DR P-PSDB; ADL26676.

XX Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.
 PS Disclosure; SEQ ID NO 112; 205pp; English.
 CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing haematopoietic cells and hematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor17lig-induced proliferation or differentiation
 CC of hematopoietic cells and hematopoietic progenitor cells; reducing
 CC zcytor17lig-induced inflammation; treating a mammal afflicted with an
 CC inflammatory disease in which zcytor17lig plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC psoriasis. The disease is acute inflammatory disease such as
 CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.
 CC An immune response inhibiting composition is useful for inhibiting an
 CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (I) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a human zcytor17 cytokine receptor that can be used
 CC in a comparison with other zcytor17 receptors.
 CC
 XX
 SQ Sequence 1299 BP; 402 A; 276 C; 306 G; 315 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3.2e-133 Length: 1299
 Score: 1282.00 Matches: 236
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.40% Indels: 0
 DB: 11 Gaps: 0
 US-10-006-265-4 (1-252) x ADL26675 (1-1299)
 Qy 3 LeuSerProGlnProSerCysValaenLeuGlyWecMetTrpThrTPAlaLeuTrpMet 22
 Db 129 CTCTCTCCCGAGCTTATGTTATGTTACCTGGGATGATGTGGACCTGGCACTGTGATG 188
 Qy 23 LeuProSerLeuCyLysPheSerLeuAlaaleuProAlaLysProGluAanLleSer 42
 Db 189 CTCCTCCACCTGCAATTCAGCTGTGCAAGCTGTGCAGTAAAGCTGAGAAACATTTC 248
 Qy 43 CysVallyrTyrTyrAaglysaenLeuThrCysThrTrpSerProGlyLysGluThrSer 62
 Db 249 TGTGCTTACTACTATAGAAAAATTAACTGCACCTTGAGAGTCCAGAAAAAGAAACAGT 308
 Qy 63 TyrThrGlnTyrThrVallysaenLeuThrTyrAlaPheGlyGluLysHSAAPAsnCyThr 82
 Db 309 TATACCAAGTACAGATAGAGAACTTACGCTTTTGGAGAAAACATGATTAATTGACA 368
 Qy 83 ThrAanSerSerThrSerGluAanArgAlaSerCysSerPhePheLeuProArgLleThr 102
 Db 369 ACCAATAGTCTCAAGTGAATAATCGTTCGTCCTTTTCTTCCCAAGATAACG 428
 Qy 103 IleProAspAsnTyrThrIleGluValaGluAenGlyAspGlyValIleLysSer 122
 Db 429 ATCCCAATATATATATACATTAAGGTGGAAGCTGAAAAATGAGATGTGTAAATTAATCT 488
 Qy 123 HisWecThrTyrTrpAagLeuGluAanIleAlaLysThrGluProProLysIlePheArg 142

Db 489 CATATGACATACATGAGATTAGAGAACATAGCGAAAACTGAACCACTTAAGATTTTCCT 548
 Qy 143 ValIysProValIleuGIYIleYsArgMeIleGIInIleGIuTrpIleYsProGIuIleu 162
 Db 549 GTGAACCAAGTTTGGGCAATCAACCAATGATTCAATGATTGAATTAAGCTGTGATTG 608
 Qy 163 AlaProValSerSerAspIleuYsTYrThrIleuArgPheArgThrValAsnSerThrSer 182
 Db 609 GGGCTGTTTCATCTGATTTAAATAACACACTTCGATTGAGACAGTCAACAGTACCAAG 668
 Qy 183 TrpMetGIuValAsnPheAlaIysAsnArgIysAspIysAsnGIInThrYrAsnIleuThr 202
 Db 669 TGGATGGAAGTCAACTTCGCTAAGAACCGTAAGATAAAACCAACGTAACAACCTCAAG 728
 Qy 203 GYIleuGIuProPheThrGIuTYrValIleAlaIleuArgCYsAlaValIysGIuSerIys 222
 Db 729 GGGCTCAGCCTTTTACAGAAATATGTCTATGCTCTGCGATGTCCGGTCAAGAGTCAAG 788
 Qy 223 PheTrpSerAspTrpSerGIuIysMeGIuMetThrGIuGIuIu 238
 Db 789 TTCTGAGTGAAGTGAAGCCAGCAAAAAAATGGAAATGACGTAGAGAGAA 836
 RESULT 15
 ID ABA93767 standard; cDNA; 2386 BP.
 AC ABA93767;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human zcytor17 cDNA sequence SEQ ID NO:1.
 XX
 KM zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KM antiinflammatory; antiviral; antirheumatic; antiarthritic; cycostatic;
 KM muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KM infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KM autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KM inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200721-A2.
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001MO-US020484.
 XX
 PR 26-JUN-2000; 2000US-0214282P.
 PR 29-JUN-2000; 2000US-0214955P.
 PR 08-FEB-2001; 2001US-0267963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Prensell SR, Gao Z, Whitmore TE, Kuijper JL;
 PI Maurer MF;
 PI
 DR MPI; 2002-090519/12.
 DR P-PSDB; ABB05730.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 XX
 PS Claim 2; Page 161-166; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cycostatic,
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral

CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention

SO Sequence 2386 BP; 711 A; 525 C; 575 G; 575 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
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Query Match:	94.40%	Indels:	0
DB:	6	Gaps:	0

US-10-006-265-4 (1-252) x ABA93767 (1-2386)

Qy 3 LeuSerProGIuProSerCyValAsnIleuGIuMetTrpThrTrpAlaIleuTrpMet 22
 Db 138 CTCTCTCCCAAGCCTTCATGTGTAACTGGGAGATGATGAGACCTGGCACTGGAGTG 197
 Qy 23 LeuProSerLeuCYsIleYsPheSerIleuAlaIleuProAlaIysProGIuAsnIleSer 42
 Db 198 CTCCTCCTCAGCTGCAAAATTCAGCTGGCAGCTCTGCCAGCTAAGCTAGAAACATTTCC 257
 Qy 43 CyValTYrTYrArgIysAsnIleuThrCYsThrTrpSerProGIuYsGIuThrSer 62
 Db 258 TGTGTCTACTACTATATGAAAAATTTAACTCTCAGTGAATGTCAGAAAGAAACCACT 317
 Qy 63 TYrThrGIuTYrThValIysArgThrTYrAlaPheGIuIleYsHisAspAsnCYsThr 82
 Db 318 TATACCACTATACAGTTTAAGAACTTACGCTTTTGGAGAAACATGATATATGTACA 377
 Qy 83 ThrAsnSerSerThrSerGIuAsnArgIasSerCYsSerPhePheIleuProArgIleThr 102
 Db 378 ACCAATAGTTTCNCAAGTAAGTAATGCTGCTGTCTCTTTCTTCCAGAAATTAAG 437
 Qy 103 IleProAspAsnTYrThrIleGIuValGIuIleAsnGIuAspGIuValIleYsSer 122
 Db 438 ATCCAGATAATTAATACATTAGAGTGAACCTGAATAATGAGATGTATAATTAATCT 497
 Qy 123 HisMetThrTYrTrpArgIleuIleAlaIysThrGIuProProIysIlePheArg 142
 Db 498 CATATGACATACATGAGATTAGAGAACATAGCAAACTGAACCACTTAAGATTTCCGT 557
 Qy 143 ValIysProValIleuGIYIleYsArgMeIleGIInIleGIuTrpIleYsProGIuIleu 162
 Db 558 GTGAACCAAGTTTGGGCAATCAACCAATGATTCAATGATTGAATTAAGCTGTGATTG 617
 Qy 163 AlaProValSerSerAspIleuYsTYrThrIleuArgPheArgThrValAsnSerThrSer 182
 Db 618 GGGCTGTTTCATCTGATTTAAATAACACACTTCGATTGAGACAGTCAACAGTACCAAG 677
 Qy 183 TrpMetGIuValAsnPheAlaIysAsnArgIysAspIysAsnGIInThrYrAsnIleuThr 202
 Db 678 TGGATGGAAGTCAACTTCGCTAAGAACCGTAAGATAAAACCAACGTAACAACCTCAAG 737
 Qy 203 GYIleuGIuProPheThrGIuTYrValIleAlaIleuArgCYsAlaValIysGIuSerIys 222
 Db 738 GGGCTCAGCCTTTTACAGAAATATGTCTATGCTCTGCGATGTCCGGTCAAGAGTCAAG 797
 Qy 223 PheTrpSerAspTrpSerGIuIysMeGIuMetThrGIuGIuIu 238
 Db 798 TTCTGAGTGAAGTGAAGCCAGCAAAAAAATGGAAATGACGTAGAGAGAA 845

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 Job time : 382.207 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:59:57 / Search time 116.023 Seconds
(without alignments)
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Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 240568

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	262.5	19.3	1977	2	US-08-825-558-3
3	262.5	19.3	1977	2	US-09-312-611-3
4	262.5	19.3	2369	1	US-07-797-556-1
5	262.5	19.3	2369	1	US-08-308-881-1
6	262.5	19.3	2369	2	US-09-058-263-1
7	262.5	19.3	2369	2	US-09-059-099-1
8	262.5	19.3	2369	2	US-09-058-264-1
9	262.5	19.3	2369	4	US-09-455-962-1
10	262.5	19.3	2369	5	PCR-US95-06530-1
11	262.5	19.3	2754	2	US-08-825-558-5
12	262.5	19.3	2754	3	US-09-312-611-5

13	262.5	19.3	3085	3	US-08-795-473B-4	Sequence 4, Appli
14	262.5	19.3	3085	4	US-09-439-856-4	Sequence 4, Appli
15	262.5	19.3	3085	4	US-09-023-655-1131	Sequence 1131, Ap
16	262.5	19.3	3477	4	US-09-313-942-25	Sequence 25, Appli
17	262.5	19.3	3507	4	US-09-313-942-23	Sequence 23, Appli
18	262.5	19.3	1218	3	US-09-012-072-1	Sequence 1, Appli
19	233	17.2	1218	3	US-09-120-601-1	Sequence 1, Appli
20	231	17.0	1690	3	US-09-071-224-1	Sequence 1, Appli
21	231	17.0	1724	3	US-09-071-224-5	Sequence 5, Appli
22	231	17.0	1790	4	US-09-866-028-31	Sequence 31, Appli
23	231	17.0	1790	4	US-09-944-457-31	Sequence 31, Appli
24	231	17.0	1813	3	US-09-071-224-3	Sequence 3, Appli
25	211	15.5	1305	3	US-09-012-072-3	Sequence 3, Appli
26	211	15.5	1305	3	US-09-120-601-3	Sequence 3, Appli
27	211	15.5	1347	3	US-09-120-601-5	Sequence 5, Appli
28	178	13.1	4040	2	US-08-685-118-1	Sequence 1, Appli
29	178	13.1	4040	2	US-08-915-459-1	Sequence 1, Appli
30	178	13.1	4040	2	US-08-914-520-1	Sequence 1, Appli
31	178	13.1	4040	4	US-09-949-016-1887	Sequence 1887, Ap
32	171	12.6	1525	1	US-08-609-572-1	Sequence 1, Appli
33	171	12.6	1525	3	US-08-841-751-1	Sequence 1, Appli
34	171	12.6	1525	3	US-08-846-344-1	Sequence 1, Appli
35	171	12.6	1525	3	US-08-846-344-1	Sequence 1, Appli
36	171	12.6	1525	4	US-09-301-808-1	Sequence 1, Appli
37	171	12.6	1525	4	US-09-828-995B-95	Sequence 95, Appli
38	171	12.6	1525	4	US-09-828-995B-97	Sequence 97, Appli
39	160.5	11.8	1050	3	US-08-806-557A-13	Sequence 13, Appli
40	160.5	11.8	1050	3	US-08-970-428A-13	Sequence 13, Appli
41	160.5	11.8	2724	4	US-09-949-016-4257	Sequence 4257, Ap
42	159	11.7	1800	3	US-08-702-665A-4	Sequence 4, Appli
43	156.5	11.5	2855	1	US-07-923-976-5	Sequence 5, Appli
44	156.5	11.5	2943	1	US-07-923-976-3	Sequence 3, Appli
45	156.5	11.5	2943	4	US-09-023-655-1086	Sequence 1086, Ap

ALIGNMENTS

RESULT 1
US-09-700-820C-17
; Sequence 17, Application US/09700820C
; Patent No. 6610485
; GENERAL INFORMATION:
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Saito, Makiyoshi
; APPLICANT: Ohtomo, Toshihiko
; TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
; FILE REFERENCE: 06501-070001
; CURRENT APPLICATION NUMBER: US/09/700,820C
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/138652
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/JP99/02341
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/279876
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 17
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) .. (2839)
US-09-700-820C-17

Alignment Scores:
Pred. No.: 7.63e-22
Score: 265.50
Percent Similarity: 52.88%
Best Local Similarity: 31.25%
Query Match: 19.55%
DB: 4
Length: 2995
Matches: 65
Conservative: 45
Mismatch: 83
Indels: 15
Gaps: 9

US-10-006-265-4 (1-252) X US-09-700-820C-17 (1-2995)

Oy		35	ProblalysrPrOgluaSnllseSrCyValylTyrrYryaraglylsAsnLeuthCyrthr	54
Dd		464	CcArAtnaAActtCAAAATTTACTGCTGTGAATTGAGGGAGAAMATTCCTGGCCAG	523
Oy		55	TpsErPrOgIlySgrJuthSerTyr---ThrgInTrThrvalLySarGrThrTYRla	73
Dd		524	TGGGACCCCCGGAAGGAGACTTAACCCTTGAAAACAATACTAACCTTTGAAATCAGAGCGCCA	583
Oy		74	PheGIyIlulyshIsaSpasnCytHrThrXrsnsEsrTrhsErgluasnAlaser	93
Dd		584	--ACAgAGAgaGTTTTCTCATGTGCAGCAAAGAcATGCCACT-----TCA	625
Oy		94	CysErPhe---PhelEuPROArgILEhrtLEPRoaPaenTryTHrlEGlVAlGlU	112
Dd		626	TGTAATGTGCAGCTACATGCCCACTATTATGTC-----AACATTGAAGTCTGGGTGAA	679
Oy		113	AAlaGlunaglYaapGLyVALIIleYSerHisMetHYrTRYTPARgleugluasnlL	132
Dd		680	GCAAGAGATGCCCTTGGGAGAGCTCCCTCAAGACTATCAATTTTAGACCCCCTGGATMAA	739
Oy		133	ALalevthrgLuPROPOLySlEphearGalysPrOVallEugLYlleLYsarGMet	152
Dd		740	GTGAHAACCCACCCCAACCTAATATTATCAAGTGAACCACTGAAGAATTTACAGTAYTA	799
Oy		153	IIEglILeIgUrTpILeySPROglULeuAlaproVAISerASPLEuLYSThyTRhr	172
Dd		800	TTAAGCTATCATGGGTCAAGTTCAGGGCTGGCGGCTTT--TTAGACTMAAGCTCAG	856
Oy		173	LenaUrPheaGrTHRvaIAmsErThserTriPMetGLUVAlaEnPhalaLYsaMARG	192
Dd		857	ATCCAAATATAGCACCAAGAGCCTCAACTGGATCCAGTCCCTCTT--GAAGATACA	913
Oy		193	lysApHySaengINThrTYraShLUethRGlyleUGlnPropHeThRGlturyVAlle	212
Dd		914	ATGCTCTCTCGAactcttcTCACTGTGAGAGacCTCAAGccTTttTACAGATATGTCTT	973
Oy		213	AlAleuargCYaLaVaLLygLSer----LysPHETPSERASPtyrSERIngIU	230
Dd		974	AGGATCCGG--TTCATTAAAGACAAGTGGAGGAGCTACTGTGAGTCACTGAGTGAAGAGAG	1030
Oy		231	LYsmEtglyMEThrgLUngLU	238
Dd		1031	GCTAGTGGAGCACCATACGAAGAC	1054
		RESULT 2		
		US-08-825-558-3		
:		: Sequence 3, Application US/08825558		
:		: Patent No. 5965724		
:		: GENERAL INFORMATION:		
:		: APPLICANT: SHARKEY, ANDREW		
:		: APPLICANT: SMITH, STEPHEN K.		
:		: APPLICANT: DELLOW, KIMBERLEY A.		
:		: TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain		
:		: NUMBER OF SEQUENCES: 14		
:		: CORRESPONDENCE ADDRESS:		
:		: ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX		
:		: STREET: 1100 NEW YORK AVENUE		
:		: CITY: WASHINGTON		
:		: STATE: DC		
:		: COUNTRY: USA		
:		: ZIP: 20005		
:		: COMPUTER READABLE FORM:		
:		: MEDIUM TYPE: Floppy disk		
:		: COMPUTER: IBM PC compatible		
:		: OPERATING SYSTEM: PC-DOS/MS-DOS		
:		: SOFTWARE: Patentin Release #1.0, Version #1.30		
:		: CURRENT APPLICATION DATA:		
:		: FILING DATE: 19-MAR-1997		
:		: CLASSIFICATION: 536		
:		: ATTORNEY/AGENT INFORMATION:		

```

? NAME: ESMOND, ROBERT W.
? REGISTRATION NUMBER: 32, 893
? REFERENCE/DOCKET NUMBER: 0623, 0530002
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202)371-2600
? TELEFAX: (202)371-2540
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1977 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1974
? US-08-825-558-3

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QY 33 ProAlaIysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
 Db 376 CCGAAGAAACCTTAAATAATTTGAGTTGCTCATTTGGACGAGGGGAGAAAATAGAGTGTGAG 435
 QY 55 TrpSerProGluLysGluThrSerTyr--ThrglnTyrThrValLys-----Arg 70
 Db 436 TGGGATGTGGGAAGGGAAAAACACTTGGAGACAAACTTCACITTAATAATCTGAATGGCA 495
 QY 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnGlyThrThrAsn 84
 Db 496 ACGACACAGTTGCTGGATTGTCAGAACAAACGTCACACCCCACTCATGACGTTGAT 555
 QY 85 SerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArgIleThrIlePro 100
 Db 556 TATCTTACT-----GTGATTTTGTG----- 576
 QY 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer--His 122
 Db 577 ---AACTTGAAGCTCGGTGAGAACAGAGATGCCCTTGGAGAGTTACATCTGATCAT 633
 QY 124 MetThrTyrTrpArgGluGluAsnIleAlaLysThrGluProPheLysIlePheArgVal 143
 Db 634 ATCAATTGTGATCTGTATATTAAGT--AAGCCCATCCGCCCATTAATTATTCAGTG 690
 QY 144 LysProValLeuGlyTleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
 Db 691 ATCAACTCAGAGGAAGCTGCTAGTATCTTAAATATGACATGACGACCAACCCAAATTAAG 750
 QY 164 ProValSerSerAspLeuLysTyrThrIleuArgPheArgThrValAsnSerThrSerTrp 183
 Db 751 AGTGTATATATA--CTAAATAATATACATCAATATAGACCAAAAGATGCTCAACTGG 807
 QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnTrpTyrAsnLeuThrGly 203
 Db 808 AGCCAGATTCT--CTGGAAGACACAGATCCACCGCATCTTCATCATCTGTCCAGAC 864
 QY 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
 Db 865 CTTAAACCTTTTACAAATATGTGTATTGAGATCTCGCTATGAAGAGAAAGATGTAGGGA 924
 QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
 Db 925 TACTGGAGTACGTGAGGTAGAAAGCAAGTGGGATCACTTATGAAGAT 972


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US-09-312-611-3
; Sequence 3, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gpi30 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,611
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32, 893
; REFERENCE/DOCKET NUMBER: 0633.0530002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1974
;
US-09-312-611-3

Alignment Scores:
Pred. No.:          9.2e-22      length:      1977
Score:             262.50       Matches:     65
Percent Similarity: 51.85%      Conservative: 47
Best Local Similarity: 30.09%    Mismatches: 75
Query Match:        19.33%      Indels:      29
DB:                  3          Gaps:           11

US-10-006-265-4 (1-252) x US-09-312-611-3 (1-1977)

QY      35   ProAlaLySPProGluAsnIleSerCySValTYrTYrTYrArgLyAsnLeuthrCYsrThr 54
         |||  |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db      376   CCAGAAAACCTAAATAATTGAAGTTCATGTGCAGAACGAGGGGAAAGAAATGAGGTGAG 435

QY      55   TTPserPrcGlyLVyGLuThrseryTyrr---ThrgInTyThrVallys-----Arg 70
         |||  |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db      436   TGGcATGcTGGAAGGGAACAACACTTGAGAGCAAACTTCATTAAATCTCGAATGGCCA 495S

QY      71   ThrTyralaphPhgIyGLu-----LYvSHtASP-----ASnCYsrThrHraSn 84
         |||  |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db      496   ACACACAAAGTTTGcGTGcATTGCAAGACAAACGTCAGACACCcCCTCATGcACTGTGGAT 555S

QY      85   SerSerThrSerGluAsnArgIlaSerCySserPhePheLeuProArgIleThrIlePro 104S
         |||  |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db      556   TATCTTACT-----GNGTATTTTGTCT-----                    576S

QY      105 AspaenTyrrThrillegluValgluaIagluasnglyaspGlYvalllleyser---His 123S
         |||  |||||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db      577   ---AACATTGAAGTCTGGcGTGcAGAGCAATGCCCTTGGGAAAGGTTTACATCAGATCAT 633S

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Oy      124 MetcHrYrTTPPaRgLeuGlaAnlIleAlaYstHnGlUProCPrIoLySlEPhEaYgl 143
        .....:::   :::   :::   ..:::   |||
Db      634 ATCAATTTTGATCTCGTATTATAAGTG--AAGCCCAATTCGCCACATATTTATCAGTG 690
        .....:::   :::   ..:::   |||
Oy      144 LysPProvAlleuGLylleLysaRgmEtIeGlnIleGUTrPlleYsPFOGIuleAUa 163
        .....:::   :::   ..:::   |||
Db      641 ATCAACTCAGAGAGACTGTCTAGTATCTTTAAATTAAGTACATGGACCACCAAGTATTAAAG 756
        .....:::   :::   ..:::   |||
Oy      164 ProVAlSerSeRaepLeuLlySTyrThrIleaRgPhaeRgTh-ValAsnSerThSerTrp 183
        ||||.....:::   :::   ..:::   |||
Db      751 AGTGTATAAAYN---CTAAAATATATAACATTCAATATAGGACCAAAGATCCTCAACTGG 807
        .....:::   :::   ..:::   |||
Oy      184 MetGIuVaLaenPhelAlaLysAsnRgrLysApLySaEnGIUnThTrZsAmLeuthRgLy 203
        .....:::   :::   ..:::   |||
Db      808 AGCCAGGATTCCT--CCTGAAGACAACAGCATCCACCCGATCTTCATTCAGTGCAGAC 864
        .....:::   :::   ..:::   |||
Oy      204 LeuGInPropheThrGlUtyrValIlleAlaLeuARgCYsaAlaVallyseGluBerLYs--- 222
        .....:::   :::   ..:::   |||
Db      865 CTTAAACCTTTTACGATATATGTGTTTAGGATTCCTGTATAGAAGAAATGTTAAGGA 924
        .....:::   :::   ..:::   |||
Oy      223 PhETTPSeraPTIPSeRGInGluLySMetGlyMeCrThnGlUGlu 238
        .....:::   :::   ..:::   |||
Db      925 TACTGAGTGACTGAGTAGAAGAACCAAGTGGGATCACCTTAGAAGAT 972
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RESULT 4
US-07-797-556-1
; Sequence 1, Application US/07797556
; Patent No. 5262522
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
; TITLE OF INVENTION: Inhibitory Factor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,556
; FILING DATE: 19911122
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; TELEFAX: 206-587-0606
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2369 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; TISSUE TYPE: human placenta
; IMMEDIATE SOURCE:
; CLONE: B10G/pDC303
; FEATURE:
; NAME/KEY: CDS
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/ LOCATION: 244..2369
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 310..2369
/
/ FEATURE: sig_peptide
/ NAME/KEY:
/ LOCATION: 244..309
/
US-07-797-556-1

Alignment Scores:
Pred. No.: 1,23e-21 Length: 2369
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 1 Gaps: 11

US-10-006-265-4 (1-252) x US-07-797-556-1 (1-2369)
QY 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
Db 619 CCGAAGAAACCTAAATTTGAGTTGCATTGTGACGAGCGGAGAAATGAGGTGTGAG 678
QY 55 TTPSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
Db 679 TGGGATGTGGAGGAAACACACTTGGAGACAACTTCACTTAAATCTGAATGGGCA 738
QY 71 ThTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 739 ACACAGCAAGTTGCTGATTGCAGAAAGCAAAAGCGACCAACCCCACTCAGCAGCTTTGAT 798
QY 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 799 TATTCTACT-----GTGTATTTTGTCT----- 819
QY 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
Db 820 ---AACATTGAAGTCTGGTAGAGAGAGAAATGCCCTTGGGAAAGTTACATCAGATCAT 876
QY 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
Db 877 ATCAATTTTGATCCTGTATATAAGTG---AGCCCAATCCGCCACATAATTTATCATG 933
QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 934 ATCAACTCAGAGGAACTGCTACTATCTTAATTTGACATGACCAACCAAGTATTAAG 993
QY 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTyr 183
Db 994 AGTGTTATATA---CTAAATATTAACATTCATATATAGGACCAAGATGCCCTCACTTGG 1050
QY 184 MetGluValAsnIleAlaLysAsnArgLysAspLysAsnGlnIleThrValAsnLeuThrGly 203
Db 1051 AGCCAGATTCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCAGTCCCAAGAC 1107
QY 204 LeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 1108 CTTAAACCTTTTACAGAAATATGTGTTAGGATTCGCTGATATGAAGAGATGTTAAGGGA 1167
QY 223 PheTTPSerAspTTPSerGlnGluLysMetGlyMetThrGluGluGlu 238
Db 1168 TACTGAGATGACTGAGTGAAGAAAGCAAGTGGATCACCTATGAAAT 1215

RESULT 5
US-08-308-881-1
/ Sequence 1, Application US/08308881
/ Patent No. 5783672
/ GENERAL INFORMATION:
/ APPLICANT: Mosley, Bruce
/ APPLICANT: Mosley, David J.
/ TITLE OF INVENTION: Receptor for Oncostatin M
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:

```

```

/ ADDRESSER: Immunex Corporation
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Apple 7.1
/ SOFTWARE: Microsoft Word, Version 5.1a
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/308,881
/ FILING DATE: 12-SEP-1994
/ CLASSIFICATION: 435
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/249,553
/ FILING DATE: 26-MAY-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seese, Kathryn A.
/ REGISTRATION NUMBER: 32,172
/ REFERENCE/DOCKET NUMBER: 2614-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 587-0430
/ TELEFAX: (206) 233-0644
/ TELEX: 756822
/
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2369 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHEICAL: NO
/
/ ANTI-SENSE: NO
/
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ TISSUE TYPE: human placenta
/ IMMEDIATE SOURCE:
/ CLONE: B10G/pDC303
/
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 244..2369
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 310..2369
/
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 244..309
/
US-08-308-881-1

Alignment Scores:
Pred. No.: 1,23e-21 Length: 2369
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 1 Gaps: 11

US-10-006-265-4 (1-252) x US-08-308-881-1 (1-2369)
QY 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
Db 619 CCGAAGAAACCTAAATTTGAGTTGCATTGTGACGAGCGGAGAAATGAGGTGTGAG 678
QY 55 TTPSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
Db 679 TGGGATGTGGAGGAAACACACTTGGAGACAACTTCACTTAAATCTGAATGGGCA 738
QY 71 ThTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 739 ACACAGCAAGTTGCTGATTGCAGAAAGCAAAAGCGACCAACCCCACTCAGCAGCTTTGAT 798

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Qy 85 SerSerThrSerGluAenArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
    |||||
Db 799 TATTTCTACT-----GTGATTTTGTCT----- 819
Qy 105 AspaenTyrrThrIleGluValGluAlaGluAenGlyAspGlyValIleLysSer---His 123
    |||||
Db 820 ---AACATTGAAGTCTGGGTAGAGAGAGAAATGCCCTTGGGAAGGTTACATCAGATCAT 876
Qy 124 MetThrTyrrTPArgLeuGluAenIleAlaLysThrGluProProLysIlePheArgVal 143
    |||||
Db 877 ATCAATTTTGATTCCTGATATATAAGG---AAGCCCAATCCGCCCATATATTATTCAGAG 933
Qy 144 LysProValIleGluIlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
    |||||
Db 934 ATCAACTCAGAGAAATGCTGATATCTTAAATTCAGACATGACCAACCAAGTATTAAAG 993
Qy 164 ProValSerSerAspLeuLysTyrrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
    |||||
Db 994 AGTGTTATATA---CTAAATATATAACATTCATATATAGAGCAAGATGCTCAACTTGG 1050
Qy 184 MetGluValAenPheAlaLysAenArgLysAspLysAenGlnThrTyrrAsnLeuThrGly 203
    |||||
Db 1051 AGCCAGATTCTCT---CTGAAGACACAGCATCCACCCGATCTTCATCTCCTCCAGAC 1107
Qy 204 LeuGlnProPheThrGluTyrrValIleAlaLeuArgCysAlaValIleGluSerLys--- 222
    |||||
Db 1108 CTTAAACCTTTTACAGAAATATGTGTTTAGGATTCGCTGATATAGAGAAAGATGTTAAGGGA 1167
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
    |||||
Db 1168 TACTGAGTGAAGTGAAGTGAAGACAGCAAGTGGATCAGCTATGAAAGAT 1215

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RESULT 6
US-09-058-263-1
Sequence 1, Application US/09058263
Patent No. 5891997

GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2644-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs

```

/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ TISSUE TYPE: human placenta
/ IMMEDIATE SOURCE:
/ CLONE: B106/pDC303
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 244..2369
/ FEATURE:
/ NAME/KEY: mac_peptide
/ LOCATION: 310..2369
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 244..309
/ US-09-058-263-1

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Alignment Scores:
Pred. No.: 1.23e-21 Length: 2369
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 50.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 2 Gaps: 11

US-10-006-265-4 (1-252) x US-09-058-263-1 (1-2369)

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Qy 35 ProAlaLysProGluAenIleSerCysValTyrrTyrrArgLysAenLeuThrCysThr 54
    |||||
Db 619 CCAGAAAAACCTAAATAATTGATGCTGTGAACGAGGGAAGAAATAGAGTGTGAG 678
Qy 55 TrpSerProGlyLysGluThrSerTyrr---ThrGlnTyrrThrValLys-----Arg 70
    |||||
Db 679 TGGAGTGTGGAAGGGAACACACTTGGAGCAAACTTCATCTTAAATTCGAATGGGCA 738
Qy 71 ThrTyrrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
    |||||
Db 739 ACACACAGATTGCTGATGTGAAGCAAAAGTGAACCCCACTCATGCACTGTTGAT 798
Qy 85 SerSerThrSerGluAenArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
    |||||
Db 799 TATTTCTACT-----GTGATTTTGTCT----- 819
Qy 105 AspaenTyrrThrIleGluValGluAlaGluAenGlyAspGlyValIleLysSer---His 123
    |||||
Db 820 ---AACATTGAAGTCTGGGTAGAGAGAGAAATGCCCTTGGGAAGGTTACATCAGATCAT 876
Qy 124 MetThrTyrrTPArgLeuGluAenIleAlaLysThrGluProProLysIlePheArgVal 143
    |||||
Db 877 ATCAATTTTGATTCCTGATATATAAGG---AAGCCCAATCCGCCCATATATTATCAGTG 933
Qy 144 LysProValIleGluIlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
    |||||
Db 934 ATCAACTCAGAGAAATGCTGATATCTTAAATTCAGACATGACCAACCAAGTATTAAAG 993
Qy 164 ProValSerSerAspLeuLysTyrrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
    |||||
Db 994 AGTGTTATATA---CTAAATATATAACATTCATATATAGAGCAAGATGCTCAACTTGG 1050
Qy 184 MetGluValAenPheAlaLysAenArgLysAspLysAenGlnThrTyrrAsnLeuThrGly 203
    |||||
Db 1051 AGCCAGATTCTCT---CTGAAGACACAGCATCCACCCGATCTTCATCTCCTCCAGAC 1107
Qy 204 LeuGlnProPheThrGluTyrrValIleAlaLeuArgCysAlaValIleGluSerLys--- 222
    |||||
Db 1108 CTTAAACCTTTTACAGAAATATGTGTTTAGGATTCGCTGATATAGAGAAAGATGTTAAGGGA 1167
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238

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Db 1168 TACTGAGTCTGAGTGAAGCAAGGATCCTATGAAGAT 1215

RESULT 7

US-09-059-099-1

/ Sequence 1, Application US/09059099

/ Patent No. 5925740

/ GENERAL INFORMATION:

/ APPLICANT: Mosley, Bruce

/ APPLICANT: Cosman, David J.

/ TITLE OF INVENTION: Receptor for Oncostatin M

/ NUMBER OF SEQUENCES: 11

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Immunex Corporation

/ STREET: 51 University Street

/ CITY: Seattle

/ STATE: WA

/ COUNTRY: USA

/ ZIP: 98101

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: Apple Macintosh

/ OPERATING SYSTEM: Apple 7.1

/ SOFTWARE: Microsoft Word, Version 5.1a

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/059,099

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US/08/308,881

/ FILING DATE: 12-SEP-1994

/ APPLICATION NUMBER: US 08/249,553

/ FILING DATE: 26-MAY-1994

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Seese, Kathryn A.

/ REGISTRATION NUMBER: 32,172

/ REFERENCE/DOCKET NUMBER: 2614-A

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (206) 587-0430

/ TELEFAX: (206) 233-0644

/ TELEFAX: 756822

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 2369 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA to mRNA

/ HYPOTHETICAL: NO

/ ANTI-SENSE: NO

/ FRAGMENT TYPE: N-terminal

/ ORIGINAL SOURCE:

/ TISSUE TYPE: human placenta

/ IMMEDIATE SOURCE:

/ CLONE: B10G/PDC303

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: 244..2369

/ FEATURE:

/ NAME/KEY: mat_peptide

/ LOCATION: 310..2369

/ FEATURE:

/ NAME/KEY: sig_peptide

/ LOCATION: 244..309

US-09-059-099-1

Alignment Scores:

Pred. No.: 1.23e-21

Score: 262.50

Percent Similarity: 51.85%

Best Local Similarity: 30.09%

Query Match: 19.33%

DB: 2

Length: 2369

Matches: 65

Conservative: 47

Mismatches: 75

Indels: 29

Gaps: 11

US-10-006-265-4 (1-252) x US-09-059-099-1 (1-2369)

QY 35 ProAlaLysProGluAsnLLeSerCysValTYRTRYrArgLysAsnLeuThrCysThr 54

Db 619 CCAGAAAACCTTAAATTTGAGTTGATGAAACGAGGAGGAAATGAGGTGTGAG 678

QY 55 TPSPserProGlyLysGluThrSerTYR---ThrGlnTYrThValLys-----Arg 70

Db 679 TGGAGTGTGAGGAGGAAACACCTTGAGACAACTTAAACTGAAATGGGCA 738

QY 71 ThrTYrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThraSn 84

Db 739 ACACACAAAGTTGCTGATTCGAAAGCAAAACGTGACACCCCACTGACATGCTGTGAT 798

QY 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgLLeThrIlePro 104

Db 799 TATTTCTACT-----GTTGATTTTGTG----- 819

QY 105 AspAsnTYrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123

Db 820 ---AACATTGAAGTCTGGGTAGAGAGAGATGCCCTTGGAGAGGTTATCATCATGATCAT 876

QY 124 MetThrTYrTYrArgLysGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143

Db 877 ATCAATTTTGAATCCTGTATATATAAGTG---AAGCCCAATCCGCCACATATTTATCATG 933

QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163

Db 934 ATCAACTCAGAGAACTGCTAGTACTTAAATTGACATGAGCAACCAACCAAGTATTAG 993

QY 164 ProValSerSerAspLeuLysTYrThrLeuArgPheArgThrValAsnSerThrSerTrp 183

Db 994 AGGTGTTAATA---CTAAATATTAACATTCATATAGACCAAAAGATCCCTCAACTGG 1050

QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTYrAsnLeuThrGly 203

Db 1051 AGCCAGATTCCG---CCTGAGACACAGCATCCACCCGATCTTCATTCATCTGCCAAGAC 1107

QY 204 LeuGlnProPheThrGluTrpValIleAlaLeuArgCysAlaValLysGluSerLys--- 222

Db 1108 CTTAAACCTTTTACAAATATGTGTAGCATTCGCTGTATGAAGAAAGATGGTAAAGGA 1167

QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238

Db 1168 TACTGAGTCTGAGTGAAGCAAGGATCCTATGAAGAT 1215

RESULT 8

US-09-058-264-1

/ Sequence 1, Application US/09058264

/ Patent No. 6010866

/ GENERAL INFORMATION:

/ APPLICANT: Mosley, Bruce

/ APPLICANT: Cosman, David J.

/ TITLE OF INVENTION: Receptor for Oncostatin M

/ NUMBER OF SEQUENCES: 11

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Immunex Corporation

/ STREET: 51 University Street

/ CITY: Seattle

/ STATE: WA

/ COUNTRY: USA

/ ZIP: 98101

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: Apple Macintosh

/ OPERATING SYSTEM: Apple 7.1

/ SOFTWARE: Microsoft Word, Version 5.1a

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/058,264

/ FILING DATE:

/ CLASSIFICATION:

/ PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-09-058-264-1
Alignment Scores:
Pred. No: 1,23e-21 Length: 2369
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 3 Gaps: 11
US-10-006-265-4 (1-252) x US-09-058-264-1 (1-2369)
Qy 35 ProAlaLysPProGluAenIleSerCyseValTyrTyrTyrArgLysAenLeuThrCythr 54
Db 619 CCAAGAAACCTTAATAATTGAGTGTGAAACGAGGGAAGAAATGAGTGTAG 678
Qy 55 TysPserProGlyLysGluThrSerTyr---ThrgInTyrThrValLys-----Arg 70
Db 679 TGGGATGGTGGAGGAAGCAACACTGTGAGACAACCTTAAATCGAATGGCA 738
Qy 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AenCythrThrasn 84
Db 739 ACACACAGATTGCTGATTGCMAAGCAAAAGTGCACCCCACTCATGACATGTTGAT 798
Qy 85 SerSerThrSerGluAenArgAlaSerCysePhePheLeuProArgIleThrIlePro 104
Db 799 TATTCTACT-----GTGTAATTGTC----- 819
Qy 105 AspaenTyrThrIleGluValGluAlaGluAenGlyAspGlyValIleLysSer---His 123
Db 820 ---AACTTGAAGTGGTGAAGCAGAGATGCCCTGGGAAGGTATACATCATCAT 876
Qy 124 MetThrTyrTrpAlaGluAenIleAlaLysThrGluProPheGlySilePheArgVal 143
Db 877 ATCAATTTCCTGATATATAAAGTG---AAGCCCAATCCGCAATATTTATCAAGTG 933
Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTyrPileLysProGluLeuAla 163

Db 934 ATCAACTGACGAGAACTGTCTAGTATCTTAAATTGACATGAGCAACCAAGATATTAG 993
Qy 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrTyr 183
Db 994 AGTGTATTATATA---CTAAATATATACATTCATAATATGAGACCAAGATGCTCAACTGG 1050
Qy 184 MetGluValAenPheAlaLysAenArgLysAspLysAenGlnThrTyrAsnLeuThrGly 203
Db 1051 AGCCAGATTCT---CTGAAAGACACAGCATCCACCGCATTTCACTTCATGCTCAAGAC 1107
Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 1108 CTTAAACCTTTTACGATATATGTGTTAGATTGCGCTGTATGAAGGAAGATGTAAGGA 1167
Qy 223 PheTyrSerAspTyrPserGlnGluLysMetGlyMetThrGluGlu 238
Db 1168 TACTGAGTGTACTGAGTGAAGAAAGCAAGTGGATCACTATGAAGAT 1215
RESULT 9
US-09-455-962-1
Sequence 1, Application US/09455962
Patent No. 6524817
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/455,962
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/058,264
FILING DATE:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369

FEATURE:	NAME/KEY:	mat_peptide
LOCATION:	310..2369	
FEATURE:	NAME/KEY:	sig_peptide
LOCATION:	244..309	
US-09-455-962-1		

Alignment Scores:	Pred. No.:	1,23e-21	Length:	2369
Score:		262.50	Matches:	65
Percent Similarity:		51.85%	Conservative:	47
Best Local Similarity:		30.09%	Mismatches:	75
Query Match:		19.33%	Indels:	29
DB:		4	Gaps:	11

US-10-006-265-4 (1-252)	x US-09-455-962-1 (1-2369)
QY	35
DB	619
QY	55
DB	679
QY	71
DB	739
QY	85
DB	799
QY	105
DB	820
QY	124
DB	877
QY	144
DB	934
QY	164
DB	994
QY	184
DB	1051
QY	204
DB	1108
QY	223
DB	1168

RESULT 10
PCT-US95-06530-1
Sequence 1, Application PC/TUS9506530
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street

```

City: Seattle
State: WA
Country: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06530
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,881
FILING DATE: 09-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-NO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10C/pDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
PCT-US95-06530-1

Alignment Scores:
Pred. No.: 1.23e-21 Length: 2369
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: 5 Gaps: 11

US-10-006-265-4 (1-252) x PCT-US95-06530-1 (1-2369)
QY ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
Db ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| 678
619 CCGAAGAAACCTAAATAATTGAGTTGCATTGTGAACGAGGGAAGAAATGAGGTGAG
QY TTPSeProGlyLysGluThrSerTyr---ThrIntYrThrValLys-----Arg 70
Db TGGGATGTGGGAAGGAAACACACTTGAGACAAACTTCACTTAATCTGATGGCA 738
679
71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| 798
739 ACGCAACAAGTCTGCTGATTCGCAAGCAAAACGTGACACCCCACTCATGACGCTGTGAT

```

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Oy 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 799 TATTTCTACT-----GTGTAATTTTGTG----- 819
Oy 105 AsparnTyrrHrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
Db 820 ---AACATTGAAGCTGGGTAGAGACAGAAATGCCCTTGGAGAGATTACATCAGATCAT 876
Oy 124 MetThrTyrrPArgLeuGluAsnIleAlaLysThrGluProProGlyIlePheArgVal 143
Db 877 ATCAATTTTGATCCGTATATTAAGTG---AAGCCCAATCCGCCCAATTAATTTATCATGTG 933
Oy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluIleLysProGluLeuAla 163
Db 934 ATCAACTGAGAGAACTGTAGTATCTTAATAATTGACATGACCAACCAAGTATTAG 993
Oy 164 ProValSerSerAspLeuLysTyrrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 994 AGTGTTATATA---CTAAATATATACATTCATATATAGACCAAGATGCCCTCAACTGG 1050
Oy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrrAsnLeuThrGly 203
Db 1051 AGCCAGATTCT---CTGAAGACACAGCATCCACCAGTCTTCACTGTCAGAC 1107
Oy 204 LeuGlnProPheThrGluTyrrValIleAlaLeuArgCysAlaValIleGluSerLys--- 222
Db 1108 CTTAAACCTTTTACGATATATGTGTTAGCATTCCTCTATGAAAGAAATGCTTAAGGA 1167
Oy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
Db 1168 TACTGAGTACTGAGTGAAGAAAGCAAGTGGATCACTATGAAGAT 1215

```

RESULT 11

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US-08-825-558-5
: Sequence 5, Application US/08825558
: Patent No. 5965724
: GENERAL INFORMATION:
: APPLICANT: SHARKEY, ANDREW
: APPLICANT: SMITH, STEPHEN K.
: APPLICANT: DELLOW, KIMBERLEY A.
: TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 NEW YORK AVENUE
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/825,558
: FILING DATE: 19-MAR-1997
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: ESMOND, ROBERT W.
: REGISTRATION NUMBER: 32,893
: REFERENCE/DOCKET NUMBER: 0623.0530001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)371-2600
: TELEFAX: (202)371-2540
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2754 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:

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: NAME/KEY: CDS
: LOCATION: 1..2754
US-08-825-558-5

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Alignment Scores:
Pred. No.: 1.56e-21 Length: 2754
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
Gaps: 11

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US-10-006-265-4 (1-252) x US-08-825-558-5 (1-2754)

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Oy 35 ProValLysProGluAsnIleSerCysValTyrrTyrrArgLysAsnLeuThrCysThr 54
Db 376 CCAAGAAAACCTAAATAATTGATGATTCGTGAACGAGGAAAGAAAATGAGGTGTAG 435
Oy 55 TrpSerProGlyLysGluThrSerTyrr---ThrGlnTyrrValLys-----Arg 70
Db 436 TGGGATGTGGAGGAAACACACTTGGAGCAAACTTCACTTAAATCTGAATGGCA 495
Oy 71 ThrTyrrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 496 ACACACAAGTTTGCTGATTCGAAGCAAAAGTGAACACCCCACTCATGACGTTGAT 555
Oy 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 556 TATTTCTACT-----GTGTAATTTTGTG----- 576
Oy 105 AsparnTyrrHrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
Db 577 ---AACATTGAAGCTGGGTAGAGACAGAAATGCCCTTGGAGAGTTCATCAGATCAT 633
Oy 124 MetThrTyrrPArgLeuGluAsnIleAlaLysThrGluProProGlyIlePheArgVal 143
Db 634 ATCAATTTTGATCCGTATATTAAGTG---AAGCCCAATCCGCCCAATTAATTTATCAGTG 690
Oy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluIleLysProGluLeuAla 163
Db 691 ATCAACTGAGAGAACTGTAGTATCTTAATAATTGACATGAGCAACCAAGTATTAG 750
Oy 164 ProValSerSerAspLeuLysTyrrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 751 AGTGTTATATA---CTAAATATATACATTCATATATGACCAAGATGCCCTCAACTGG 807
Oy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrrAsnLeuThrGly 203
Db 808 AGCCAGATTCT---CTGAAGACACAGCATCCACCAGTCTTCACTGTCAGAC 864
Oy 204 LeuGlnProPheThrGluTyrrValIleAlaLeuArgCysAlaValIleGluSerLys--- 222
Db 865 CTTAAACCTTTTACGATATATGTGTTAGGATTCGCTGATGAAAGAAATGTTAAGGA 924
Oy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
Db 925 TACTGAGTACTGAGTGAAGAAAGCAAGTGGATCACTATGAAGAT 972

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RESULT 12

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US-09-312-611-5
: Sequence 5, Application US/09312611
: Patent No. 6380160
: GENERAL INFORMATION:
: APPLICANT: SHARKEY, ANDREW
: APPLICANT: SMITH, STEPHEN K.
: APPLICANT: DELLOW, KIMBERLEY A.
: TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 NEW YORK AVENUE
: CITY: WASHINGTON
: STATE: DC

```



```

COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,611
FILING DATE: 17-MAY-1999
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0623.0530002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2754 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2754
IS-09-312-611-5

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Db 751 ACACACAGTTGCTGATTGCAAAACGACACCCCACTGACCTGAT 810
Qy 85 SerSerThrSerGluAsnArgLysSerPhePheLeuProArgIleThrIlePro 104
Db 811 TATCTACT-----GTGATTTTGTCT----- 831
Qy 105 AspAsnTrpThrIleGluValGluIleValAsnGlyValIleLysSer---His 123
Db 832 ---AACATTGAAGTCTGGGTAGACAGAGATGCCCTTGGGAAGTTCATCATCATCAT 888
Qy 124 MetThrTrpArgLeuGluAsnIleAlaIleValProProLysIlePheArgVal 143
Db 889 ATCAATTTTGATCCCTGATATTAAGTG---AAGCCCAATCCCGCATATTAATATCAGG 945
Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 946 ATCAACTGACAGGAAGTCTGATCTGATCTTAATAATTGACATGACCAACCAAGTATTAG 1005
Qy 164 ProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 1006 AGTGTATTAATA---CTAAATATTAACATTCATATAGACCAAGATGCCCTCAACTGG 1062
Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnTrpTrpAsnLeuThrGly 203
Db 1063 AGCCAGATTCT---CTGAAGACACACAGCATCCCGATCTTCACTGCTCAAGAC 1119
Qy 204 LeuGlnProPheThrGluTrpValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 1120 CTAAACCTTTTAACTGAATATGTGTAGATTCCTCTATGACAAAGATGTAAAGGA 1179
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetCysLeuGluGlu 238
Db 1180 TACTGAGTGACTGAGTGAAGACAAAGTGGATCCTATGAAGAT 1227

RESULT 14
; Sequence 4, Application US/09439856
; Patent No. 6410009
; GENERAL INFORMATION:
; APPLICANT: Galun, Ethan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/439, 856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,473
; FILING DATE: 11-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963,1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 3085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-09-439-856-4

Alignment Scores:
Pred. No.: 1,87e-21 Length: 3085
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: Gaps: 11

US-10-006-265-4 (1-252) x US-09-439-856-4 (1-3085)
Qy 35 ProValLysProGluAsnIleSerCysValTrpTrpArgLysAsnLeuThrCysThr 54
Db 631 CCAAGAAAACCTAAATAATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 690
Qy 55 TrpSerProGlyLysGluThrSerTrp---ThrGlnTrpValLys-----Arg 70
Db 691 TGGGATGGTGGGAAGGAAACACTGAGAGCAAACTTCACTTAATAATCTGAATGGCA 750
Qy 71 ThrTrpAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 751 ACACACAGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 810
Qy 85 SerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 811 TATCTACT-----GTGATTTTGTCT----- 831
Qy 105 AspAsnTrpThrIleGluValGluIleValAsnGlyValIleLysSer---His 123
Db 832 ---AACATTGAAGTCTGGGTAGACAGAGATGCCCTTGGGAAGTTCATCATCATCAT 888
Qy 124 MetThrTrpArgLeuGluAsnIleAlaIleValProProLysIlePheArgVal 143
Db 889 ATCAATTTTGATCCCTGATATTAAGTG---AAGCCCAATCCCGCATATTAATATCAGG 945
Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 946 ATCAACTGACAGGAAGTCTGATCTGATCTTAATAATTGACATGACCAACCAAGTATTAG 1005
Qy 164 ProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 1006 AGTGTATTAATA---CTAAATATTAACATTCATATAGACCAAGATGCCCTCAACTGG 1062
Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnTrpTrpAsnLeuThrGly 203
Db 1063 AGCCAGATTCT---CTGAAGACACACAGCATCCCGATCTTCACTGCTCAAGAC 1119
Qy 204 LeuGlnProPheThrGluTrpValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 1120 CTAAACCTTTTAACTGAATATGTGTAGATTCCTCTATGACAAAGATGTAAAGGA 1179
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetCysLeuGluGlu 238
Db 1180 TACTGAGTGACTGAGTGAAGACAAAGTGGATCCTATGAAGAT 1227

RESULT 15
; US-09-023-655-1131
; Sequence 1131, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEO ID NO: 1131:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g186353
US-09-023-655-1131

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Alignment Scores:
Pred. No.: 1.87e-21 Length: 3085
Score: 262.50 Matches: 65
Percent Similarity: 51.85% Conservative: 47
Best Local Similarity: 30.09% Mismatches: 75
Query Match: 19.33% Indels: 29
DB: Gaps: 11

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US-10-006-265-4 (1-252) x US-09-023-655-1131 (1-3085)

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DB 631 CCAGAAAACCTTAATAATTGAGTTCATGTGACACGAGGGAAGAAATGAGGTGTGAG 690
QY 55 TrpSerProGlyLysGluThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
DB 691 TGGGATGGTGGAGGGAACACCTTGAGACAACTTCACTTAAATCTGAATGGCA 750
QY 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCystrHisAsn 84
DB 751 ACACACAGATTTCCTGATTCGAACAAACGACACCCCACTCATCTGATTGAT 810
QY 85 SerSerThrSerGluAsnArgAlaSerCyserPhePheLeuProArgIleThrIlePro 104
DB 811 TATTCTACT-----GTGTATTTCCTC----- 831
QY 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
DB 832 ---AACATTGAAGTCTGGGAGACAGAGATGCCCTTGGGAAGTTACATCATGATCAT 888
QY 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
DB 889 ATCAATTTTATCTCTGATATTAAGTG--AAGCCCAATCCGCAATATTTATCATG 945
QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
DB 946 ATCAACTCAGAGAACTGTCTAGTATCTTAAATTGACATGACCAACCAAGTATTAAG 1005

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QY 164 ProValSerSerAspLeuIleuTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
DB 1006 AGTGTTATTAATA---CTAATAATATAACATTCAATATAGACCAAGATGCCCACTTG 1062
QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
DB 1063 AGCCAGATTCCCT---CCTGAAGACACAGCATCCACCCGATCTTCATTCACTGTCCAAAGAC 1119
QY 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCyserAlaValLysGluSerLys--- 222
DB 1120 CTTAAACCTTTTACAGAAATATGTGTGATTCCGCTGATATGAAGAGATGTAAAGGA 1179
QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGlu 238
DB 1180 TACTGAGTGAAGTGTGAAGTGAAGCAAGTGGGATCACCATTAGAAAGAT 1227

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Search completed: February 23, 2005, 19:36:05
Job time : 126.023 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p1us2 model

Run on: February 23, 2005, 09:15:27 ; Search time 392.322 Seconds
(without alignments)
3796.488 Million cell updates/sec

Title: US-10-006-265-4

Perfect score: 1358

Sequence: 1 MKUSPQSCVNLGMWMTMAL.....GMEBEGLALPAIVLSTIV 252

Scoring table:
BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 538458 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-Q=/cgn2_1/USPRO.spool/US10006265/runat.18022005.094659.22236/app.query.fasta_1.2069
-DB=Published Applications NA -OPMT=fastlap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCNALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MALEN=200000000 -USER=US10006265@cgn.1.1175 @runat.18022005.094659.22236
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSELOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAREXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
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- 10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
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- 18: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US10F_NEW_PUB.seq:*
- 20: /cgn2_6/prodata/1/pubpna/US10F_NEW_PUB.seq:*
- 21: /cgn2_6/prodata/1/pubpna/US10F_NEW_PUB.seq:*
- 22: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1358	100.0	2470	15 US-10-006-265-3	Sequence 3, Appl1
2	1343	98.9	1476	10 US-09-892-949-21	Sequence 21, Appl
3	1343	98.9	1476	17 US-10-351-157-114	Sequence 11, App
4	1343	98.9	1476	18 US-10-772-531-121	Sequence 21, Appl
5	1292	95.1	2119	15 US-10-006-265-16	Sequence 16, Appl
6	1292	95.1	2238	10 US-09-892-949-5	Sequence 5, Appl1
7	1292	95.1	2238	10 US-09-892-949-68	Sequence 5, Appl1
8	1292	95.1	2295	10 US-09-892-949-68	Sequence 68, Appl
9	1292	95.1	2295	17 US-10-351-157-38	Sequence 38, Appl
10	1292	95.1	2295	17 US-10-352-554-38	Sequence 38, Appl
11	1292	95.1	2295	18 US-10-772-531-68	Sequence 68, Appl
12	1292	95.1	2480	10 US-09-892-949-3	Sequence 3, Appl1
13	1292	95.1	2480	18 US-10-715-667-3	Sequence 3, Appl1
14	1292	95.1	2903	10 US-09-892-949-53	Sequence 53, Appl
15	1292	95.1	2903	17 US-10-351-157-4	Sequence 4, Appl1
16	1292	95.1	2903	17 US-10-352-554-4	Sequence 4, Appl1
17	1292	95.1	2903	18 US-10-772-531-53	Sequence 53, Appl
18	1292	95.1	2969	15 US-10-006-265-1	Sequence 1, Appl1
19	1282	94.4	1299	10 US-09-892-949-17	Sequence 17, Appl
20	1282	94.4	1299	17 US-10-351-157-112	Sequence 112, App
21	1282	94.4	1299	18 US-10-772-531-17	Sequence 17, Appl
22	1282	94.4	2402	10 US-09-892-949-1	Sequence 1, Appl1
23	1282	94.4	2402	17 US-10-351-157-110	Sequence 110, App
24	1282	94.4	2402	18 US-10-772-531-1	Sequence 1, Appl1
25	1282	94.4	2445	14 US-10-227-884-91	Sequence 91, Appl
26	1282	94.4	2445	14 US-10-330-163-91	Sequence 91, Appl
27	1282	94.4	2445	14 US-10-230-338-91	Sequence 91, Appl
28	1282	94.4	2445	14 US-10-218-631-91	Sequence 91, Appl
29	1282	94.4	2445	14 US-10-230-414-91	Sequence 91, Appl
30	1282	94.4	2445	14 US-10-232-224-91	Sequence 91, Appl
31	1282	94.4	2445	14 US-10-216-1594-91	Sequence 91, Appl
32	1282	94.4	2445	14 US-10-218-849-91	Sequence 91, Appl
33	1282	94.4	2445	14 US-10-227-883-91	Sequence 91, Appl
34	1282	94.4	2445	14 US-10-227-883-91	Sequence 91, Appl
35	1282	94.4	2445	14 US-10-219-076-91	Sequence 91, Appl
36	1282	94.4	2445	14 US-10-230-434-91	Sequence 91, Appl
37	1282	94.4	2445	14 US-10-219-003-91	Sequence 91, Appl
38	1282	94.4	2445	14 US-10-219-075-91	Sequence 91, Appl
39	1282	94.4	2445	14 US-10-219-464-91	Sequence 91, Appl
40	1282	94.4	2445	14 US-10-219-466-91	Sequence 91, Appl
41	1282	94.4	2445	14 US-10-219-479-91	Sequence 91, Appl
42	1282	94.4	2445	14 US-10-219-481-91	Sequence 91, Appl
43	1282	94.4	2445	14 US-10-230-260-91	Sequence 91, Appl
44	1282	94.4	2445	14 US-10-232-231-91	Sequence 91, Appl
45	1282	94.4	2445	14 US-10-232-233-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-10-006-265-3
Sequence 3, Application US/10006265
Publication No. US20030125520A1
GENERAL INFORMATION:
APPLICANT: Yaguchi, No. US20030125520A1iko
TITLE OF INVENTION: NOVEL HEMOPROTEIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
CURRENT APPLICATION NUMBER: US/10/006.265
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

; LENGTH: 2440
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (523)...(1278)
 ; US-10-006-265-3

Alignment Scores:

Pred. No.:	135e-161	Length:	2440
Score:	1358.00	Matches:	252
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-10-006-265-4 (1-252) x US-10-006-265-3 (1-2440)

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DB      523 ATGAAGCTCTCTCCAGCCTTCATGTGTTAACTGGGGATGATGTGACCTGGCAGCTG 582

QY      21 TrpMetLeuProSerLeuGlySlysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
DB      583 TGGATGCTCCCTCCAGCTGCAAAATTCAGCTGGCAGCTCTGCACCTAAGCTGAGAAC 642

QY      41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB      643 ATTTCTGTGTCTACTACTACTAGAAAATTTTAACTGCACCTGGAGTCCAGAAAGGAA 702

QY      61 ThrSerTyrTrgIntTyrTrgValLysArgThrTyrAlaPheGlyLysLysAspAsn 80
DB      703 ACCAGTTATACCCAGTACACAGATTAGAGAACTTACGCTTGGAGAAAACATGATTAAT 762

QY      81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB      763 TGTACACCAAAATGATCTCAAGTGAATAATCGTTCGCTCTTTTCTTCCCAAGA 822

QY      101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
DB      823 ATACACATCCCAATATTTATACATTGAGCTGAAAGCTGAAAATGAGATGATGTAAT 882

QY      121 LysSerHisMetThrTyrTrpArgLysGluAsnIleAlaLysThrGluProLysIle 140
DB      883 AATCTCATATGACATACGAGATTAGAGAACATAGCGAAACTGAACACCTAAGATT 942

QY      141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
DB      943 TTCGGTGTGAACCAAGTTTGGGCATCAACGAAATGATTCMAATGAAATGATTAAGCCCT 1002

QY      161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB      1003 GAGTTGGCGCTTTTCACTCTGATTTAAATATACACCTTCGATTCCAGACAGTCAACAGT 1062

QY      181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrpAsn 200
DB      1063 ACCAGCTGATGAGATCAACTTCGCTAAGAACCGTAAGATTAACCAACCAAGTCAAC 1122

QY      201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB      1123 CTCACGAGGGGTGAGAGCTTTTACAGAAATGTCTATGCTCTGCGAGTGTGGGTCACAGGAG 1182

QY      221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluLys 240
DB      1183 TCAAAGTTCTGGAGTGACTGGAGCCCAAGAAAATGGAAATGACTGAGGAGAGAGCGAAG 1242

QY      241 LeuLeuProAlaIleProValLeuSerTrpLeuVal 252
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RESULT 2
 US-09-892-949-21
 ; Sequence 21, Application US/09892949

; Publication No. US20030096339A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sprecher, Cindy A.
 ; APPLICANT: Preenell, Scott R.
 ; APPLICANT: Gao, Zeren
 ; APPLICANT: Whitmore, Theodore E.
 ; APPLICANT: Kuiper, Joseph L.
 ; APPLICANT: Maurer, Mark F.
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
 ; FILE REFERENCE: 00-42
 ; CURRENT APPLICATION NUMBER: US/09/892,949
 ; CURRENT FILING DATE: 2001-06-26
 ; PRIOR APPLICATION NUMBER: US 60/214,282
 ; PRIOR FILING DATE: 2000-06-26
 ; PRIOR APPLICATION NUMBER: US 60/214,955
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: US 60/267,963
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 93
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 1476
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (162)...(878)
 ; US-09-892-949-21

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Best Local Similarity:	99.60%	Mismatches:	1
Query Match:	98.90%	Indels:	0
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US-10-006-265-4 (1-252) x US-09-892-949-21 (1-1476)

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QY      23 LeuProSerLeuGlySlysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
DB      189 CTCCTCTACTCTGCAAAATTCAGCTGGCAGCTCTGCCAGCTAAGCTGAGAACATTTCC 248

QY      43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
DB      249 TGTGTCTACTACTATAGAAAATTTTAACTGCACCTGGAGTCCAGAAAGAACACAGT 308

QY      63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyLysLysAspAsnCysThr 82
DB      309 TATACCCAGTACACAGTTAAGAACTTACGCTTTTGGAGAAAACATGATTAATGTACA 368

QY      83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB      369 ACCAATAGTCTTCAAGTGAATAATCGCTGTGTCTCTTTTCTTCCAGAAATTAAG 428

QY      103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB      429 ATCCAGATAATTAATATACATGAGGTGAAAGCTGAAAATGAGATGAGTAAATTAATCT 488

QY      123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
DB      489 CATATGACATCTACTGAGATTAGAGAACATAGGAAAACGAAACCACTTAAGATTTTCCGT 548

QY      143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
DB      549 GTGAACCAAGTTTGGGCATCAACGATGATTCAAATGAAATGATTAAGCTGAGTGG 608

QY      163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
  
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Db 609 GCGCGCTTTCATCTGATTTAAATACACACTTCGATTGAGACAGTCAAGTACAGC 668
Qy 183 TTPMETGLUVALAENPHEALALYASNAAGLYSAPLYSAENGINTHTYRASNLEUTHR 202
Db 669 TGGATGGAAAGTCMACTTGCTTAAGAAAGGTAAGTAACCAACCTACAACTCAGC 728
Qy 203 GLYLEUGINPPOPHETHRGLUTYRVALILEALALEUAQCYSAALAVALLYGUSERTYLS 222
Db 729 GGGCTGCAGCCTTTTACGAATATATCTCATAGCTCTGCCATGTGCGGTCAAGAGTCAAG 788
Qy 223 PHEITPSEARPTPSPERGINGULYSMEGLYMETHRGUGUGUGLYLYSLEULEU 242
Db 789 TTCTGGAGTGACTGGAGCCAAAGAAATGGGAATGATGAGAGAAAGGCAAGTACTC 848
Qy 243 PROALALEPROVALLEUSERTHRLEUVAL 252
Db 849 CCTGCGATTCCCGTCTGCTGCTGTG 878

RESULT 3
US-10-351-157-114
; Sequence 114, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kujiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(878)
US-10-351-157-114

Alignment Scores:
Pred. No.: 5.02e-160 Length: 1476
Score: 1343.00 Matches: 249
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 98.90% Indels: 0
DB: 17 Gaps: 0

US-10-006-265-4 (1-252) x US-10-351-157-114 (1-1476)
Qy 3 LEUSERPROGINPPOSERCYSAVALASMLEUGLYMEWETTPHRTTPALALEUTHR 22
Db 129 CTCTCTCCCGCCTTTCATGTTTAACTGGGGAATGATGTGACCTGGGCACTGTGATG 188
Qy 23 LEUPROSERLEUCYLYSPHESERLEUALAALALEUPROVALYSPROGLUASNI 42
Db 189 CTCCCTCACTCTCAATTCAAGCTGACCTCTGCGACGTAAGCCGAGAACATTTCC 248
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Qy 43 CYSAVALTYRTYRTRYARGLYSASMLEUTHRCYSTRTPSPERPROGLYLYEGLUTHSER 62
Db 249 TGTGTCTACTACTTATAGAAAAATTTAACTTGCACTTGAGATCCAGAAAAAGAAACAGT 308
Qy 63 TYRTHRGINTYRTHRVALYSAAGTHRTRYALAEHGLYGLUYSNHAASPAASNCYS 82
Db 309 TATACCCGATCACAGTTAAGAGAACTTACGCTTTTGGAGAAAAATGATTAATTGTACA 368
Qy 83 THRANSESERTHRSERGUASNAAGALASECYASERPHIELEUPROVALILETHR 102
Db 369 ACCAATGTTTACAAAGTAAATCGCTTCGCTCTTTTTCCTCCAAAGATACG 428
Qy 103 ILEPROSPAENYTYRTHRIEGLUVALIGLUALAGLUNENGLYASBPGLYVALILEY 122
Db 429 ATCCAGATTAATTAACATTGAGGTGAGACTGAATGAGATGATTAATTAATCT 488
Qy 123 HISMETHRTRYTPARGLEUGLUASNI 1EALYSTRHGIUPROPOLY 1LEPHEARG 142
Db 489 CATATGACATACCTGAGATTAGAGACATAGCGAAAACTGAACCACTTAAGATTTCCGT 548
Qy 143 VALYSPROVALILEUGLYILEYSAAGMETLLEGLINTPILGLUTPILGLYSPROGL 162
Db 549 GTGAACCAAGTTTGGGCATCAACGAATGATTCMAATTGATGATTAACCTGAGTTG 608
Qy 163 ALAPROVALSERSEARAPLEULYSERYTHRLEUARGPHEARGTHRVALASNSERT 182
Db 609 GCGCTGTTTCATCTGATTTAAATACACACTTGATTCAGAGACGTCAACAGTACAGC 668
Qy 183 TTPMETGLUVALAENPHEALALYASNAAGLYSAPLYSAENGINTHTYRASNLEUTHR 202
Db 669 TGGATGGAAAGTCMACTTGCTTAAGAAAGGTAAGTAACCAACCTACAACTCAGC 728
Qy 203 GLYLEUGINPPOPHETHRGLUTYRVALILEALALEUAQCYSAALAVALLYGUSERT 222
Db 729 GGGCTGCAGCCTTTTACGAATATATGATGATGCTGCGATGTGCGTCAAGAGACTCAAG 788
Qy 223 PHEITPSEARPTPSPERGINGULYSMEGLYMETHRGUGUGUGLYLYSLEULEU 242
Db 789 TTCTGGAGTGACTGGAGCCAAAGAAATGGGAATGATGAGAGAAAGGCAAGTACTC 848
Qy 243 PROALALEPROVALLEUSERTHRLEUVAL 252
Db 849 CCTGCGATTCCCGTCTGCTGCTGTG 878

RESULT 4
US-10-772-531-21
; Sequence 21, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kujiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Homo sapiens
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(878)
US-10-772-531-21

Alignment Scores:
Pred. No.: 5,02e-160 Length: 1476
Score: 1343.00 Matches: 249
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 98.90% Indels: 0
DB: 18 Gaps: 0

US-10-006-265-4 (1-252) x US-10-772-531-21 (1-1476)

QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
DB 129 CTCTCTCCCGAGCTTCATGTGTTAACTGGGGATGATGTGAGCTGGGCACTGTGGATG 188
QY 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGlnLysLeuSer 42
DB 189 CTCCCTCACTCGCAAAATTCAGCTGGCAGCTCTGCCAGCTAAGCTGAGAACATTTCC 248
QY 43 CysValTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 62
DB 249 TGTGTCTACTACTATAGAAAATTTAACTGCACTTGAGCTCAGAGAAAGCAACAGT 308
QY 63 TyTyThGlnTyTyThTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 82
DB 309 TAAACCCAGTACAGATTAAAGAACTTTCGCTTTGGAGAAAACAATGATTAATTTGATCA 368
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB 369 ACCAATAGTTCTTCAAGTGAATTCGTGCTTCGCTCTTTTCTTCCCAAGAAATAGC 428
QY 103 IleProAspAsnTyThrIleGluValGluValGluValGluValGluValGluValGluVal 122
DB 429 ATCCAGATTAATTAATACATTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 488
QY 123 HisMetThrTyTyThTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 142
DB 489 CATATACATACATCGAGATTAGAGAACTAAGCAAAATGAAACCACTTAAGATTTTCCGT 548
QY 143 ValIleProValLeuGlyIleLysArgMetIleGlnIleGlnIleGlnIleGlnIleGlnIle 162
DB 549 GTGAAACCACTTTGGGCAATCAACGATATTCAAATTCGATGATGATGATGATGATGATGATG 608
QY 163 AlaProValSerSerAspLeuTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 182
DB 609 GCGCCTGTTTCATCTGATTTAAATACACACTTCGATTGAGACAGTCAACAGTACAGC 668
QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnIleThrTyAsnLeuThr 202
DB 669 TGGATGAAAGTCAACTTCGCTAAGAACTGTAAGATTAAGAACTGTAAGATTAAGATTAAGAT 728
QY 203 GlyLeuGlnProPheThrGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 222
DB 729 GGGCTGAGGCTTTTACAGATATGTCATAGCTCTGCGATGTCGCTGCGTCAAGAGTCAAG 788
QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGlnGlnGlnGlnGlnGlnGlnGln 242
DB 789 TTCTGGAGTGACTGAGAGCAAAAGAAATGGAATGACTGAGAGAAAGCAAGTACTC 848
QY 243 ProAlaIleProValLeuSerThrLeuVal 252
DB 849 CCTGCGATTCCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 878

RESULT 5
US-10-006-265-16
; Sequence 16, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masaatsu
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APPLICANT: Yaguchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006,265
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2119
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)...(1996)
US-10-006-265-16

Alignment Scores:
Pred. No.: 2.73e-153 Length: 2119
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 15 Gaps: 0

US-10-006-265-4 (1-252) x US-10-006-265-16 (1-2119)

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
DB 11 ATGAAAGCTCTCTCCCGAGCTTCATGTGTTAACTGGGGATGATGTGAGCTGGGCACTG 70
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGlnLys 40
DB 71 TGGATGCTCCCTCACTCGCAAAATTCAGCTGGCAGCTCTGCCAGCTAAGCTGAGAAC 130
QY 41 IleSerCysValTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 60
DB 131 ATTTCTGTGCTCTACTACTATAGAGAAATTTAACTGCTGAGTGAAGTCAAGAGAAAGAA 190
QY 113 SerCysValTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 60
DB 191 ACCAGTTATACCACTGATCACTTAAGACACTTCGCTTTGGAGAAAACAATGATTAAT 250
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 251 TGTACACCAATAGTTCTTCAAGTGAATTCGTGCTGCTCTTTTCTTCCAGAA 310
QY 101 IleThrIleProAspAsnTyThrIleGluValGluValGluValGluValGluValGluVal 120
DB 311 ATTAAGATCCAGATTAATTAATCAATTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 370
QY 121 LysSerHisMetThrTyTyThTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 140
DB 371 AAATCTCATATACATCTGAGATTTAGAACATTAAGCAAACTGAAACCTTAAGATT 430
QY 141 PheArgValIleProValLeuGlyIleLysArgMetIleGlnIleGlnIleGlnIleGlnIle 160
DB 431 TTCCGTGTAAACCACTTTGGGCAATCAACGATGATTCAAATTCGATTAAGTAAAGCT 490
QY 161 GluLeuAlaProValSerSerAspLeuTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 180
DB 491 GAGTTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCAACAGT 550
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnIleThrTyAsn 200
DB 551 ACCAGCTGATGATGATCACTTCGTTAAGAACTGTAAGATTAAGAACTGTAAGATTAAGAACTG 610
QY 201 LeuThrGlyLeuGlnProPheThrGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 220
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Db 611 CTCACGGGGCTGCAGACCTTTTACAGATATGCTAGCTGCGATGCGGTCAAGAG 670
Qy 221 SerlypPheTTPSerAspTTPSerGlnGluYsmetGlyMetThrGluGlu 238
Db 671 TCAAGTTCTGGAGTGAAGTGAAGCCAGAAAAATGGGAATGATGAGGAAGAA 724

RESULT 6
US-09-972-708-5
; Sequence 5, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-5

Alignment Scores:
Pred. No.: 2,98e-153 Length: 2238
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 10 Gaps: 0

US-10-006-265-4 (1-252) x US-09-972-708-5 (1-2238)

Qy 1 MetlyseuSerProGlnProSerCyvalaIsenleuGlyMetMetTTPThrTPAlaleu 20
Db 1 ATGAAGCTCTCTCCCGACCTTCACTGTTAACTGGGAGATGATGAGCACTGGGCACTG 60
Qy 21 TTPMetleuProSerleuCylyvPheSerleuAlaIaleuProAlaIyleProGluasn 40
Db 61 TGGATGCTCCCTTCACTGCAAAATTCAGCTGGCAGCTGCGCAAGCTGAGAAC 120
Qy 41 IleserCyvalaIyleTyrTyrAryGlyAsnleuThrCystrThrTPSerProGlyLyasglu 60
Db 121 ATTTCCTGCTGCTACTACTATAGAAATAATTAACCTGCACTGGAGTCCAGAAAGGAA 180
Qy 61 ThseTyrThrgInlyrThrValIysArgThrTyrAlaPheGlyGlyLysH;AspAsn 80
Db 181 ACCAGTTATACCCGATACACAGTTAAGGAACCTTACGCTTTGGAGAAAAACATGATAT 240
Qy 81 CystrThrAsnSerSerThrSerGluAsnArgAlaSerCyserPhePheleuProArg 100
Db 241 TGTACACCAATATGCTTACAAAGTGAATAATGCTGCTCTCTTTTCTTCCACAGA 300
Qy 101 IletHrIleProAspAenlyrThrIleGluValaGluIleAsnGlyAspGlyValIle 120
Db 301 ATTAACGATCCCAAGTAAATTAATACCAATGAGGTGAAGCTGAATAATGGAGTGTAAAT 360
Qy 121 LysSerHisMetThrTyrTyrPargLeuGluAsnIleAlaIyleThrgluProProLysIle 140
Db 361 AAATCTCATATGACATACCTGAGATTAGAAACATAGCAAACTGAACCACTTAAGATT 420
Qy 141 PheArgValIyleProValleuGlyIleLysArgMetIleGlnIleGluTTPAlaIylePro 160
Db 421 TTCGGTGTGAACCAAGTTTGGGATCAAAAGAAATGATTAATTAATGATTAAGCT 480
Qy 161 GluIleuAlaProValSerSerAspLeuIyleTyrThrIleuArgPheArgThrValAsnSer 180

Db 481 GAGTTGGGCTGCTGTTACTGATTTAAATACACACTTCATTCAGACAGTCAACAGT 540
Qy 181 ThseTTPMetGluValaIsenPheAlaIysAsnArglyAspIyleAsnGlnThrTyrAsn 200
Db 541 ACCGCTGAGTGAAGATCACTGCTTAAGAACCGTAAGGATTAATAAACCAACGTACAC 600
Qy 201 LeuThrglyLeuGlnProPheThrGluTyrValIleAlaIleuArgCyvalaValIysglu 220
Db 601 CTCACGGGGCTGCAGACCTTTTACAGATATGCTAGCTTGCAGATGCGGTCAAGAG 660
Qy 221 SerlypPheTTPSerAspTTPSerGlnGluYsmetGlyMetThrGluGlu 238
Db 661 TCAAGTTCTGGAGTGAAGTGAAGCCAGAAAAATGGGAATGATGAGGAAGAA 714

RESULT 7
US-10-715-667-5
; Sequence 5, Application US/10715667
; Publication No. US20040152161A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/10/715,667
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/972,708
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-715-667-5

Alignment Scores:
Pred. No.: 2,98e-153 Length: 2238
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 18 Gaps: 0

US-10-006-265-4 (1-252) x US-10-715-667-5 (1-2238)

Qy 1 MetlyseuSerProGlnProSerCyvalaIsenleuGlyMetMetTTPThrTPAlaleu 20
Db 1 ATGAAGCTCTCTCCCGACCTTCACTGTTAACTGGGAGATGATGAGCACTGGGCACTG 60
Qy 21 TTPMetleuProSerleuCylyvPheSerleuAlaIaleuProAlaIyleProGluasn 40
Db 61 TGGATGCTCCCTTCACTGCAAAATTCAGCTGGCAGCTGCGCAAGCTGAGAAC 120
Qy 41 IleserCyvalaIyleTyrTyrAryGlyAsnleuThrCystrThrTPSerProGlyLyasglu 60
Db 121 ATTTCCTGCTGCTACTACTATAGAAATAATTAACCTGCACTGGAGTCCAGAAAGGAA 180
Qy 61 ThseTyrThrgInlyrThrValIysArgThrTyrAlaPheGlyGlyLysH;AspAsn 80
Db 181 ACCAGTTATACCCGATACACAGTTAAGGAACCTTACGCTTTGGAGAAAAACATGATAT 240
Qy 81 CystrThrAsnSerSerThrSerGluAsnArgAlaSerCyserPhePheleuProArg 100
Db 241 TGTACACCAATATGCTTACAAAGTGAATAATGCTGCTCTCTTTTCTTCCACAGA 300
Qy 101 IletHrIleProAspAenlyrThrIleGluValaGluIleAsnGlyAspGlyValIle 120
Db 301 ATTAACGATCCCAAGTAAATTAATACCAATGAGGTGAAGCTGAATAATGGAGTGTAAAT 360

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QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
DB 361 AATCTCATATGACATGACTGAGATTAGAGAACTAGCGGAAAACCTAACCTTAAGATT 420
QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
DB 421 TTCCTGGTGAACCAATTTTGGGCTCAACAAACGAAATATTCAAATTTAAAGATGAAGCCCT 480
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB 481 GAGTTGGCCCTGTTTCATCTGATTTAAATACACCTTCGATTCCAGACAGTCAACAGT 540
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
DB 541 ACCAGCTGATGAGAACTCAACTTCGCTAAGAACCGTAAGGAATAAAACCAACGTAACAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB 601 CTCACGGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGGGTCAAGAG 660
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGluMetThrGluGluGlu 238
DB 661 TCAAAGTTCTGAGTGACTGAGACCAAGAAAATGGGAATGACTGAGGAGAGA 714

RESULT 8
US-09-892-949-68
; Sequence 68, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide encoding human zcytor17-FC4 fusion
; NAME/KEY: CDS
; LOCATION: (1)...(2295)
US-09-892-949-68

Alignment Scores:
Pred. No.: 3,1e-153 Length: 2295
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 10 Gaps: 0

US-10-006-265-4 (1-252) x US-09-892-949-68 (1-2295)
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
DB 1 ATGAACTCTCTCCCAAGCCTTATATGTATTACCTGGGAGATATATGGACCTTGGGACATG 60
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40

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DB 61 TCGAGTCTCCCTTCACTGCAAAATTCAGCCCTGGGACGCTCTCCAGCTTAAGCTTGAAC 120
QY 41 IleserCysValLysTyrTrpArgLysAsnLeuThrCysThrTrpSerProGluLysGlu 60
DB 121 ATTTCTGTGTCTACTACTATAGAAAATTTAACTGCACTTGGATGTCAGAAAAGAA 180
QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
DB 181 ACCAGTTATACCAGTACAGTAAAGAACTTAACGCTTTTGGAGAAAATCATGTAAT 240
QY 81 CysThrThrAsnSerSerThrSerGluAsnAlaSerCysSerPhePheLeuProArg 100
DB 241 TGTACAAACCAATAGTCTTACCAAGTAAATCTGCTTCCTTTTCTTCCCAAA 300
QY 101 ILeThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
DB 301 ATAAAGATCCAGATTAATTAATTCATTGAGTGAAGCTGAAAATGGAGATGATGTAAT 360
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
DB 361 AATCTCATATGACATGACTGAGATTAGAGAACTAGCGGAAAACCTAACCTTAAGATT 420
QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
DB 421 TTCCTGGTGAACCAATTTTGGGCTCAACAAACGAAATATTCAAATTTAAAGATGAAGCCCT 480
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB 481 GAGTTGGCCCTGTTTCATCTGATTTAAATACACCTTCGATTCCAGACAGTCAACAGT 540
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
DB 541 ACCAGCTGATGAGAACTCAACTTCGCTAAGAACCGTAAGGAATAAAACCAACGTAACAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB 601 CTCACGGGGCTGACGCTTTTACAGAAATATGTCATAGCTCTGCGATGTGGGTCAAGAG 660
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGluMetThrGluGluGlu 238
DB 661 TCAAAGTTCTGAGTGACTGAGACCAAGAAAATGGGAATGACTGAGGAGAGA 714

RESULT 9
US-10-351-157-38
; Sequence 38, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Grose, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2295

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human zcytor17-Fc4 fusion polynucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2295)
US-10-351-157-38

Alignment Scores:
Pred. No.: 3,1e-153 Length: 2295
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 17 Gaps: 0

US-10-006-265-4 (1-252) x US-10-351-157-38 (1-2295)
Qy 1 MetLysLeuSerProGlnProSerCyValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db 1 ATGAAGCTCTCTCCCGAGCTTCAATGTTAACTGGGAGATGATGAGTGGACCTGGGCACTG 60
Qy 21 TrpMetLeuProSerLeuCyValAsnLeuAlaLeuProAlaLysProGluAsn 40
Db 61 TGGATGCTCCCTTCACTCTGCAAAATTCAGCTGGAGCTTGGCCAGCTAAAGCTGAGAAC 120
Qy 41 LLeSerCyValLysTrpTrpArgLysAsnLeuThrCyThrTrpSerProGlyLysGlu 60
Db 121 ATTTCCTGTCTACTACTATAGCAAAATTTAACTCTCACTGGAGTCCAGGAAGGAA 180
Qy 61 ThrSerTrpThrGlnTrpThrValLysArgThrTrpAlaPheGlyLysLysAspAsn 80
Db 181 ACCGATTATACCCAGTACACAGTTAAGAACTTAAGCTTTTGGAGAAAACATGATAT 240
Qy 81 CySerThrAsnSerSerThrSerGluAsnArgLaserCySerPhePheLeuProArg 100
Db 241 TGTACAAACCAATATCTTCAAGTGAAGAAATGCTGCTCTCTTTTCTTCCCAAGA 300
Qy 101 LLeThrLLeProAspAsnTrpThrLLeGluValGluAlaGluAsnGlyAspGlyValIle 120
Db 301 ATAAAGATCCCAAGATAATTAATACCATTTGAGAGCTGAAATGAGATGGTATAT 360
Qy 121 LysSerHisMetTrpTrpTrpArgLysAsnLLeAlaLysTrpGluProProLysIle 140
Db 361 AAATCTCATATGACATACCTGAGATTAAGAAACATAGGAAACCTGAACCTTAAGATT 420
Qy 141 PheArgValLysProValLLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
Db 421 TTCCGTGTGAACCAAGTTTGGGCATCAACGAATGATTTCAATTTGAATGATTAAGCT 480
Qy 161 GluLeuAlaProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSer 180
Db 481 GAGTGTGGCGCTGTTTCATCTGATTTAAATPACACATTCGATTCAGGACGCTCAACAGT 540
Qy 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrpAsn 200
Db 541 ACCAGCTGAGAGGAAAGTCACTTGTCTAAGAACCTGAAGATAAAACCAAAACCTAACAC 600
Qy 201 LeuThrGlyLeuGlnProPheThrGlyLysValLLeAlaLeuArgCyValAlaValLysGlu 220
Db 601 CTCACGGGGCTGCAGCTTTTACAGAAATATCTCACTGCTGCAATGTGGGTCAAGAG 660
Qy 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
Db 661 TCAAAAGTTCTGAGTGAAGTGAAGCAAGAAAATGGGAATGACTGAGGAAGAA 714

RESULT 10
US-10-352-554-38
; Sequence 38, Application US/10352554
; Publication No. US20030224487A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
```

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; APPLICANT: Kujiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Novak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: NOVEL CYTOKINE ZCYTOR17 LIGAND
; FILE REFERENCE: 02-01
; CURRENT APPLICATION NUMBER: US/10/352,554
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/375,323
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/435,315
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human zcytor17-Fc4 fusion polynucleotide
; NAME/KEY: CDS
; LOCATION: (1) ... (2295)
US-10-352-554-38

Alignment Scores:
Pred. No.: 3,1e-153 Length: 2295
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 17 Gaps: 0

US-10-006-265-4 (1-252) x US-10-352-554-38 (1-2295)
Qy 1 MetLysLeuSerProGlnProSerCyValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db 1 ATGAAGCTCTCTCCCGAGCTTCAATGTTAACTGGGAGATGATGAGTGGACCTGGGCACTG 60
Qy 21 TrpMetLeuProSerLeuCyValAsnLeuAlaLeuProAlaLysProGluAsn 40
Db 61 TGGATGCTCCCTTCACTCTGCAAAATTCAGCTGGAGCTTGGCCAGCTAAAGCTGAGAAC 120
Qy 41 LLeSerCyValLysTrpTrpArgLysAsnLeuThrCyThrTrpSerProGlyLysGlu 60
Db 121 ATTTCCTGTCTACTACTATAGCAAAATTTAACTCTCACTGGAGTCCAGGAAGGAA 180
Qy 61 ThrSerTrpThrGlnTrpThrValLysArgThrTrpAlaPheGlyLysLysAspAsn 80
Db 181 ACCGATTATACCCAGTACACAGTTAAGAACTTAAGCTTTTGGAGAAAACATGATAT 240
Qy 81 CySerThrAsnSerSerThrSerGluAsnArgLaserCySerPhePheLeuProArg 100
Db 241 TGTACAAACCAATATCTTCAAGTGAAGAAATGCTGCTCTCTTTTCTTCCCAAGA 300
Qy 101 LLeThrLLeProAspAsnTrpThrLLeGluValGluAlaGluAsnGlyAspGlyValIle 120
Db 301 ATAAAGATCCCAAGATAATTAATACCATTTGAGAGCTGAAATGAGATGGTATAT 360
Qy 121 LysSerHisMetTrpTrpTrpArgLysAsnLLeAlaLysTrpGluProProLysIle 140
Db 361 AAATCTCATATGACATACCTGAGATTAAGAAACATAGGAAACCTGAACCTTAAGATT 420
Qy 141 PheArgValLysProValLLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
Db 421 TTCCGTGTGAACCAAGTTTGGGCATCAACGAATGATTTCAATTTGAATGATTAAGCT 480
Qy 161 GluLeuAlaProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSer 180
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DB 481 GAGTTGGCCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGACAGTCAACAGT 540
QY 181 ThrSerTrpMetGluValAsnPheAlaValAsnArgLysAspLysAsnGlnThrTyrAsn 200
DB 541 ACCAGCTGGATGGAATCACTTCGCTAAGAACCCGTAAGGATTAACCAACGTAACAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB 601 CTCACGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAGAG 660
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
DB 661 TCAAAAGTCTGAGTGACTGAGCCCAAGAAAATGGAATGACTGAGGAAGAA 714

RESULT 11
US-10-772-531-68
; Sequence 68, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prensell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide encoding human zcytor17-Fc4 fusion
; NAME/KEY: CDS
; LOCATION: (1)...(2295)
US-10-772-531-68

Alignment Scores:
Pred. No.: 3,1e-153 Length: 2295
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 18 Gaps: 0

US-10-006-265-4 (1-252) x US-10-772-531-68 (1-2295)
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
DB 1 ATGAAGCTCTCTCCACAGCCTTCATGTGTAACTGGGATGATGTGAACCTGGGACACTG 60
QY 21 TrpMetLeuProSerLeuGlySerPheSerLeuAlaIleLeuProAlaLysProGluAsn 40
DB 61 TGGATGCTCCCTTCACATCTGCAAAATTCAGCTGGGAGCTCTGCACTAAGCTGGAAC 120
QY 41 IleSerCysValLysTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 121 ATTTCTGTGTCTACTACTATATGAAAAATTTAACTGCACTTGAGTCCAGAAAAAGAA 180
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QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
DB 181 ACCAGTTATACCACTATACAGATTAAAGAACTTAAGCTTTTGGAGAAAAACATGATAT 240
QY 81 CysThrThrAsnSerSerThrSerGluAsnAlaSerCysSerPhePheLeuProArg 100
DB 241 TGTACAAACCAATAGTTCTTACAGATGAATAATCGTGTCTCTTTTCCCTCCAAA 300
QY 101 IleThrIleProAspAsnTyrThrIleGluValIleGluAlaGluAsnGlyAspGlyValIle 120
DB 301 ATTAAGATCCAGATTAATTAATACATGAGTGGAAGCTGAAAATGAGATGTGTAAAT 360
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
DB 361 AATCTCATATGACATACACTGAGATTAAGAAACATATAGGAAATCGAACCACTTAAGAT 420
QY 141 PheArgValLysProValLeuGlyTyrLysArgMetIleGlnIleGluTrpIleLysPro 160
DB 421 TTCCTGTGAAACCAAGTTTGGGCATCAACCAATGATTCAAATTCGAATGAAGTAAGCCT 480
QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB 481 GAGTTGGCCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGACAGTCAACAGT 540
QY 181 ThrSerTrpMetGluValAsnPheAlaValAsnArgLysAspLysAsnGlnThrTyrAsn 200
DB 541 ACCAGCTGGATGGAATCACTTCGCTAAGAACCCGTAAGGATTAACCAACGTAACAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
DB 601 CTCACGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAGAG 660
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGlu 238
DB 661 TCAAAAGTCTGAGTGACTGAGCCCAAGAAAATGGAATGACTGAGGAAGAA 714

RESULT 12
US-09-972-708-3
; Sequence 3, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-3

Alignment Scores:
Pred. No.: 3,49e-153 Length: 2480
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 10 Gaps: 0

US-10-006-265-4 (1-252) x US-09-972-708-3 (1-2480)
QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
DB 132 ATGAAGCTCTCTCCACAGCCTTCATGTGTAACTGGGATGATGTGACCTGGGACACTG 191
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Qy 21 TrpMetLeuProSerLeuCyAlaPheSerLeuAlaAlaLeuProAlaLeuProGluLeu 40
Db 192 TGAATGCTCCCTTCACTCTGCAAAATTCAGCCCTGGACGCTCCGACGTAAGCTTAGAAC 251
Qy 41 ILeSerCyValIYrTYrTYrAglYaaNleuThrCySerThrTrpSerProGlyValGlu 60
Db 252 ATTTCCTGTCTACTACTAATAAGAAATTTAACTCCACTTGAGCTGAGCAAGAAAGAA 311
Qy 61 ThrSerYrThrGlnTYrThrValIYaaRghThrYrAlaPheGlyGluLeuHisAspAsn 80
Db 312 ACCAGTTATACCCAGTACACAGTTAAGAACTTAAGCTTTTGGAGAAACATGATATAT 371
Qy 81 CysThrThraenSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 372 TGTACAACCAATAGTTCTACAAAGTAAATGCTGCTTCTCTCTTTCTTCTTCCACAA 431
Qy 101 ILeThrIleProAspAsnTYrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db 432 ATTAAGATCCAGATTAATTATACCACTGAGGTGGAACTGAAATGAGATGCTGTAATT 491
Qy 121 LysSerHisMetThrTYrTYrTrpArgLeuGluAsnIleAlaIleYrThrGluProProIle 140
Db 492 AAATCTCATATGACATCTGAGATTAAGAAACATAGCGAAACCTGAACCTTAAGATT 551
Qy 141 PheArgValIysProValIleuGlyIleYsaRgMetIleGlnIleGluTrpIleYsaPro 160
Db 552 TTCCTGTGAAACCAAGTTTGGGCATCAACCAATGATTCAAATTGAATGAATAAAGCTT 611
Qy 161 GluLeuAlaProValSerSerAspLeuYrTYrThrLeuArgPheArgThrValAsnSer 180
Db 612 GAGTTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGACAGTCAACAGT 671
Qy 181 ThrSerTrpMetGluValAsnPheAlaYsaAsnArgYsaAspYsaAsnGlnThrTYrAsn 200
Db 672 ACCAGCTGAGATGAAGTCACTGCTAAGAACCGTAAGATTAAGAAACGTAACAC 731
Qy 201 LeuThrGlyLeuGlnProPheThrGluTYrValIleAlaLeuArgCysAlaValIleGlu 220
Db 732 CTCACGGGGCTGCAGCCTTTTACGAATATGTCTATAGCTTGCATGTGCGGTCAAGAG 791
Qy 221 SerIYsaPheTrpSerAspTrpSerGlnGluIYsaMetGlyMetThrGluGluGlu 238
Db 792 TCANAAGTTCTGAGTGAAGTGAAGCCAAAGAAAATGGAAATGACGAGAGAA 845

RESULT 13
US-10-715-667-3
; Sequence 3, Application US/10715667
; Publication No. US20040152161A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/10/715,667
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/972,708
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-715-667-3

Alignment Scores: 3,49e-153 Length: 2480
Score: 1292.00 Matches: 238
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.14% Indels: 0
DB: 18 Gaps: 0

US-10-006-265-4 (1-252) x US-10-715-667-3 (1-2480)
Qy 1 MetIYsaSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
Db 132 ATGAAGCTCTTCCCGACCTTCACTGTATTAACTGGGAGATGATGACCTGGGCACTG 191
Qy 21 TrpMetLeuProSerLeuCyAlaPheSerLeuAlaAlaLeuProAlaLeuProGluLeu 40
Db 192 TGAATGCTCCCTTCACTCTGCAAAATTCAGCCCTGGACGCTCCGACGTAAGCTTAGAAC 251
Qy 41 ILeSerCyValIYrTYrTYrAglYaaNleuThrCySerThrTrpSerProGlyValGlu 60
Db 252 ATTTCCTGTCTACTACTAATAAGAAATTTAACTCCACTTGAGCTGAGCAAGAAAGAA 311
Qy 61 ThrSerYrThrGlnTYrThrValIYaaRghThrYrAlaPheGlyGluLeuHisAspAsn 80
Db 312 ACCAGTTATACCCAGTACACAGTTAAGAACTTAAGCTTTTGGAGAAACATGATATAT 371
Qy 81 CysThrThraenSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
Db 372 TGTACAACCAATAGTTCTACAAAGTAAATGCTGCTTCTCTCTTTCTTCTTCCACAA 431
Qy 101 ILeThrIleProAspAsnTYrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
Db 432 ATTAAGATCCAGATTAATTATACCACTGAGGTGGAACTGAAATGAGATGCTGTAATT 491
Qy 121 LysSerHisMetThrTYrTYrTrpArgLeuGluAsnIleAlaIleYrThrGluProProIle 140
Db 492 AAATCTCATATGACATCTGAGATTAAGAAACATAGCGAAACCTGAACCTTAAGATT 551
Qy 141 PheArgValIysProValIleuGlyIleYsaRgMetIleGlnIleGluTrpIleYsaPro 160
Db 552 TTCCTGTGAAACCAAGTTTGGGCATCAACCAATGATTCAAATTGAATGAATAAAGCTT 611
Qy 161 GluLeuAlaProValSerSerAspLeuYrTYrThrLeuArgPheArgThrValAsnSer 180
Db 612 GAGTTGGCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGACAGTCAACAGT 671
Qy 181 ThrSerTrpMetGluValAsnPheAlaYsaAsnArgYsaAspYsaAsnGlnThrTYrAsn 200
Db 672 ACCAGCTGAGATGAAGTCACTGCTAAGAACCGTAAGATTAAGAAACGTAACAC 731
Qy 201 LeuThrGlyLeuGlnProPheThrGluTYrValIleAlaLeuArgCysAlaValIleGlu 220
Db 732 CTCACGGGGCTGCAGCCTTTTACGAATATGTCTATAGCTTGCATGTGCGGTCAAGAG 791
Qy 221 SerIYsaPheTrpSerAspTrpSerGlnGluIYsaMetGlyMetThrGluGluGlu 238
Db 792 TCANAAGTTCTGAGTGAAGTGAAGCCAAAGAAAATGGAAATGACGAGAGAA 845

RESULT 14
US-09-892-949-53
; Sequence 53, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore B.
; APPLICANT: Kuljper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29

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Qy 141 PheArgValIysProValLeuGlyIleYsArgMetIleGlnIleGluTrpIleYsPro 160
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Db 917 TTCGCTGTGAAACCAAGTTTGGGCATCAACGAATGATTCAAAATTGAATGATAAAGCCT 976
    |||||
Qy 161 GluLeuAlaProValSerSerAspLeuIleYrThrLeuArgPheArgThrValAsnSer 180
    |||||
Db 977 GAGTTGGCGCCTGTTTCATCTGATTTAAATACACACTTCGATTCAGGACAGTCACACAGT 1036
    |||||
Qy 181 ThrSerTrpMetGluValAsnPheAlaIleYsAsnArgIysAspIysAsnGlnThrTyrAsn 200
    |||||
Db 1037 ACCAGCTGAGTGAAGTCACTCGCTAAGAACCGTAAGATAAACCAACGTAACAC 1096
    |||||
Qy 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIysGlu 220
    |||||
Db 1097 CTCACGGGGGCTGCAAGCCTTTACAGAAATATGTCAATAGCTTGCAGATGTCCGGTCAAGAG 1156
    |||||
Qy 221 SerIysPheTrpSerAspTrpSerGlnGluIysMetGlyMetThrGluGluGlu 238
    |||||
Db 1157 TCAAAATTCTGAGTGAAGTGAAGCAAGAAAAAATGGGAATGACTGAGAGAAAGAA 1210
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Job time : 400.322 secs

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OM protein - nucleic search, using frame_p2n model

Run on: February 23, 2005, 08:54:07 ; Search time 2316.44 Seconds
(without alignments)
4140.927 Million cell updates/sec

Title: US-10-006-265-4
Perfect score: 1358
Sequence: 1 MKLSPQPSCVNLGMWMTWL.....GMEEGKLPLAIVLSTLV 252

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 segs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seg length: 0
Maximum DB seg length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+g2n.model -DEV=x1h
-O=/cgnt_1/USPRO.epool/US10006265/runat_18022005_094658_22193/app_query.fasta_1.2069
-DB=EST -QFMT=fastcap -SUFFIX=rest -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=humand40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006265_QCGN_1_1_7723_@runat_18022005_094658_22193 -NCPU=6 -ICPU=3
-NO MMAP -LARGEDBPRY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST+
1: gb_est1:.*
2: gb_est2:.*
3: gb_hic:.*
4: gb_est3:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_ges1:.*
9: gb_ges2:.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468.5	34.5	637	7	CF174021 B0932D09-
2	397	29.2	651	2	CF915066 B0973F04-
3	347	25.6	592	6	CA561173 K0283D09-
4	345	25.4	459	8	A0022781 HS_2180 A
5	342	25.2	479	6	CA560924 K0279C07-
6	302	22.2	546	6	CA555774 K0202F08-
7	298.5	22.0	628	6	CB427282 K02850 MA
8	297	21.9	553	6	CA559989 K026C03-
9	270.5	19.9	699	6	CB168262 HSF603268

10	270	19.9	518	6	CA561193 K0283F09-
11	270	19.9	523	6	CA559290 K0256G09-
12	265.5	19.6	1512	3	BC020454 BC020454
13	265	19.5	487	5	B0560019 H4061G10-
14	262.5	19.3	5264	7	CF780723 AGENCOURT
15	262.5	19.3	5264	3	BC071555 Homo sapi
16	257	18.9	3055	3	AY310138 Rattus no
17	235	17.3	948	5	BU956443 AGENCOURT
18	228	16.8	1069	5	BM928529 AGENCOURT
19	221.5	16.3	923	5	B0644443 AGENCOURT
20	215	15.8	876	5	B0646417 AGENCOURT
21	207	15.2	588	7	CN265170 170004243
22	207	15.2	761	7	CN265171 170004240
23	196	14.4	515	8	CC144782 NST002_Ba
24	196	14.4	911	5	B0647489 AGENCOURT
25	194.5	14.3	420	1	AU233305 AU233305
26	194.5	14.3	3436	3	AK050317 Mus muscu
27	193.5	14.2	420	1	AJ689818 AJ689818
28	193	14.2	761	5	BU460413 B03369157
29	191.5	14.1	3536	3	AK054381 Mus muscu
30	191.5	14.1	3812	3	AK052679 Mus muscu
31	190	14.0	695	5	BX849563 BX849563
32	189	13.9	909	9	AY416683 Pan trogl
33	183.5	13.5	757	7	CO807600 AGENCOURT
34	181.5	13.4	626	6	CA893723 B0181A01-
35	181.5	13.4	947	5	B0652548 AGENCOURT
36	180.5	13.3	3207	3	AK054551 Mus muscu
37	179	13.2	828	9	AY416684 Mus muscu
38	176	13.0	1456	3	CR686776 Tetradon
39	176	13.0	1859	3	CR650198 Tetradon
40	174.5	12.8	681	5	BU443017 603019102
41	174.5	12.8	718	5	BU288806 604163450
42	172	12.7	939	5	BU248460 603780593
43	171	12.6	939	5	B0649117 AGENCOURT
44	170	12.5	1677	3	AK080147 Mus muscu
45	168.5	12.4	931	5	BU190038 AGENCOURT

ALIGNMENTS

RESULT 1
LOCUS CF174021 637 bp mRNA linear EST 25-JUL-2003
DEFINITION B0932D09-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
ACCESSION CF174021
VERSION CF174021.1 GI:33283570
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORANISM Mus musculus

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Piao, Y., Ko, N.T., Lim, M.K., and Ko, M.S.H.
TITLE Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method

JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE 21429098
PUBMED 11544199
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun-grc.nia.nih.gov
Plate: B0932 row: D column: 09
Seq primer: M13 Reversease
High quality sequence stop: 637
POLYA=No.

FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"

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/strain="C57BL/6J"
/db_xref="nlaEST:B0932D09-5"
/db_xref="taxon:10090"
/clone="NIA:B0932D09 IMAGE:30475340"
/dev_stage="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
1)"

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/Note="Vector: PCMV-SPORT6 (Invitrogen) ; Site 1: SalI;
Site 2: NotI. Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgun.gsc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer [Invitrogen:
5'-pGACTAGTCTAGATCGCGAGCGCGCCCTTTT-3'],
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of PCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.5 kb. The library was
constructed by Yulan Piao."

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ORIGIN

Alignment Scores:

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Pred. No.: 6,76e-42 Length: 637
Score: 468.50 Matches: 96
Percent Similarity: 63.59% Conservative: 21
Best Local Similarity: 52.17% Mismatches: 54
Query Match: 34.50% Indels: 13
DB: 7 Gaps: 4

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US-10-006-265-4 (1-252) x CF174021 (1-637)

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QY 7 ProSerCysValAsnLeuGlyMetCysThrTrpAlaLeuTrpMetLeuProSerLeu 26
Db 119 CCTCGGTGTGAAACCTGGAATATGTGACCTTGCGCACTTGCGCACTTCCTTCCTC 178
QY 27 CysLeuPheSerLeuAlaLeuProAlaLeuProGluAsnLeuSerCysValTyrTyr 46
Db 179 TGCAAATTCAGCTGCGACGCTGCGCACTTAACCAAGAAACATTCCTGCGCTTTAC 238
QY 47 TyrArgValAsnLeuThrCysThrTrpSerProGlyValGluThrSerTyrTrpGlnTyr 66
Db 239 TTCGACAGAAATCTGACTGCTGAGACCGAGAAAGAAACCAATGATACCACTAT 298
QY 67 ThrValIysArgThrTyrAlaPheGlyGluValHisAspAsnCysThrThrAsnSerSer 86
Db 299 ATTGTACTTGACTTACTTACTTGTGAAA-----AGCAAT 334
QY 87 ThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle-----Pro 104
Db 335 TATAGTACATCTCAAGAGGCTCATATTTCTTCCCGCTTCGTCGATGCCCCA 394
QY 105 AspAsnTyrThrIleGluValAlaGluAsnGlyAspGlyValIleLeuSerHisMet 124
Db 395 GACATCTGCAGTGTAAAGTAAAGCTCAAAATGAGATGTGTAATCTGACATC 454
QY 125 ThrTyrTrpArgLeuGluAsnIleAlaValThrGluProProIysIlePheArgValys 144
Db 455 ACATATTTGGATTATATCTCATAGCAAAACCGAACCACTTAATTTTAAAGTGAAT 514
QY 145 ProValIleuGlyIleLeuArgMetIleGlnIleGluTrpIleLeuProGluLeuAlaPro 164

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Db 515 CCMAAT-----TGATATGAAATGTTCCAGATACAAATG---AAACCGGTGAAAAAGACT 565
QY 165 ValSerSerAspLeuIysTyrThrIleuArgPheArgThrValAsnSerThrTrpMet 184
Db 566 CGTGGCTTCCCTTTGATATGATGATGCTTGGCTTCAAGACTGTAAACGATGACCACTGACG 625
QY 185 GluValAsnPhe 188
Db 626 GAAGTCAATTTT 637

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RESULT 2
CF915066 651 bp mRNA linear EST 05-NOV-2003
LOCUS B0973F04-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
DEFINITION musculus cDNA clone NIA:B0973F04 IMAGE:30479295 5', mRNA sequence.
CF915066
ACCESSION CF915066.1 GI:38186268
VERSION EST.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 651)
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Piao, Y., Ko, N.-T., Lim, M.K. and Ko, M.S.H.
CONSTRUCTION OF long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)
JOURNAL 21429098
MEDLINE 11544199
PUBMED
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgun.gsc.nia.nih.gov
Plate: B0973 Row: F Column: 04
Seq primer: M13 Reverse
High quality sequence stop: 651
POLVA=No.

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FEATURES

source

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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="nlaEST:B0973F04-5"
/clone="NIA:B0973F04 IMAGE:30479295"
/dev_stage="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
1)"
/Note="Vector: PCMV-SPORT6 (Invitrogen) ; Site 1: SalI;
Site 2: NotI. Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgun.gsc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer [Invitrogen:
5'-pGACTAGTCTAGATCGCGAGCGCGCCCTTTT-3'],
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of PCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.5 kb. The library was

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ORIGIN constructed by Yulan Piao."

Alignment Scores:
 Pred. No.: 7.64e-34 Length: 651
 Score: 397.00 Matches: 79
 Percent Similarity: 64.90% Conservative: 19
 Best Local Similarity: 52.32% Mismatches: 41
 Query Match: 29.23% Indels: 12
 DB: 7 Gaps: 3

US-10-006-265-4 (1-252) x CF915066 (1-651)

Qy 6 GlnProSerCyValAsnLeuGlyMeMetTrpThrAlaLeuTrpMetLeuProSer 25
 Db 229 CAGCCTCGGGTGTGAACCGTGAATTAATGTGACCTTGGCAGCTGTGGCATTCTCTTC 288
 Qy 26 LeuCyAlpPheSerLeuAlaLeuProAlaLysProGluAsnIleSerCyValTyr 45
 Db 289 CTCTGCAAAATTCAGCTGTGAGTCTGCGCACTAAGCCAGAAACATTTCCTGGCTCTT 348
 Qy 46 TyrTrpAlaGlyAsnLeuThrCySerThrTrpSerProGlyLysGluThrSerTyrThrGln 65
 Db 349 TACTTCGACAGAAATCTGACTTGCACCTTGGAGACCAAGAAAGAAACCAATGATACGAC 408
 Qy 66 TyrThrValLysArgThrTyrAlaPheGlyGlyLysIleAspAsnCySerThrThrAsnSer 85
 Db 409 TACATTGTGACTTGTGACTTACTCTTATGAGAAA-----AGC 444
 Qy 86 SerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThrIle----- 103
 Db 445 AATTATAGTGAACAATGTCAAGAGCGCTCATATCTTTCCCGTCTCTGCAATGCC 504
 Qy 104 ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis 123
 Db 505 CCAGACATCTGCAGTGTGAAGTCAAGCTCAAAATGAGATGATGAAGTTAAATCTGAC 564
 Qy 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProlLysIlePheArgVal 143
 Db 565 ATCAATATGTGACATTATATCTCCATAGCAAAACCAACCTATATATTTAAGTGTG 624
 Qy 144 LysProValLeuGlyIleLysArgMetIleGln 154
 Db 625 AATCCAATT-----TGTATAGAAATGTTCCAG 651

RESULT 3
 CAS61173 592 bp mRNA linear EST 19-NOV-2002
 LOCUS K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library (long) Mus
 DEFINITION musculus cDNA clone NIA:K0283D09 IMAGE:30052652 5', mRNA sequence.
 ACCESSION CAS61173.1 GI:25105828
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 592)
 AUTHORS Piao, Y., Kargul, G.U., Dudekula, D.B., Qian, Y., Luo, A., Steag, C.A., Martin, P., Alpa, K., Tanaka, T. and Ko, M.S.H.
 TITLE Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (long)
 JOURNAL Unpublished (2001)
 COMMENT Other ESTs: K0283D09-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@gsun.grc.nia.nih.gov
 Plate: K0283 row: D column: 09
 Seq primer: M13 Reverse
 High quality sequence stop: 592
 POLY-A-No.

FEATURES
 source

Location/Qualifiers

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/organism="Mus musculus"

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/db_xref="taxon:K0283D09-5N"

/db_xref="taxon:10090"

/clone="NIA:K0283D09 IMAGE:30052652"

/tissue_type="Unfertilized Egg"

/lab_host="DH10B"

/clone_id="NIA Mouse Unfertilized Egg cDNA Library (long)"

/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI. Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research, Program, NIH (http://gsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 148 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGAGCGGCCCTTTTCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker l3-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 Kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:

Pred. No.: 2.79e-28 Length: 592
 Score: 347.00 Matches: 67
 Percent Similarity: 65.89% Conservative: 18
 Best Local Similarity: 51.94% Mismatches: 34
 Query Match: 25.55% Indels: 10
 DB: 6 Gaps: 2

US-10-006-265-4 (1-252) x CAS61173 (1-592)

Qy 6 GlnProSerCyValAsnLeuGlyMeMetTrpThrAlaLeuTrpMetLeuProSer 25
 Db 229 CAGCCTCGGGTGTGAACCGTGAATTAATGTGACCTTGGCAGCTGTGGCATTCTCTTC 288
 Qy 26 LeuCyAlpPheSerLeuAlaLeuProAlaLysProGluAsnIleSerCyValTyr 45
 Db 289 CTCTGCAAAATTCAGCTGTGAGTCTGCGCACTAAGCCAGAAACATTTCCTGGCTCTT 348
 Qy 46 TyrTrpAlaGlyAsnLeuThrCySerThrTrpSerProGlyLysGluThrSerTyrThrGln 65
 Db 349 TACTTCGACAGAAATCTGACTTGCACCTTGGAGACCAAGAAAGAAACCAATGATACGAC 408
 Qy 66 TyrThrValLysArgThrTyrAlaPheGlyGlyLysIleAspAsnCySerThrThrAsnSer 85
 Db 409 TACATTGTGACTTGTGACTTACTCTTATGAGAAA-----AGC 444
 Qy 86 SerThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThrIle----- 103
 Db 445 AATTATAGTGAACAATGTCAAGAGCGCTCATATCTTTCCCGTCTCTGCAATGCC 504
 Qy 104 ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSerHis 123
 Db 505 CCAGACATCTGCAGTGTGAAGTCAAGCTCAAAATGAGATGATGAAGTTAAATCTGAC 564
 Qy 124 MetThrTyrTrpArgLeuGluAsnIle 132
 Db 132

Db 565 ATCACATATTGGCATTTAATCTCCATA 591

RESULT 4
LOCUS A0022781 459 bp DNA linear GSS 16-JUN-1998
DEFINITION HS_2180_A2_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2180 Col=22 Row=C, genomic survey sequence.

ACCESSION A0022781
VERSION A0022781
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,U., Young,U., Zhao,S., Adams,W.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PubMed 10449764

COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2180 row: C column: 22
Class: BAC ends
High quality sequence stop: 459.

FEATURES
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1. .459
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/clone="Plate=2180 Col=22 Row=C"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: Sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN
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Score: 345.00 Matches: 68
Percent Similarity: 90.79% Conservative: 1
Best Local Similarity: 89.47% Mismatches: 7
Query Match: 25.41% Indels: 0
Gaps: 0

US-10-006-265-4 (1-252) x A0022781 (1-459)

QY 177 ThrValAsnSerThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsn 196
Db |||:|||||
190 ACGATTGCTCTGTTCTTAGATGAGAGTCACTTGCTPAAGACGTAAAGGTTAAAC 249
QY 197 GlnThrTyAsnLeuThrGlyLeuGlnProPheThrGluTyValAlaLeuArgCys 216
Db |||:|||||
250 CAAACGTACACTCAGCGGGCTGCACCTTNTACAGATATGTCTAGCTCGCATGT 309
QY 217 AlaValLysGluSerLysPheTrpSerArgTrpSerGlnGluLysMetGlyMetThrGlu 236
Db |||:|||||
310 GCGGTCAAGAGAGCAAGTTCTGAGTGACTGAGCCAGAAAAATGGGAATGACTGAG 369
QY 237 GlnGluGlyLysLeuLeuProAlaLeuProValLeuSerThrLeuVal 252
Db |||:|||||
370 GAAGANCGACGACTCTCTCGATTCCGTCCTGCTGCTGTGG 417

RESULT 5
LOCUS CA560924 479 bp mRNA linear EST 19-NOV-2002
DEFINITION K0279C07-SN NIA Mouse Unfertilized Egg cDNA Library (long) Mus musculus cDNA clone NIA:K0279C07 IMAGE:30052254 5', mRNA sequence.

ACCESSION CA560924
VERSION CA560924
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Steagy,C.A., Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.
TITLE Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (Long)
JOURNAL Unpublished (2001)
COMMENT Other ESTs: K0279C07-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0279 row: C column: 07
Seq primer: M13 Reverse
High quality sequence stop: 479
POLYA-No.

FEATURES
source
1. .479
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taabst:K0279C07-5N"
/db_xref="taxon:10090"
/clone="NIA:K0279C07 IMAGE:30052254"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544191]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen):
5'-pGACATGTTCTAGTCGCGAGCGCGCCCTTTTCTTTTCTTTT-3', treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN
Alignment Scores:
Pred. No.: 7.49e-28 Length: 479
Score: 342.00 Matches: 66
Percent Similarity: 65.62% Conservative: 18
Best Local Similarity: 51.56% Mismatches: 34
Query Match: 25.16% Indels: 10
Gaps: 2

TITLE	Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries	
Unpublished (2003)	

OY	6	GINP	ProSerCysValAsnIleuGluMetMetTyrThrTrrAlaLeuTrrPheLeuProSer	25
		229	CAGCCCTCGGGGTGTGAACCGCTGGAAATATGTGACCTTGGCACTGTGGCATTTCTTTTC	288
Db				
OY	26	LeuCysLysPheSerIleuAlaLeuProAlaLysPheGluAsnIleSerCysValTyr	45	
		289	CTCTGGAAATTCAGCGCTGGCAGTCTCGCGACATACGACAGAGAAACATTTCTCAGCTCTT	348
Db				
OY	46	TyrTyrArgLysAsnIleuThrCysThrTrrPseProGluLysGluThrIserTyrThrGln	65	
		349	TACTTCGACAGAAATGTGAACCTTGACCTTGGAGACCCAGAGAGAAACCAATGATACCCAGC	408
Db				
OY	66	TyrThrValLysArgThrTyrAlaPheGluLysLysIleAspAsnCysThrThrAsnSer	85	
		409	TACATGTGACTTTGACTTACTACTCTGTGAAA-----AGC	444
Db				
OY	86	SerThrIserGluAsnArgLaserCysSerPhePheLeuProArgIleThrIle-----	103	
		445	AATTATAGTGACATGCTCTACAGAGGTTTCAATATCTTTTCCCGCTCTGTGCAATGCC	504
Db				
OY	104	ProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGly	118	
		505	CCAGACATCTGCAGTGTGAAATGACAGCTCAAAATGAGAGATGT	549
Db				

FEATURES

Source

Alignment Scores:

[illegible]

RESULT	10
LOCUS	CAS61193
DEFINITION	CASE1193 518 bp mRNA linear EST_19-NOV-2007 K0283f09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
ACCESSION	Musculus cdna clone NIA:K0283F09 IMAGE:30052676 5' mRNA sequence.
VERSION	CAS61193
KEYWORDS	CAS61193..1 GI:25105848
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 518)
TITLE	Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Seagg,C.A., Martin,P., Alida,K., Tanaka,T. and Ko,M.S.H. Systematic Analyses of NIA Mouse Unfertilized Egg cDNA library (long) Unpublished (2001)
JOURNAL COMMENT	Other ESTs: K0283F09-3
	Contact: Dawood B. Dudekula

Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0283 Row: F Column: 09
Seq primer: M13 Reverse
High quality sequence stop: 518
POLYA=No.

FEATURES

Location/Qualifiers
1..518
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:K0283F09-5N"
/db_xref="taxon:10090"
/clone="NIA:K0283F09 IMAGE:30052676"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_1ib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544191]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an oligo(dT) primer (Invitrogen): 5'-pGACTAGTCTAGATCGCAGCGCGCCCTTTTCTTTT-3', treated with T4 DNA polymerase, and ligated to ethanol-precipitation. The cDNAs were purified by Lone-linker Lf-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:

Pred. No.: 1.04e-19 Length: 518
Score: 270.00 Matches: 51
Percent Similarity: 65.26% Conservative: 11
Best Local Similarity: 53.68% Mismatches: 25
Query Match: 19.88% Indels: 8
DB: 6 Gaps: 1

US-10-006-265-4 (1-252) x CA561193 (1-518)

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Oy 6 GlnProSerCyValAsnLeuGlyMetMetTrpThrTrrAlaLeuTrpMetLeuProSer 25
    |||||
Db 223 CAGCCTCTGGGTGTGAACCTGGAATTAATGTGACCTTGCACTGGGCACTTCCTTC 288
    |||||
Oy 26 LeuCyValPheSerLeuAlaAlaLeuProAlaLysProGluAsnLysSerCyValTyr 45
    |||||
Db 289 CTTCTGAAATTCAGCTGCGACGTCGCCGACTTAACCAAGAAACATTCCTCGTCTT 348
    |||||
Oy 46 TyrTyrArgLysAsnLeuThrCySerThrTrpSerProGlyLysGluThrSerTyrTrnGln 65
    |||||
Db 349 TACTTGCAGAAATCTGACTTGCACTTGAGACCCAGAAAGGAAACCAATACCAAC 408
    |||||
Oy 66 TyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCySerThrTrnAsnSer 85
    |||||
Db 409 TACATGTGACTTTCCTTACTTCTTATGAAAA-----AGC 444
    |||||
Oy 86 SerThrSerGluAsnArgAlaSerCySerPhePheLeuProArg 100
    |||||
DB: 6

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Db 445 AATTATAGTACATGCTACAGAGGCTTCATATCTTTCCCGT 489

RESULT 11
CA559290 523 bp mRNA linear EST 19-NOV-2002
LOCUS K0256G09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
DEFINITION musculus cDNA clone NIA:K0256G09 IMAGE:30050096 5', mRNA sequence.
ACCESSION CA559290
VERSION CA559290.1 GI:25103871
KEYWORDS EST
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 523)
REFERENCE Martin,P., Alpa,K., Tanaka,T. and Ko,M.S.H.
Authors Systeatic Analyses of NIA Mouse Unfertilized Egg cDNA Library
Title (Long)
Journal Unpublished (2001)
Comment Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0256 Row: G Column: 09
Seq primer: M13 Reverse
High quality sequence stop: 523
POLYA=No.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:K0256G09-5N"
/db_xref="taxon:10090"
/clone="NIA:K0256G09 IMAGE:30050096"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_1ib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544191]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an oligo(dT) primer (Invitrogen): 5'-pGACTAGTCTAGATCGCAGCGCGCCCTTTTCTTTT-3', treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Lf-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:

Pred. No.: 1.06e-19 Length: 523
Score: 270.00 Matches: 51
Percent Similarity: 65.26% Conservative: 11
Best Local Similarity: 53.68% Mismatches: 25
Query Match: 19.88% Indels: 8
DB: 6 Gaps: 1

US-10-006-265-4 (1-252) x CA559290 (1-523)

Qy 6 GlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSer 25
 |||||
 Db 229 CAGCCTCTGGGTGTGACGCTGGAAATATGTGGACCTTGGCACTGTGGCACTCTCTTTC 288
 |||||

Qy 26 LeuCysIysPheSerLeuAlaLeuProAlaIysProGluAsnIleSerCysValTyr 45
 |||||
 Db 289 CTCGCAAAATTCACGCTGGCAGTCTGCGCACTAAGCCAGAAACATTCTCTGCTCTT 348
 |||||

Qy 46 TyrTrArgIysAsnLeuThrCysThrTrpSerProGlyIysGluThrSerTyrTrgIn 65
 |||||
 Db 349 TACTTCACAGAAATCGACTTGCACCTGGAGACAGAGAAACCAATGATATCCAGC 408
 |||||

Qy 66 TyrThrValIysAsnGlyTrpAlaPheGlyGluIysHsAspAsnCysThrThrAsnSer 85
 |||||
 Db 409 TACATTTGTGCTTGTACTTACTTACTTGTGAAA-----AGC 444
 |||||

Qy 86 SerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 |||||
 Db 445 AATTATAGTGCATTCCTACAGAGCTTCAATCTTCTTCCCGT 489
 |||||

RESULT 12
 BC020454 1512 bp mRNA linear HTC 19-NOV-2003
 LOCUS Mus musculus interleukin 6 signal transducer, mRNA (CDNA clone
 IMAGE:3598166).

ACCESSION BC020454
 VERSION BC020454.1 GI:18045025
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Dergs, J.G.,
 Altschuler, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J.J., Heien, F.,
 Dapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Uedl, T.B., Toshiki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Boeck, S.A., McEwan, P.J.,
 McKernan, K.O., Malek, U.A., Gunaratne, P.H., Richards, S.,
 Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J.J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalins, D.E.,
 Schenck, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 22388257
 12477932
 2 (bases 1 to 1512)
 Strausberg, R.
 Direct Submission
 Submitted (03-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://ngc.ncbi.nih.gov>
 Contact: MGC help desk
 Email: gcgabs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome

REMARK
 COMMENT

Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgobcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Namballi,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 16 Row: K Column: 14
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 6754337
 This clone has the following problem: no poly-a-tail.

FEATURES
 source
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:3598166"
 /issue_type="Mammary tumor, C3(1)-Tag model, Infiltrating
 ductal carcinoma, 5 month old virgin mouse."
 /clone_id="NCI CGAP_Mam6"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN
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 Pred. No.: 1,57e-18 Length: 1512
 Score: 265.50 Matches: 65
 Percent Similarity: 52.88% Conservative: 45
 Best Local Similarity: 31.25% Mismatches: 83
 Query Match: 19.55% Indels: 15
 DB: 3 Gaps: 9

US-10-006-265-4 (1-252) x BC020454 (1-1512)

Qy 35 ProAlaIysProGluAsnIleSerCysValTyrTyrTrArgIysAsnLeuThrCysThr 54
 |||||
 Db 613 CCAGATTAACCTTCAAAATTTGACTTGTGATGATGAGGAGGAAATATCTGTGCCAG 672
 |||||

Qy 55 TrpSerProGlyIysGluThrSerTyr---ThrGlnTyrThrValIysArgThrTyrAla 73
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 Db 673 TGGACCCCGGAGAGGAGGACTTACCTTGAACCAACTACCTTGAATTCAGAGTGGCA 732
 |||||

Qy 74 PheGlyIysIysHsAspAsnCysThrThrAsnSerSerThrSerGluAsnArgAlaSer 93
 |||||
 Db 733 ---ACAGAGAAAGTTCCGTGATGTCAGTCAAGACATGGCACT-----TCA 774
 |||||

Qy 94 CysSerPhe---PheLeuProAlaGlyIleThrIleProAspAsnTyrThrIleGluValGlu 112
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 Db 775 TGTATGTGTCAGTCAAGGACCCACCTATATATGTC-----AACATGAAGTCTGGGTGAA 828
 |||||

Qy 113 AlaGluAsnGlyAspGlyValIleIysSerHsMetThrTyrTrpArgLeuGluAsnIle 132
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 Db 829 GCAGAGATGCCCTTGGAGAGGTCTCTCAAGCTTATCAATTTTGAACCCCGTGATAA 888
 |||||

Qy 133 AlaIysThrGluProProlIysIlePheArgValIysProValIleGluIleIysArgMet 152
 |||||
 Db 889 GTGAAACCCACCCACCATATATATTCAGTGCACCACTCAGAGAAATTTACAGATTA 948
 |||||

Qy 153 IleGlnIleGluTrpIleIysProGluLeuAlaProValSerSerAspLeuIysTyrThr 172
 |||||
 Db 949 TTAAAGCTATCATCGGTGACGTTCAGGCTGGCGGTCTT---TTAGATCTTAAAGTCTGAC 1005
 |||||

Qy 173 LeuArgPheArgThrValAsnSerThrSerTrpMetIysValAsnPheAlaIysAsnArg 192
 |||||
 Db 1006 ATCCAAATATAGAGCAAAAGATGCTTCACTTGGATCCAGGTCCTCTT---GAAGATACA 1062
 |||||

Qy 193 LysAspIysAsnGlnThrTyrAsnLeuThrGlyLeuGlnProPheThrGlyTyrValIle 212
 |||||
 Db 1063 ATGCTCTCTGGAACCTTCTTCACTGTCAGAGACCTCAAGCTTTTACAGATATGTCTT 1122
 |||||

QY 213 ALaLeuArgCyAlaValIyGser-----LySPhetRpsrAspTrpSerGlnGlu 230
 Db 1123 AAGATCCGG---TCCATTAAAGACACTGGGAAGCGCTACTGAGTACTGAGTACGAG 1179
 QY 231 LySMetGlyMetThrGlnGluGlu 238
 Db 1180 GCTAGTGGAGCACATACAGAGAC 1203

RESULT 13
 BOS60019
 LOCUS BOS60019 487 bp mRNA linear EST 20-JUN-2002
 DEFINITION H4061G10-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
 H4061G10 5', mRNA sequence.
 ACCESSION BOS60019
 VERSION BOS60019.1 GI:21460904
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 487)
 VanBuren,V., Pao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,
 Martin,P.R., Steag,C.A., Baasey,U., Alba,K., Hamatani,T.,
 Kargul,G.U., Luo,A.G., Kelso,J., Hide,W. and Ko,M.S.H.
 Assembly, verification, and initial annotation of NIA 7.4K mouse
 cDNA clone set
 Genome Res. 12 (12), 1999-2003 (2002)
 MEDLINE 22354164
 PUBMED 12466305
 COMMENT Other ESTs: H4061G10-3
 Contact: Yong Qian
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Casell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
 Email: cna@igsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit http://igsun.grc.nia.nih.gov/cDNA/NIA_7.4K.html for details.
 Plate: H4061 row: G column: 10
 Seq primer: -21M13 Reverse
 High quality sequence stop: 487
 POLY=A=No.

FEATURES
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 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
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 /clone="H4061G10"
 /sex="mixed"
 /dev_stage="mixed"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
 clone is among a rearranged set of 7,407 clones from more
 than 20 cDNA libraries."

ORIGIN
 Alignment Scores:
 Pred. No.: 3,49e-19 Length: 487
 Score: 265.00 Matches: 50
 Percent Similarity: 64.89% Conservative: 11
 Best Local Similarity: 53.19% Mismatches: 25
 Query Match: 19.51% Indels: 8
 Gaps: 1

US-10-006-265-4 (1-252) x BOS60019 (1-487)

QY 6 GlnProSerCyValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMetLeuProSer 25
 Db 229 CAGCCTCGGTGTGAACCTGGAAATATATGTGAGCCTTGCCACTGTGGCATTTCTTTTC 288

QY 26 LeuCyAlaPheSerLeuAlaAlaLeuProAlaIyPProGluAsnIleSerCyValIyR 45
 Db 289 CTTGTGAATTCAGCTGGCAGTCTGCGGACTTAAGCCAGAGAACTTTCTGCGCTTT 348
 QY 46 TTYTyrAglAsnLeuThrCySthTrpSerProGlyIyGlnIuThSerIyThrgln 65
 Db 349 TACTTCGACAGAAATCTGACTTGACCTGGAGACAGAGAGAAACCAATATACACAGC 408
 QY 66 TTYThrValIyArgThrTyralaPheGlyGluIySHisAspAsnCysThrIhrAsnSer 85
 Db 409 TACATTGTGACTTGTGACTTCTCTATGAAA-----AAC 444
 QY 86 SerTrpSerGluAsnArgAlaSerCySerPhePheLeuPro 99
 Db 445 AATTATAGTGAACAATGCTACAGAGCTTCATATCTTTCCC 486

RESULT 14
 CF780723
 LOCUS CF780723 887 bp mRNA linear EST 20-OCT-2003
 DEFINITION AGENCOURT 15873120 NIH MGC 219 Homo sapiens cDNA clone
 IMAGE:30523682 5', mRNA sequence.
 ACCESSION CF780723
 VERSION CF780723.1 GI:37740344
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 887)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@bhs-remail.nih.gov
 Tissue Procurement: James Martin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDM602 row: a column: 03
 High quality sequence stop: 683.

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 /db_xref="taxon:9606"
 /clone="IMAGE:30523682"
 /tissue_type="Pooled Chondrosarcoma Tumor cells"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 219"
 /note="Vector: pYX-AecI; Site 1: EcoRI; Site 2: NotI;
 library is oligo-dT primed and directionally cloned
 library is oligo-dT primed and directionally cloned
 Denatured RNA was size fractionated on a 1% agarose gel.
 First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated with
 EcoR I adaptor, digested with Not I and then cloned
 directionally into pYX-AecI vector. Average insert size
 0.5-1kb. Adaptors 5' (AATTCGACACAGG)3' and 5'd
 (CTCTGTGCG)3'. 3' Linker sequence - GCGGCGCTGAGGCC T18.
 Sequencing primers 3' end: T3 promoter primer 5'd
 (ATTACCTCCTTAAGGA)3', 5' End: T7 promoter primer 5'd
 (TAATACGCTCATTAAGG)3'. Library was constructed in the
 laboratory of M. Bento Soares. Average insert size 2-3kb.
 Note: this is a NIH_MGC library."

ORIGIN
 Alignment Scores:

Pred. No.:	1.56e-18	length:	883
Score:	262.50	Matches:	65
Percent Similarity:	51.85%	Conservative:	47
Best Local Similarity:	30.09%	Mismatches:	75
Query Match:	19.33%	Indels:	11
DB:	7	Gaps:	11

US-10-006-265-4 (1-252) X CF780723 (1-887)

Oy 35 ProxIatylsProGIllasnilleSerCysValtYrTYrtYrArgIgsAsnLeuthnCysThr 54
||| ::::: ||| :::
Db 85 CCAGAAACCTTAAAATTGTGATTCcATTgncAACCGGGGAGnAAlAAATGAAGTGtGAG 144

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Oy      55  Tpsrprrogllylgesluthrseryr---Thnqlnrythvallys-----Arg 70
      145  TGGAGTGTGGAGGGAAACACACTTGGAGCAAACCTTCACTTTAAATCTGAATGGGCA  200

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Oy 71 Thr Tyr Ala Phe Gly - - - - - Lys His Asp - - - - - Asn Cys Thr Thr Ser 84
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 205 ACACACACAGTTGCTGCAATGTCAAAGCAAAACGACACACCCCCCACCCTCTGTCACCTGTTGAT 266

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Oy	85	serSerThrserGluasnarglna	glaSerCysSerPhe	MetIlePro	104
			::: :::		
Db	265	TATTTCTACT	-----GTCGATTTTGTG	-----	288

Oy 105 AspaerlyrthrilegluvalcglualglaenglylmapgiValIlelySser---His 122

Db 286 ---AACATTGAAGTCCTGGTAGACGACAGAATGCCCTTGGGAAAGTTACATCATCAGTATC 342

```

Oy 124 MetThyTrrPargLugLuanIleAlaIleThrGluProProLysIlePheArgVal 133
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 343 ATCATTTTGATCCGTATATAAGT---AGGCCCAATCCGCCACATTAATTATCAAGT 359

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OY 144 LysProvalleugliyllysargmetilleginutriplelysprogluleula 165
DB 400 ATCACTCAGGGACTGTCTAAGTATCTTTAAATTGCATGACCCACCCTTAATTAG 455

QY 164 ProValSerSerAspLeuLysTrpHisLeuArgPheArgThrValAsnSerHisSerTrp 163
 |||||
 460 AGTGTATTATAA---CTAAATATTAACATTCTCAATATGACCCCAAGATGCCCTCAACTGG 516
 Db

Qy 184 MetGluValAsnPheAlaIysAsnArgLysAspLysAsnGlnThrTrpAsnLeuThrGly 203
::: : :::
Db 517 AGCGAGATTCT--CCTGAACACACAGCATCCGCCGATCTTCATTACTGTCCAAAGC 573

Qy	Db
204	574
leuglnprophethrcsurtyralilaealaleargcysalavallvsgluserlys---	CTTAACCTTTTACAGATATGCTTTAGGATTCGCGCTGTATGAAAGAAAGATGCTAAAGCA
222	633

Qy 223 phetpserasptpserginglulymetciylmethnglulgu 238
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Db 634 TACTGAGTGTCTGCACTGAAACAAGCAAGTGATCATCTATGAGAT 681

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DECONTAMINATION	BC071555	5264 bp	mrna	linear	HTC 02-JUN-2001
RESULT 15	BC071555				

errorB.	
ACCESSION	BC071555
VERSION	BC071555.1
VERUSAPPc	
WUC	GI:47938807

SOURCE ORGANISM	Source Organism
Homo sapiens (human)	Homo sapiens (human)
Homo sapiens	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria

REFERENCE
1 (bases 1 to 5264)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.
Mitsch, S.P., Zeeberg, K., Shokat, D.R., Chishti, A.H., Chishti, N.K.

Datchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldi, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Ussin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abrahamson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hultkr, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalka, U., Smilins, D.E.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL
PROC. NATL. ACAD. SCI. U.S.A. 99 (26), 16899-16903 (2002)
12477932
REFERENCE
2 (Pages 1 to 5264)

REMARK	
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk
JOURNAL	Direct Submission
TITLE	Submitted (01-JUN-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
AUTHORS	Strausberg, R.

Email: cgapds-remail.nih.gov
Tissue procurement: Miklos Pakovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shitaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@axl1.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILM; at: <http://image.llnl.gov>
Series: IRAP Plate: 167 Row: A Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 28610144
This clone has the following problem: frame shifted.
Location/Qualifiers

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Query Match:	19.33%
DB:	3
Length:	5264
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Conservative:	47
Mismatches:	75
Indels:	29
Gaps:	11

US-10-006-265-4 (1-252) x BC071555 (1-5264)

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Db 521 CCGAAGAAACCTAAAAATTGGATTCCTGTGAACGAGGGAGAATAATAGGTGTGAG 580
55 TipSerProGluIlysGluThrSerTyr--ThrglnTyrThaLys-----Arg 70
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Db 581 TGGATGTGTGAAGGAAAACAACCTTGAGAGCAAACTCATTTAAAAATGTGAATGGCA 640
Oy 71 ThrTyAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThraAn 84

[illegible]

FEATURES
source

Location/Qualifiers
1. .2119
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ORIGIN

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Score: 3528.00 Matches: 662
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-006-265-17 (1-662) x BD091877 (1-2119)

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QY 41 LLeSerCysValTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
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QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 251 TGTACAAACCAATAGTTCTACAGTGAATCGTGCTTGTCTTTTCTTCCAAAGA 310
QY 101 LLeThrLLeProAspAsnTyrThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
DB 311 ATAAAGTCCCAATATATTAACATTGAGTGGAAAGCTGAAAAATGGAGATGGTGTAT 370
QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnLLeAlaLysThrGluProProlLysLLe 140
DB 371 AAATTCATATGACAATACTGAGATTAGAAACATAGCGAAAACTGAACCACTTAAGATT 430
QY 141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
DB 431 TTCGGTGTAAACCAAGTTTGGGCAATCAACGAATGATTCAAATGTGAATGATTAAGCCT 490
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QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
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Db      1991 TCAATTA 1996

RESULT 2
AX365201
LOCUS   AX365201 53 from Patent WO0200721.
DEFINITION
ACCESSION AX365201
VERSION   AX365201.1 GI:18696955
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE
AUTHORS  Sprecher, C.A., Presnell, S.R., Gao, Z., Whitmore, T.E., Kuiper, J.L.
          and Maurer, M.F.
          Cytokine receptor zcytor17
          Patent: WO 0200721-A 53 03-JAN-2002;
          ZymoGenetics, Inc. (US)
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ORIGIN
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Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
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US-10-006-265-17 (1-662) x AX365201 (1-2903)

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Qy	461	GUuYrYsgIyIleIleCyAsnIYrThrllePheTYrGlnAgluGlyIylylyly	480
Db	1877	GAAGAAAGGGTTCATCTGCAACTACACATCTTTTACCACTGAGGTGAGAAAGCA	1936
Qy	481	PheSerIleThrValAsnSerSerIleleuGlnTYrGlyleuGluSerleuYsAglYs	500
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Qy	501	ThlSerTYrIleValGlnValMetAlaserThlSerAlaGlyIyThrAsnGlyThrSer	520
Db	1997	ACCTTACATTTGTCAGGTCATGGCCAGACACAGTGTGGGGAACCAACGGGACAG	2056
Qy	521	IleAsnPhelYsThrlleuSerPheSerValPheGluIleIleleuIleThrSerleuIle	540
Db	2057	ATTAATTTCAAGACATGTCATTCAGTCTTGAAGATTATCCTCATTAATCTTGATTT	2116
Qy	541	GLYGLYGLYleuIleuIleleuIleIleleuThrValAlaTYrGlyleuYslySProaAn	560
Db	2117	GGTGGAGGCTTTCTTATTTCTCATTTATCTGACAGTGCATATGATCTCAAAAAACCAAC	2176
Qy	561	lyeIleuThrlleuCystrProThrValProaSnProAlaGluSerSerIleAlaThr	580
Db	2177	AAATTCATCATCTGATGTTGGCCACCGTTCCCAACCTGCTGAAGTAGTATAGCCACA	2236
Qy	581	TrpHIGLYAspAspPheIyAspIyAspIyAspIyAspIyAspIyAspIyAspIyAsp	600
Db	2237	TGCGATGGAATATATTCAGAGTAAGCTAAACCTGAAGAGCTGATGATCTGTGAAAC	2296
Qy	601	ThlGlaAspArgIleleuYsProCySerThlProSerAspIyIleuValIleAspIy	620
Db	2297	ACGAAAGACGAGATCTTAAACCATGTTCCACCCCACTGACAGATTTGGATTGACAG	2356
Qy	621	IleuValIleAsnPhelGlyAsnValIleuGlnIyIlePheThrAspGlnAlaArgTrgIy	640
Db	2357	TTGGTGTGAACTTTGGGAAATGTTCTGCAGAAATTTTTCACATGATGAGCCAGACGGGT	2416
Qy	641	GlnGluAsnAsnIleuGlyIyGlyIyAsnGlyThrArgIleleuSerSerCystrProThr	660
Db	2417	CAGAAACCAATTTAGAGGGGAAAGAAAGAAAGAAAGTAATTCCTTCTCCCAACT	2476
Qy	661	SeTlle 662	
Db	2477	TCAATA 2482	
RESULT 3			
LOCUS	AY499342	2903 bp	mRNA linear PRI 10-JUL-2004
DEFINITION			Homo sapiens interleukin 3lra splice variant x4 (IL3lRA) mRNA.
ACCESSION	AY499342		Complete cds, alternatively spliced.
VERSION	AY499342.1	GI:46276462	
KEYWORDS			
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			
AUTHORS			Bukayocsa, Metazoa; Choradata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
			1 (bases 1 to 2903)
			Dillon,S.R., Sprecher,C., Hammond,A., Bileborough,J., Maurer,M., Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Harder,B., Johnston,J., Bort,S., Mudri,S., Kuljper,J.L., Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J., Lockwood,L., Levin,S.D., Leckel,C., Waggle,K., Day,H., Topouzis,S., Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and Gross,J.A.
			Interleukin 3l, a cytokine produced by activated T cells, induces dermalitis in mice
			Nat. Immunol. 5 (7), 752-760 (2004)
			2 (bases 1 to 2903)

AUTHORS	Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H., Bileborough,J., Maurer,M., Harder,B., Johnston,J., Bort,S., Mudri,S., Kuljper,J., Bukowski,T., Shea,P., Dong,D., Dasovich,M., Lockwood,L., Levin,S., Leckel,C., Waggle,K., Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and Gross,J.A.		
TITLE	Direct Submision		
JOURNAL	Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA		
FEATURES	Location/Qualifiers		
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 REFERENCE
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 Sprecher, C.A., Prensell, S.R., Gao, Z., Whitmore, T.E., Kuiper, J.L.
 and Maurer, M.F.
 Cytokine receptor zcytor17
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 QY 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
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 QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
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RESULT 8
 AX467335 2238 bp DNA linear PAT 16-JUL-2002
 LOCUS
 DEFINITION Sequence 5 from Patent WO0229060.
 ACCESSION AX467335
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.
 Hematopoietic receptors hprt and hprt2

JOURNAL Patent: WO 0229060-A 5 11-APR-2002;
Immunex Corporation (US)
FEATURES Location/Qualifiers
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Percent Similarity: 99.09% Conservative: 2
Best Local Similarity: 98.79% Mismatches: 3
Query Match: 98.23% Indels: 3
DB: 6 Gaps: 1

US-10-006-265-17 (1-662) x AX467335 (1-2238)

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RESULT 9
AY499341

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DEFINITION Homo sapiens interleukin 31RA splice variant x3 (IL31RA) mRNA,
complete cds, alternatively spliced.

ACCESSION AY499341
VERSION AY499341.1 GI:46276460

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 2393)
Dillon,S.R., Sprecher,C., Hammond,A., Bilborough,J.,
Rosenfeld-Franklin,M., Presnell,S.R., Haugen,H.S., Maurer,M.,
Harder,B., Johnston,J., Bort,S., Mudri,S., Kujiper,J.L.,
Bukowski,T., Shea,P., Dong,D.L., Dasovich,M., Grant,F.J.,
Lockwood,L., Levin,S.D., Beciel,C., Maggle,K., Day,H., Topouzis,S.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.

TITLE Interleukin 31, a cytokine produced by activated T cells, induces
dermatitis in mice
JOURNAL Nat. Immunol. 5 (7), 752-760 (2004)
PUBMED 15184896

REFERENCE
AUTHORS 2 (bases 1 to 2393)
Dillon,S.R., Sprecher,C., Hammond,A., Rosenfeld-Franklin,M.,
Presnell,S.R., Haugen,H., Bilborough,J., Maurer,M., Harder,B.,
Johnston,J., Bort,S., Mudri,S., Kujiper,J., Shea,P.,
Dong,D., Dasovich,M., Lockwood,L., Levin,S., Beciel,C., Maggle,K.,
Kramer,J., Kuestner,R., Chen,Z., Foster,D., Parrish-Novak,J. and
Gross,J.A.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-2003) Bioinformatics, ZymoGenetics, Inc., 1201
Eastlake Avenue East, Seattle, WA 98102, USA
FEATURES
source location/Qualifiers

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US-10-006-265-17 (1-662) x AY499341 (1-2393)

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 DEFINITION Sequence 1 from Patent WO0200721.
 ACCESSION AX365149

VERSION AX365149.1 GI:18696908
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Sprecher, C.A., Preenell, S.R., Gao, Z., Whitmore, T.E., Kujper, J.L.,
 and Maurer, M.F.
 TITLE Cytokine receptor zcytor17
 JOURNAL Patent: WO 0200721-A 1 03-JAN-2002;
 ZymoGenetics, Inc. (US)
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 Db 558 GTAAACCACTTTGGGCATCAACGATATTCATTAATGATGATGAAAGGCTGAGTTG 617
 Qy 163 AlaProValSerSerAspLeuYsTYrThrLeuArgPheArgThrValAsnSerThrSer 182
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 Db 678 TGGATGAAATCAACTTCCTGTAAGAACCCGTAAAGATTAACCAACAGTCAACCTCACG 737
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 Db 738 GGGCTGACGCTTTTACAGAAATGTCTATGCTCTGCGATGTGCGTCAAGAGTCAAG 797
 Qy 223 PheTrpSerAspTrpSerGIuYsMetGIuMetThrGIuGIuAlaProCysGIy 242
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 Qy 363 LeuAspValAsnThrTrpMetIleGIuTrpPheProAspValAspSerGIuProThrThr 382
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 ACCESSION AK467333
 VERSION AX467333.1 GI:21900584
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE 1 Cosman,D.J., Mosley,B.A., Bird,T.A., Dubose,R.F. and Wiley,S.R.
 TITLE Hematopoietin receptors hprt1 and hprt2
 JOURNAL Patent: WO 0229060-A 3 11-APR-2002;
 Immunex Corporation (US)
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 Query Match: 98.23% Indels: 3
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 Db 1572 TTCTCCAAGACAGTCATTCAGCATCTTGCAGTACGCGCTGAGTCCCTGAACGAAG 1631
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 BD178872
 LOCUS BD178872 2952 bp DNA linear PAT 16-Apr-2003
 DEFINITION NR10 splicing variants.
 ACCESSION BD178872
 VERSION BD178872.1 GI:30016139
 KEYWORDS WO 02077230-A/3.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2952)
 AUTHORS Maeda,M., Yaguchi,N. and Hasegawa,M.
 TITLE NR10 splicing variants
 Patent: WO 02077230-A 3 03-OCT-2002.
 JOURNAL CHUGAI PHARMACEUTICAL CO LTD,MASATSUGU MAEDA,NORIKO YAGUCHI,
 MASAKAZU HASEGAWA
 OS Homo sapiens (human)
 PN WO 02077230-A/3
 PD 03-OCT-2002
 PF 22-MAR-2002 WO 2002JP002769

PR 26-MAR-2001 JP 01P 087298
PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
C12N5/12, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC
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PC C12P21/02, G01N33/15, G01N33/50, G01N33/53
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ORIGIN

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Query Match:	98.23%	Indels:	3
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US-10-006-265-17 (1-662) x BD178872 (1-2952)

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QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluTrpSer 62
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VERSION    BD178871.1 GI:30016138
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ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 5271)
AUTHORS   Maeda,M., Yaguchi,N. and Hasegawa,M.
TITLE     NR10 splicing variants
JOURNAL   Parent: WO 02077230-A 2 03-OCT-2002;
          CHUGAI PHARMACEUTICAL CO LTD,MASATSUGU MAEDA,NORIKO YAGUCHI,
          MASAKAZU HASEGAWA
COMMENT    OS Homo sapiens (human)
            PN WO 02077230-A/2
            PD 03-OCT-2002
            PE 22-MAR-2002 WO 2002JP002769
            PR 26-MAR-2001 JP 01P 087298
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            C12N5/10,
            PC C12P21/02,G01N33/15,G01N33/50,G01N33/53
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Best Local Similarity: 99.09%      Mismatches: 2
Query Match:    98.23%      Indels:      3
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US-10-006-265-17 (1-662) x BD178871 (1-5271)
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Qy      43 CyValaTyrrTyrrTyrrAsnleuThrCySerThrTrpSerProGlyLysGluThrSer 62
Db      190 TGTGTCTACTCTATAGGAAATTTAACTGCACTTGAAGTCCAGAGAAAGAAACCACT 249
Qy      63 TyrrThrGlnTyrrThrValaLysAsnThrTyrrAlaPheGlyGluYpPheAsnCySerThr 82
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Db      370 ATCCAGATTAATTAATACATGAGAGTGGAACTGAAATGAGATGAGATTAATTAATCT 429
Qy      123 HisMetThrTyrrTrpArgleuGluAanlleAlaYpThrGluProProlyIlePheArg 142
Db      430 CATATGACATACCTGAGATTAGAGAACATACGAAACCTGAAACCACTTAAGATTTTCCGT 489
Qy      143 ValLySProValleuGlyIleYpArgMetIleGlnIleGluTrpIleYpProGluLeu 162
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Qy      163 AlaProValSerSerAaPleuYpTyrrThrLeuArgPheArgThrValaAnSerThrSer 182
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Qy      283 TyrrTyrrProGluSerAanThrAsnleuThrcIuThrMetAanThrAsnGlnleu 302
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Qy      323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluYpSerPheGlnCyAlle 342
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Qy      423 TyrrSerIleGlnAlaTyrrAlaYpGluGlyValProSerGluGlyProGluThrLysVal 442
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Db 1510 AAGACAGTCATTCACGACATCTTGAGTACGGCTGGAGTCCCTGAAAGCAAAAGACTCT 1569
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LOCUS NR10 splicing variants.
DEFINITION BD178873.1 GI:30016140
ACCESSION BD178873.1
VERSION WO 02077230-A/4.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Maeda,M., Yaguchi,N. and Hasegawa,M.
TITLE NR10 splicing variants
JOURNAL Patient: WO 02077230-A 4 03-OCT-2002;
CHUGAI PHARMACEUTICAL CO LTD, MASATSUGU MAEDA, NORIKO YAGUCHI,
MASAKAZU HASEGAWA
COMMENT
OS Homo sapiens (human)
PN WO 02077230-A/4
PD 03-OCT-2002
PF 22-MAR-2002 WO 2002JP002769
PR 26-MAR-2001 JP 01P 087298
PI MASATSUGU MAEDA, NORIKO YAGUCHI, MASAKAZU HASEGAWA PC
C12N15/12, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, G01N33/15, G01N33/50, G01N33/53
CC NR10 splicing variants
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
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Best Local Similarity: 93.40 Mismatches: 2
Query Match: 97.38 Indels: 43
DB: 6 Gaps: 2
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QY 23 LeuProSerLeuCystrPheSerLeuAlaAlaLeuProAlaLysProGlnAsnIleSer 42
Db 130 CTCCTCTCATCTGCAAAATTCAGCTGGCAGCTCTGCCAGCTAAGCTGAGAACTTCC 189
QY 43 CysValYrYrYrYrArgLysAsnLeuThrCystrThrProGlyLysGlnThrSer 62
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QY 63 TyrThrGlnTyrThrValLysArgThrYrAlaPheGlyGlnLysHisAspAsnCystr 82
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QY 83 ThrAsnSerSerThrSerGlnAsnArgAlaSerCystrPhePheLeuProArgIleThr 102
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QY 103 IleProAspAsnYrThrIleGlnValGlnAlaGlnAsnGlyAspGlyValIleYsSer 122
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QY 123 HisMetThrYrThrArgLeuGlnLeuIleAlaLysThrGlnProProLysIlePheArg 142
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QY 163 AlaProValSerSerAspLeuLysYrThrLeuArgPheArgThrValAsnThrSer 182
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QY 203 GlyLeuGlnProPheThrGlnYrValIleAlaLeuArgCysAlaValLysGlnSerLys 222
Db 670 GGGCTGACCTTTTACAAATATGTCAATGCTCTGCGATGTCCGTCAAGAGTCAAG 729
QY 223 PheTrpSerAspTrpSerGlnGlnLysMetGlyMetThrGlnGlnGlnAlaProCysGly 242
Db 730 TTCTGAGATGACTGAGGCCAAGAAATGGGAATGACATGAGGAAGAACTCCATGTGC 789
QY 243 LeuGlnLeuThrArgValleuLysProAlaGlnAlaAspGlyArgArgProValAlaGlnLeu 262
Db 790 CTGGAACTGTGAGATCTCTGAACCAAGCTGAGGGGAGTGAAGAGGCGCAGTGG 849
QY 263 LeuTrpLysLeuAlaArgGlyAlaProValleuGlnLysThrLeuGlyYrThrAsnIleTrp 282
Db 850 TTTATGAGAGAGGCAAGAGAGGCCCAAGTCTTGAAGAAACACTTGGCTACAACTATGG 909
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Qy 323 LysSerProValAlaThrLeuArgLLeProAlaIleGlnGluLysSerPheGlnCysIle 342
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Db 1270 CTTTCTGTCGTATACATCTCTGTATCCAAATTTTCATGACAAAGTTGGGAGCCCA 1329
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Qy 443 G|u|a|s|e|r|l|e|g|y|v|a|l|y|e|t|h|r|v|a|l|t|h|r|e|t|h|r|p|l|y|e|g|u|l|e|r|p|l|y|s|e|r|g|u|a|g| 462
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Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
Db 1630 TTCAAGACATTTGTCATTCAGTCTTGAATATCTCATTAATCTCTGATTTGGTGA 1689
Qy 543 G|y|e|u|e|u|l|e|u|l|e|l|e|u|t|h|r|v|a|l|a|t|y|r|g|l|y|e|u|l|y|e|p|r|o|a|s|n|l|y|e|u| 562
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LOCUS Homo sapiens gp130-like monocyte receptor mRNA, complete cds.
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ACCESSION AF486620
VERSION AF486620.1 GI:20563276
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2199)
Ghildardi, N., Li, J., Hongo, J.A., Yi, S., Gurney, A. and de
Savage, F.J.
A novel type I cytokine receptor is expressed on monocytes, signals
proliferation, and activates STAT-3 and STAT-5
J. Biol. Chem. 277 (19), 16831-16836 (2002)
PUBMED 11877449
REFERENCE
2 (bases 1 to 2199)
Ghildardi, N., Li, J., Hongo, J.-A., Yi, S., Gurney, A. and de
Savage, F.J.
Direct Submission
Submitted (21-FEB-2002) Molecular Oncology, Genentech, 1 DNA Way,
South San Francisco, CA 94080, USA
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ORIGIN
Alignment Scores:
Pred. No.: 8.58e-295 Length: 2199
Score: 3405.50 Matches: 640
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Query Match: 96.53% Indels: 3
DB: 9 Gaps: 1

US-10-006-265-17 (1-662) x AF486620 (1-2199)
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QY GlnAlaGluGlyIySerIyPheSerIyThrValAsnSerSerIleLeuGlnTyrGly 493
Db CAAGGTGAAGGTGGAAGAGATTTCCAGACAGTCAATTCAGCATCTTGCAGTACGCGC 1440
QY LeuGluSerLeuIySerArgIySerTyrIleValGlnValMetAlaSerThrSerAla 513
Db CTGGAGTCCCTTAACGAAAGACCTTTACATTTGTTCAGGTATGGCCAGCACAGTGTCT 1500
QY GlyIyThrAsnGlyThrSerIleAsnPheIySerThrLeuSerPheSerValPheGluIle 533
Db GGGGAAACCAAGGAGCAAGCATTAATTTCAAGACATTTGTCAATGATCTTTGAGATT 1560
QY IleLeuIleThrSerLeuIleGlyIyGlyLeuLeuIleLeuIleIleLeuThrValAla 553
Db ATCCTCATTAATCTTCTGATGTGGAGGCTTTCTTATCTCATTAATCTGACAGTGGA 1620
QY TyrGlyLeuIySerProAsnIySerLeuThrIleuCystrProThrValIleProAsnPro 573
Db TATGTCTCAAAAAACCAACAAATTTGACTCATCTGTGTGGCCCAACCGTTCCCAACCT 1680
QY AlaGluSerSerIleAlaThrTrpHisGlyAspAspPheIyAspIySerLeuAsnLeuIyS 593
Db GCTGAAGATGATATAGCCCATGCGATGAGATGATTTCAAGATTAAGCTTAACCTGAAG 1740
QY GluSerAspAspSerValAsnThrGluAspArgIleLeuIySerProCySerThrProSer 613
Db GAGTCTGATGACTCTGTGAACACAGAAAGCAGAGATCTTAAACCATGTTCCACCCAGCT 1800
QY AspIySerLeuValIleAspIySerLeuValIleAsnPheGlyAsnValIleuGlnIyIlePhe 633
Db GACAAATTGTGTATTTGACAAAGTTGTGTGAACTTTGGGAAATGTTCTGCAAGAAATTTTC 1860
QY ThrAspGluAlaArgThrGlyGlnGluAsnAsnLeuGlyIyGlyIySerAsnGlyThrArg 653
Db ACGATGAAGCCAGAACGGGTCAAGAAACAAATTTAGAGGGGAAAGAAATGGG----- 1914
QY IleLeuSerSerCysePro 659
Db 1915 ---TATGTGACCTGGCCC 1929

Search completed: February 23, 2005, 15:25:27
Job time : 8440.27 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus2n model

Run on: February 23, 2005, 05:20:17; Search time 977.782 Seconds

(without alignments)
4007.918 Million cell updates/sec

Title: US-10-006-265-17

Perfect score: 3528
Sequence: 1 MKLSPQSPCVNLGMMTWAL.....NNLGGKNGKTRILSSCPSTI 662

Scoring table:

BLOSUM62	
Xgapop 10.0, Xgapext 0.5	
Ygapop 10.0, Ygapext 0.5	
Fgapop 6.0, Fgapext 7.0	
Delop 6.0, Delext 7.0	

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+2n.model -DEV=xlh
-Q=/cgn2.1/USPRO.spool/US10006265/runat.18022005.094657.22172/app.query.fasta_1.2069
-DB=N Geneseq.16Dec04 -QWMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOFCI=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006265.QCGN.1.1.1998 @runat.18022005.094657.22172 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=130 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N_Geneseq.16Dec04:*

1: Geneseqn1980s:*\n2: Geneseqn1990s:*\n3: Geneseqn2000s:*\n4: Geneseqn2001as:*\n5: Geneseqn2001bs:*\n6: Geneseqn2002as:*\n7: Geneseqn2002bs:*\n8: Geneseqn2003as:*\n9: Geneseqn2003bs:*\n10: Geneseqn2003cs:*\n11: Geneseqn2003ds:*\n12: Geneseqn2004as:*\n13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3528	100.0	2119	4 AAC92350	Aac92350 Human hae
2	3528	100.0	2903	6 ABA93808	Ab93808 Human zcy
3	3528	100.0	2903	10 ADD68146	Add68146 Human zcy
4	3528	100.0	2903	11 ADL26569	Adl26569 Human cyt
5	3518	99.7	2529	6 ABA93803	Ab93803 Human zcy

6	3518	99.7	2529	11 ADL26671	Adl26671 Human cyt
7	3518	99.5	4315	8 ABO83363	Ab83363 Human NRI
8	3512	99.5	2969	4 AAC92337	Aac92337 Human hae
9	3465.5	98.2	2386	6 ABA93767	Ab93767 Human zcy
10	3465.5	98.2	2402	11 ADL26673	Adl26673 Human cyt
11	3465.5	98.2	2480	6 AAD38772	Aad38772 Human hae
12	3465.5	98.2	2481	10 ACF36434	Acf36434 Human typ
13	3465.5	98.2	2952	8 ABO83365	Ab83365 Human NRI
14	3465.5	98.2	5271	8 ABO83364	Ab83364 Human NRI
15	3435.5	97.4	3072	8 ABO83366	Ab83366 Human NRI
16	3276	92.9	2858	8 ABO83368	Ab83368 Human NRI
17	3263	92.5	2870	8 ABO83367	Ab83367 Human NRI
18	3096	87.8	2776	8 ABO83369	Ab83369 Human NRI
19	3072	87.1	2108	10 ADL21969	Adl21969 Novel hum
20	2888	81.9	1986	6 ABA93809	Ab93809 Human zcy
21	2888	81.9	1986	11 ADL26685	Adl26685 Human cyt
22	2853	80.9	2295	6 ABA93821	Ab93821 Human zcy
23	2853	80.9	2295	10 ADD68179	Add68179 Human zcy
24	2853	80.9	2295	11 ADL26602	Adl26602 Human zcy
25	2836	80.4	1947	6 ABA93804	Ab93804 Human zcy
26	2836	80.4	1947	11 ADL26684	Adl26684 Human cyt
27	2806.5	79.5	2196	6 ABA93768	Ab93768 Human zcy
28	2806.5	79.5	2196	11 ADL26683	Adl26683 Human cyt
29	2782	78.9	1557	10 ADD68201	Add68201 Human zcy
30	2782	78.9	1557	11 ADL26633	Adl26633 Human cyt
31	2606	73.9	2445	6 ABA93581	Ab93581 CDNA enco
32	2606	73.9	2445	6 ABL88257	Ab188257 Human PRO
33	2606	73.9	2445	6 ABL95746	Ab195746 Human ang
34	2606	73.9	2445	8 ACA68542	Ac68542 Novel hum
35	2606	73.9	2445	9 ABA744271	Ab744271 Human PRO
36	2606	73.9	2445	9 ABA744554	Ab744554 Human PRO
37	2606	73.9	2445	9 ACD83221	Ac83221 Human sec
38	2606	73.9	2445	9 ABA743927	Ab743927 Human mem
39	2606	73.9	2445	9 ADB83581	Ad83581 Novel hum
40	2606	73.9	2445	9 ADB80687	Ad80687 Novel hum
41	2606	73.9	2445	9 ADB73228	Ad73228 Novel hum
42	2606	73.9	2445	9 ADB78310	Ad78310 Novel hum
43	2606	73.9	2445	10 ADB84958	Ad84958 Human PRO
44	2606	73.9	2445	10 ADB78064	Ad78064 Novel hum
45	2606	73.9	2445	10 ADB87130	Ad87130 Human PRO

ALIGNMENTS

RESULT 1	
AAC92350	
ID AAC92350 standard; CDNA; 2119 BP.	
XX	
XX AAC92350;	
XX	
DT 26-MAR-2001 (first entry)	
XX	
XX Human haemopoietic receptor protein NR10.3 encoding CDNA SEQ ID NO:16.	
DE	
XX Human; haemopoietic receptor; NR10.1; NR10.2; NR10.3; NR10;	
KM immunoregulation; haematopoietic cell regulation; transmembrane;	
KM immune disorder; haematopoietic disorder; autoimmune disease; allergy;	
KM metal allergy; pollen allergy; ss.	
XX	
OS Homo sapiens.	
XX	
FN W0200075314-1.	
XX	
PD 14-DEC-2000.	
XX	
PF 01-JUN-2000; 2000WO-JP003556.	
XX	
PR 02-JUN-1999; 99UP-00155797.	
PR 30-JUN-1999; 99UP-00217797.	
XX	
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.	
XX	
PI Maeda M, Yaguchi N;	

XX WPI: 2001-061720/07.
 DR P-PsDB; AAB51244.
 XX Hematopoietic receptor protein NR10 for screening potential ligands for
 PT treatment of immune and hematopoietic disorders such as autoimmune
 PT diseases and allergies.
 XX
 PS Claim 1; Fig 13-14; 127pp; Japanese.
 XX
 CC The present sequence encodes a human haemopoietin receptor protein
 CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
 CC which participates in immunoregulation and hematopoietic cell regulation
 CC in vivo, and is useful in searching for hematopoietic factors capable of
 CC binding to the receptor. NR10 can be used for the identification of
 CC substances for the treatment and prevention of immune and haematopoietic
 CC disorders including autoimmune diseases and allergies such as metal and
 CC pollen allergy
 CC
 SQ Sequence 2119 BP; 643 A; 459 C; 504 G; 513 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 2119
 Score: 3528.00 Matches: 662
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-006-265-17 (1-662) x AAC92350 (1-2119)
 QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTPAlaLeu 20
 Db 11 ATAAGCTCTCTCCCAAGCCTTCATGTAAGTGGGATGATGGAGCTGGGACCTG 70
 QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
 Db 71 TGGATGCTCCCTCCACCTGCAATTGAGCTGGAGCTGCGACGTAAAGCTGGAAC 130
 QY 41 ILSESCysValIleTyrTyrAlaGlyAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 Db 131 ATTTCCTGCTCTACTACTATAGAAAATTTAACTGCACTTGGAGTCCAGAAAGGAA 190
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysPheAspAsn 80
 Db 191 ACCAGTTATACCAAGTACAGATTAAGAGAACTTAGCGCTTTGGAGAAAACATGATTAAT 250
 QY 81 CysThrThrAsnSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 Db 251 TGTACAAACCAATAGTTCTACAACTGAAACATCGCTTCGCTCTTTTCCCTCCAAAG 310
 QY 101 ILethrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 Db 311 ATTAACATCCCAAGATTAATTATACCATTTGAGGTGAAGCTGAAAATGAGATGCTGAATT 370
 QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
 Db 371 AAATTCATATGACATACGAGATTAAGAGAACTTAGCGAAAACCTAAACCACTTAAGATT 430
 QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 Db 431 TTCGGTGAACCAAGTTTGGGCATCAACGAATGATTTCAATTGATGATTAAGCCCT 490
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db 491 GAGTTGGCCGCTTTTCATCTGATTTAAATAACACTTGCATTGAGAGCAAGCAACAGT 550
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 Db 551 ACCAGCTGGAGGAGCAACTTCGCTAAAGACCGTAAGATTAACCAACCAACGATCAAC 610
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220

Db 611 CTCACGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCATGTGCGGTCAAGAG 670
 QY 221 SerLysPheMetTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGluValPro 240
 Db 671 TCAAAAGTTCTGGAGTGAAGCTGAGGCAAGAAAAAATGGGATATACGTAGGAACAACCTCA 730
 QY 241 CysGlyLysGluLeuThrTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
 Db 731 TGTGGCTTGAACCTGTGAGAGCTCTGAAACCAAGCTGAGCCGATGGAAGAGCCAGTG 790
 QY 261 ArgLeuLeuTrpLysValAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 Db 791 CGTTGTTATGAGAAGGCAAGAGAGAGCCCAAGCTCTAGAAAACCTTGGCTTACAAC 850
 QY 281 ILethrTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db 851 ATATGCTACTATCCAGAAAACCACTAACTTCACAGAAACATGAACCTTAACACAG 910
 QY 301 GlnLeuGluLeuHisIleuGlyLysLeuSerPheTrpValSerMetIleSerTyrAsnSer 320
 Db 911 CAGCTTGAACCTGCATCTGGAGAGCCAGAGCCTTTGGGTCTATGATTTCTTATTAATGT 970
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGlyLysSerPheGln 340
 Db 971 CTGGGGAAGCTTCCAGTGGCCACCTGAGAGATTCCAGCTATTCAAGAAAATCATTTGAG 1030
 QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db 1031 TGCATTTGAGTATGACAGGCGCTGCGTCTGAGGACACAGCTAGTGATGAAGTGGCAAC 1090
 QY 361 SerAlaLeuAspValAlaAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db 1091 TCTGCTTGAAGTGAACCTTGGATGATGATGATTTCCGAGTGTGAACCTCAAGAGCCC 1150
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
 Db 1151 ACCACCCCTTCTCGGGAATCTGTCTCAGGCAAGATGAGCATGACAGCAAGATATAA 1210
 QY 401 LeuLysProPheMetProCysLeuTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
 Db 1211 TTAAAACTTTCTGTGGCTATGAACATCTGTGTATCCATATGTGATGAACAAGTTGGGC 1270
 QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
 Db 1271 GAGCCATATTCATTCAGGCTTATGCCAAAGAGGCGTTCCATCAGAGGTCTGAGAGC 1330
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 Db 1331 AAGGTGAGAAACATTTGGCGTGAAGACGTCAGATCACAATGAAAGATTCGCAAGAGT 1390
 QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 Db 1391 GAGAGAAAGGATATATCTGCAACATCAACATCTTTTCAAGCTGAAAGTGAAGAAAGGA 1450
 QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLysGluSerLeuLysArgLys 500
 Db 1451 TTCTCCAAACAGTCAATTCAGCATCTTGCGATGAGGCTGAGTCCCTGAAACGAAG 1510
 QY 501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSer 520
 Db 1511 ACCTTATACATTTGTTCAAGTATGCGCAGACACAGAGCTGGGGAACCAACGAGAC 1570
 QY 521 ILethnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db 1571 ATTAATTTTCAACACATTTGATTCAGTGTCTTTGAGATTATCTCATTAACCTTCTGATT 1630
 QY 541 GlyLysGlyLysLeuIleLeuIleIleLeuThrValAlaTyrGlyLysLysLysProAsn 560
 Db 1631 GGTGAGGCTTCTTATTTCTATTTCTGACAGTGGCATAGGTCTCAAAAACCAAC 1690
 QY 561 LysLeuThrHisLeuLysCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580

Db	1691	AAATGACATCTGTGTGGCCACCGTCCCAACCGTGGTGAAGAATGATACACAA	1750
Oy	581	TTPhISGIyAspAPSPheLyAspLySLeuAsnLeuLySGLuSerAspAspSerValAsn	600
Db	1751	TGGCATGAGATGATTTCCAGCATTAAGCTAAACCTGAAGGAGTCTGATGACTCTGTGAAC	1810
Oy	601	ThrGIuAspPAyGIIleLeuLyBProcysSerThrProSerAspLySLeuValIIeAspLyS	620
Db	1811	ACAGAAAGACAGGATTTAAACCAATGTTCCACCCAGGAGCAAGACTTGATGATTAACAAG	1870
Oy	621	LeuValValAsnPhelGyAsnValIleuGInguIlePheThrAspGluAlaArgThrSGLy	640
Db	1871	TTGCTGGTGAACCTTTGGGAATGTTCTGCACAAATTTTCACAGATGAAGCCGAAACGGGT	1930
Oy	641	GInguIuAsnAsnLeuGlyGlyGluLyAsnGlyThrArgIIeLeuSerSerCysProThr	660
Db	1931	CAGGAAACCAATTTTGAAGGGGAAAGATGGGACTTAAGATTTCTGTCTTCCGCCCACT	1990
Oy	661	SerIle 662	
Db	1991	TCAATA 1996	
RESULT 2			
ABA93808	ID	ABA93808 standard; cDNA, 2903 BP.	
XX	AC	ABA93808;	
XX	DT	01-MAY-2002 (first entry)	
XX	XX	Human zcytor17 cDNA sequence SEQ ID NO:53.	
XX	XX	zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;	
KW	KW	antiflammatory; antiviral; antithematic; antiaethritic; cytostatic;	
KW	KW	muscular; lymphoid; immune; inflammatory; splenic; blood; bone;	
KW	KW	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;	
KM	KM	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;	
KW	KW	inflammatory disease; pancreatitis; inflammatory bowel disease; ss.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	WO200200721-A2.	
PD	PD	03-JAN-2002.	
XX	XX		
PF	PF	26-JUN-2001; 2001WO-US020484.	
XX	XX		
PR	PR	26-JUN-2000; 2000US-0214282P.	
PR	PR	29-JUN-2000; 2000US-0214955P.	
PR	PR	08-FEB-2001; 2001US-0267963P.	
XX	XX		
PA	PA	(ZYMO) ZYMOGENETICS INC.	
XX	XX		
PI	PI	Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kujiiper JL,	
PI	PI	Maurer MF;	
XX	XX		
DR	DR	WPI; 2002-090519/12.	
XX	XX	P-PSDB; ABB05741.	
PT	PT		
XX	XX		
PS	PS	Example 1; Page 199-203; 235pp; English.	
CC	CC	The present invention describes a cytokine receptor designated zcytor17.	
CC	CC	Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,	
CC	CC	antirheumatic, antiaethritic and muscular activities. The zcytor17	
CC	CC	proteins are useful for treating and diagnosing lymphoid, immune,	
CC	CC	inflammatory, splenic, blood or bone disorders. Agonists or anti-	
CC	CC	zcytor17 antibodies are useful in stimulating cell-mediated immunity and	
CC	CC	for stimulating lymphocyte proliferation, such as in the treatment of	
CC	CC	infections involving immunosuppression, including certain viral	

	CC	infections. They are also useful for inducing cytotoxicity and for treating leukopenias. Antagonists of zcytoril polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytoril was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to CC ABA93843, and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention
XX	Sequence	2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;
US-10-006-265-17 (1-662) x ABA93808 (1-2903)		
OY	Alignment Scores:	
Pred. No.: 0	Length: 2903	
Score: 3528.00	Matches: 662	
Percent Similarity: 100.00%	Conservative: 0	
Best Local Similarity: 100.00%	Mismatches: 0	
Query Match: 100.00%	Indels: 0	
DB: 6	Gaps: 0	
Db	1 MetlyleuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrLalaLeu	20
Oy	497 ATGAAGCTCTCTCCCGACGCTTCAATGTATTAACTGGAGGATGANTGCACCTGGGCACTG	556
Db	21 TrpMetLeuProSerLeuCysValPheSerLeuAlaIleuProAlaLysProGluAsn	40
Oy	557 TGGANGCTCCCTTCACTCTGCATAATTCAGCTGGAGCTCTGCCAGCTTAAGCTGAGAAC	616
Db	41 IleSerCysValYrYrYrYrArgLysAsnLeuThrCysThrTrpSerProGlyLYsgLu	60
Oy	617 ATTTCGCTGTCTACTACTAAGAAGAAAATTAACTGCACCTTGAGTCCAGAAAGAA	676
Db	61 ThiserYrThrgInYrThrVallYsArgThrTyralaPheGlyGLuLyHisAspAsn	80
Oy	677 ACCGATTATACCAGTCACACAGTTAAGAGAACTTAACGCTTTTGGAGAAAACATGATAAT	736
Db	81 CysThrThraSnsaserSerSerGluAsnArgLasrCysSerPhePheLeuProArg	100
Oy	737 TGTCACACCAATAGTCTTCAAGTAGAAATGTGCTTGCTCTCTTTTCTTCCAAGA	796
Db	101 ILeThrIleProAspAsnYrThrl egluValalagluasnglyaspGlyValIle	120
Oy	797 ATAAGACATCCAGATTAATATACATGAGCTGAGAGCTGAAATGAGATGGGTATAT	856
Db	121 LysSerHlsweThrYrTrpArgLeuGluAsnIlealalythrGluProProLyBile	140
Oy	857 AAATCTCATATGACATATCTGGAGATTGAGAACTAGCGAAACCTGAACCACTTAAGATT	916
Db	141 PheArgVallysrProvalleuGlylleylsArgmetIleglnlleglutrpIlleyBPro	160
Oy	917 TTCGGTGTGAACAAGATTITGGGACATCAACAGAAATGATTCAAATTTGAATGGATTAAGCTT	976
Db	161 GluLeuAlaProValserSerAspLeuLyTrThrLeuArgPheArgThrValAsnSer	180
Oy	977 GAGTTGGGCGCTGTTTCACTGATTTTAAATATACACATTCGATTCAGAGACGTCAACGT	1036
Db	181 ThierTrfMetGluValasnPheAlalyAsnArglysAbplysaenglnThrTyrsn	200
Oy	1037 ACCAGCTGGAGAGAGCACTTGCTGCTTAAGAACCGTAAAGGATTAAMAAACCAACGTACAC	1096
Db	201 LeuThrglyLeuGlnpRopheThrGluTyrtValillealaleuaNrgCyValaValLygLu	220
Oy	1097 CTCACGGGGCTGCAGCTTCTTACGAATATGTCTAGCTCTGCGAATGTGCGGTCAAGAG	1156
Db	221 SerlyspHetirPseArpTrpSerGlngluLyswetGlywethrGlngluGluAlaPro	240
Oy	1157 TCANAAGTTCTGGAATGACTGGAGCCAAAGAAAATVGGAATGACTGAGGAAGAAGCTCCA	1216
Db	241 CygeglyLeuGluLeuTPAPArgValleuLyPProAlaGluAlaapGlyArgArgProVal	260
Oy	1217 TGTGGCTCTGGAACGTGTGAAGTCTGTAACCAAGCTGAGGGATGGAAGAAAGCCAGTG	1276


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Qy 261 ArgLeuLeuTrpIlyslYsAlaargGlyAlaProValIleuGluIlyThrIleuGlyTyrAsn 280
Db 1277 CGGTTGTTATGGAAGAAGGCAAGAGGAGCCCGAGTCTTAGAGAAAACACTGGCTACAAC 1336
Qy 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluIlyMetLeuThrThrAsnGln 300
Db 1337 ATATGGACTATACAGAAACCAACACTAACCTCACAGAAACAATGAACTACTTAACAG 1396
Qy 301 GlnLeuGluLeuHisIleuGlyGlyIlySerPheTrpValSerMetIleSerTyrAsnSer 320
Db 1397 CAGCTTGAATGCATCTGGAGAGCGAGAGCTTTGGGTGCTATGATTTCTTAATTC 1456
Qy 321 LeuGlyIlySerProValAlaThrLeuArgIleProAlaIleGlnIlyIlySerPheGln 340
Db 1457 CTGGGGAAGTCTCAGAGGCCACCTGAGGATTCAGCTATTCAGAAAATCATTTACAG 1516
Qy 341 CysIleGlnValMetGlnAlaCysValAlaGluAspGlnLeuValIlyIlyTrpGlnSer 360
Db 1517 TGCATTGAGGTACAGAGGCCCTGCTGAGAGACACAGTACGTGGAAGTGCAAAAGC 1576
Qy 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db 1577 TCGGCTCTAGACCTGAAACCTTGAGATGATGATGTTCCGATGAGACTAGAGCCC 1636
Qy 381 ThrThrIleuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIlyAspLys 400
Db 1637 ACCACCTTCTCTGGGATCTGTGCTCAGGCCACGACGATCCAGCAAGATATAA 1696
Qy 401 LeuIlyProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
Db 1697 TTAACCTTCTGAGTCTATTAACATCTGTGTATCCAAATGTGACAAAGTTGGC 1756
Qy 421 GluProIlySerIleGlnAlaTyrAlaIlyGluIlyValProSerGluGlyProGluThr 440
Db 1757 GAGCCATATTCCATCCAGGCTTATGCCAAGAAAGCGTTCCATCAGAAAGTCCTAGACC 1816
Qy 441 LysValGluAsnIleGlyValIlyThrValThrIleThrIlyIlyGluIleProLysSer 460
Db 1817 AAGGTGAGAAACATTGGCGTGAAGACGATCACATCAGTGAAGAGATTTCCCAAGAGT 1876
Qy 461 GluArgIlyGlyIleIleCysAsnTyrThrIlePheTyrGlnIleGluGlyIlyIlyGly 480
Db 1877 GAGAGAAAGGTATCATCTCACTACACATCTTTTAACTGAAGGTGAGAAAGGA 1936
Qy 481 PheSerIlyThrValAsnSerSerIleLeuGlnTyrGlyIlyLeuIlySerLysArgLys 500
Db 1937 TTCTCCAGACATCAATTCACAGATTTGCAATGCGCTGAGATCCCTGGAACCAAG 1996
Qy 501 ThrSerTyrIleValGlnValMetValAsnThrSerIleGlyIlyThrAsnGlyThrSer 520
Db 1997 ACCTCTTACATTTGTCAGTCTCATGGCCAGACACAGTCTGGGGAACCAACGGGAGCAGC 2056
Qy 521 IleAsnPheIlyThrIleuSerPheSerValPheGlnIleIleLeuIleThrSerLysIle 540
Db 2057 ATTAATTTCAAGCAATTCATTCAGTCTTTGAAGTATTCCTCAATACCTTCCTGATT 2116
Qy 541 GlyIlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyIlyLeuLysProAsn 560
Db 2117 GGTGGAGGCTTTCTTAATCTCATATTCACAGTGGCAATAGTCTCAAAAAACCAAC 2176
Qy 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db 2177 AAATTGACTATCTGTGTGGCCACCGTTCCCAACCTCTGTAAGATGATAGCCACA 2236
Qy 581 TrpHisGlyAspAspPheLysAspLysLysLeuAsnLeuLysIlySerAspAspSerValAsn 600
Db 2237 TGGCATGGAATATTTCAAGATGAAGTAAACCTGAAGAGTCTGATGTAAC 2296
Qy 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
Db 2297 ACGAAGACAGCATCTTAAACATGTTCCACCCCAAGTACAAAGTTGGTGAATTGACAG 2356
Qy 621 LeuValValAsnPheGlyAsnValLeuGlnIlyIlePheThrAspGluAlaArgThrGly 640

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Db 2357 TTGGTGGTAACTTTGGGAAATTTTCAGAAATTTTCAGAGTGAACCCGAGACGGGT 2416
Qy 641 GlnIlyAsnAsnLeuGlyIlyGlyIlyLysAsnGlyThrArgIleLeuSerSerCysProThr 660
Db 2417 CAGAAAACAAATTTAGAGGGGAAAGAAATGGGACTAGAAATCTGTCTTCTGCGCACT 2476
Qy 661 SerIle 662
Db 2477 TCAATA 2482

RESULT 3
ADD68146
ID ADD68146 standard; cDNA; 2903 BP.
XX
XX ADD68146;
AC
XX 15-JAN-2004 (first entry)
DT
XX
XX Human zcytor17 cDNA SEQ ID NO:4.
DE
XX
XX 68; gene: human; zcytor17; antiinflammatory; dermatological;
XX immunosuppressive; antimicrobial; vaccine; inflammatory disease;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;
XX atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;
XX toxic shock syndrome; infectious disease.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 497..2485
FT CDS /*tag= a
FT /product= "zcytor17"
XX
XX MO2003060090-A2.
XX
XX 24-JUL-2003.
XX
XX 21-JAN-2003; 2003WC-US001984.
XX
XX 18-JAN-2002; 2002US-0350325P.
XX 25-APR-2002; 2002US-0375323P.
XX 19-DEC-2002; 2002US-0435315P.
XX
XX (Zymo ) ZYMOGENETICS INC.
XX
XX PI Sprenger CA, Kuiper JJ, Dasovich MM, Grant FJ, Hammond AK;
XX PI Novak UE, Gross JA, Dillon SR;
XX DR P-PSDB; ADD68147.
XX
XX PT New zcytor17 ligand polypeptides, useful for treating inflammatory
XX PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
XX PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.
XX
XX PS Example 3; SEQ ID NO 4; 372pp; English.
XX
XX CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A
XX CC immunosuppressive, and antimicrobial activity, and may have a use in a
XX CC vaccine. The polypeptide is useful for treating inflammatory diseases,
XX CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
XX CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic
XX CC shock syndrome or infectious diseases. The present sequence is used in
XX CC the exemplification of the invention.
XX
XX SQ Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2903
Score: 3528.00 Matches: 662
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-10-006-265-17 (1-662) x ADD68146 (1-2903)

QY 1 MetLysLeuSerProGlnProSerCysValAlaLeuGluMetMetTrpThrTrpAlaLeu 20
 Db ATGAAGCTCTCTCCCAAGCTTCAATGTGTTAACTGGGGAATATGTGAAGCTGGGCACTG 556

QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAla 40
 Db TGGATGCTCCCTCACTCTGCAAAATTCAGCCGCGAGCTCTGCAAGCTTAAGCTGAGAAC 616

QY 41 LLeSerCysValTyrTyrTyrArgLysAlaLeuThrCysThrTrpSerProGluLysGlu 60
 Db ATTTCCTGTGCTACTACTATAGGAAAAATTTAACCTGCACCTTGAGTCCAGGAAGAA 676

QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGluGluLysHisAspAsn 80
 Db ACCAGTTATACCACTACACAGTTAAGAGAACTTACGCTTTGGAGAAACATATATAT 736

QY 81 CysThrThrAsnSerSerThrSerGluAlaAlaSerCysSerPhePheLeuProArg 100
 Db TGTACAACCAATAGTTCTACAAGTGAATGCTGCTCTTTTCTCTTCAAGA 796

QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 Db ATAACGATCCAGATTAATATACATGAGGTGAAGCAAAATGGAGATGCTGTAAAT 856

QY 121 LysSerHisMetThrTyrTrpArgLeuGluAlaLeuAlaLysThrGluProProLysIle 140
 Db AAATCTCTATGACACTACTGAGATTAGAGAACATAGGAAACTTGAACACCTTAAGATT 916

QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 Db TTCGGTGTGAACCAAGTTTGGGCAATCAAGAAATGATTCAAATTGATGATAAGCT 976

QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db GAGTGGGCGCTGTTCTCATCTGATTAAATACACACTTCAGACAGTCAACAGT 1036

QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTrpAsn 200
 Db ACCAGCTGAGTGAAGTCAACTGCTAAGAACCTTAAGATAAACCAACCGTACAC 1096

QY 201 LeuThrGlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLysGlu 220
 Db CTCACGGGGCTGCAGCCCTTTACAGAAATATGTCATAGCTCTGCCATGTGCCGTCAAGAG 1156

QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaPro 240
 Db TCAGAGTTCTGAGAGTGAAGCCAGCAAGAAAAATGGAAATGATGAGAGAAAGAGCTCCA 1216

QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProAla 260
 Db TGTGGCTGGAACTGTGAGAGTCTCTGAACCAAGTGAAGCGAGTGAAGAAAGCGCACTG 1276

QY 261 ArgLeuLeuTrpLysValArgGlyValAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 Db CGGTGTTATGGAAGAAAGCAAGAGAACCCCAAGTCCACAGAAACACTTGGCTACAC 1336

QY 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db ATATGTTACTATCCAGAAAGCAACACTCACTCAAGAAACAAATGAACTACTACAG 1396

QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSer 320
 Db CAGCTTGAACCTGCACTGGAGGCGAGAGCTTTGGGTCTATGATTTCTTAATAATCT 1456

QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 Db CTGGGAAGTCTCCAGTGGCCACCTGAGATTCACAGTATTCAAGAAATCATTTTCAG 1516

QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 Db TGCATTTGATGATGACAGCGCTGCTGTAGAGCAAGCTATGTGTAAGTGGAAAGC 1576

QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db TCTGCTACAGCGTGAACACTTGGATGATTAATGTGTTCCGAGTGTGACTCAGAGCC 1636

QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
 Db ACCACCTTTCTCGGAATCTGTGTCTCAGGCGCAGAACTGAGCATCCACCAAGTAA 1696

QY 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
 Db TTAAAACTTTCTGTGCTATACATCTGTGTATCCAAATGTGATGACAAAGTTGGC 1756

QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
 Db GAGCCTATTTCCATCCAGGCTTATGCCAAGAGCGCTTCATCAGAAAGCTCGAGACC 1816

QY 441 LysValGluAlaIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 Db AAGTGAGAACTTGGCGTGAAGACGCTCAGATCACATGGAAGAAGATCCCAAGAGT 1876

QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 Db GAGAGAAAGGTATCATCTGCACCTACACCATCTTTTACCAAGGTGAAGGTGAAGAAAGGA 1936

QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLys 500
 Db TTCTCCAGACAGTCATTCAGCATCTTGCAATCCGCTCGAGTCCCTTAACGAAAG 1996

QY 501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyIleThrAsnGlyThrSer 520
 Db ACTCTTACATTTGTCAGTCTATGCGCAGCACCGTGGGGGAAACCAAGGGAGCCAGC 2056

QY 521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db ATAAATTTCAAGACATTTGTCTAGTCTTTGAGATTTATCTCATPAACCTTCTGATT 2116

QY 541 GlyIleGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
 Db GGTGAGGCTCTTATTCTTATCTTATCTGACAGTGGCATGTGTCMAAAAAACCCAAC 2176

QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThr 580
 Db AAATTGACTATCTGTGTGGCCCAACCGTCCCAACCTGTGAAAGTATGAGCCACA 2236

QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db TGGCATGAGATGATTTTCAAGATTAAGTAACTGAAAGAGTCTGTGACTCTGTGATC 2296

QY 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
 Db ACAAGAGACAGATCTTAACACATGTTCAACCCCACTGACCAAGTTGGTATGACAG 2356

QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
 Db TTGTGTGTAACCTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAAGCAGAACGGGT 2416

QY 641 GlnGluAsnAsnLeuGlyGlyLysArgLysThrArgIleLeuSerSerCysProThr 660
 Db CAGGAAAAACAATTTAGAGGGGAAAGAAATGGGACTGAAATTCGTCTCTGCCCCAACT 2476

QY 661 SerIle 662
 Db TCAATA 2482

RESULT 4
 ADL26569
 ID ADL26569 standard; cDNA; 2903 BP.
 XX

AC ADL26569;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 DE Human cytokine receptor zcytor17 DNA seqid 4.
 XX
 KM antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;
 KM antibacterial; immunosuppressive; cell proliferation inhibitor;
 KM immune response inhibitor; inflammatory response inhibitor;
 KM multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KM cytokine-binding domain; class I cytokine receptor; haematopoietic cell;
 KM zcytor17lg-induced proliferation; zcytor17lg-induced differentiation;
 KM haematopoietic progenitor cell; zcytor17lg-induced inflammation;
 KM inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KM Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 KM septicæmia; toxic shock syndrome; zcytor17; human; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003215838-A1.
 XX
 PD 20-NOV-2003.
 XX
 PF 21-JAN-2003; 2003US-00351157.
 XX
 PR 18-JAN-2002; 2002US-0350325P.
 PR 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX
 PA (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUIJ/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNELL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX
 PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
 DR P-PSDB; ADL26570.
 XX
 PT Novel multimeric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicæmia.
 XX
 PS Example 3; SEQ ID NO 4; 205pp; English.
 XX
 CC The invention describes an isolated multimeric or heterodimeric cytokine
 CC receptor (I) having at least one polypeptide having 90 percent sequence
 CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in
 CC specification, and where (I) binds a ligand comprising a 164 (S3) amino
 CC acid sequence, given in specification, or at least one polypeptide
 CC comprising residue 20-227 of (S1). (I) is useful for killing cancer cells
 CC and producing an antibody to (I) and a cytokine-binding domain of a class
 CC I cytokine receptor. A composition (C1) comprising (I) and a cytokine-
 CC binding domain of a class I cytokine receptor and a vehicle is useful
 CC for: reducing haematopoietic cells and haematopoietic progenitor cells in
 CC a mammal; inhibiting zcytor17lg-induced proliferation or differentiation
 CC of haematopoietic cells and haematopoietic progenitor cells; reducing
 CC zcytor17lg-induced inflammation; treating a mammal afflicted with an
 CC inflammatory disease in which zcytor17lg plays a role. The disease is a
 CC chronic inflammatory disease such as inflammatory bowel disease,
 CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and
 CC psoriasis. The disease is acute inflammatory disease such as
 CC endotoxaemia, septicæmia, toxic shock syndrome and infectious disease.
 CC An immune response inhibiting composition is useful for inhibiting an

CC immune response in a mammal exposed to an antigen or pathogen. An
 CC inflammatory response inhibiting composition is useful for suppressing an
 CC inflammatory response in a mammal with inflammation. An antibody that
 CC specifically binds to (I) is useful for detecting the presence of a
 CC multimeric or heterodimeric cytokine receptor in a biological sample.
 CC This sequence encodes a human zcytor17 cytokine receptor.
 CC
 XX

Sequence 2903 BP; 862 A; 620 C; 664 G; 757 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	2903
Score:	3528.00	Matches:	662
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-006-265-17 (1-662) x ADL26569 (1-2903)

QY	1	M	e	t	l	y	s	e	r	p	r	o	g	i	n	p	r	o	s	e	r	c	y	s	a	l	a	e	n	l	e	u	g	i	y	m	e	t	r	i	p	a	l	e	n	20																				
DB	497	A	T	G	A	G	C	T	C	T	C	C	C	A	G	C	T	T	C	A	T	G	T	T	A	C	T	G	G	G	A	T	G	A	T	G	A	C	T	G	G	G	A	C	T	G	556																			
QY	21	T	r	p	M	e	t	l	e	n	P	r	o	S	e	r	i	e	u	C	y	s	a	l	y	s	p	h	e	s	e	r	l	e	u	a	l	a	l	e	u	P	r	o	A	l	a	y	s	P	r	o	G	i	u	a	n	40								
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QY	41	I	l	e	s	e	r	C	y	s	a	l	e	u	V	a	l	e	u	T	r	i	p	a	r	g	l	e	u	s	a	e	n	l	e	u	T	r	i	p	a	r	g	l	e	u	s	e	r	C	y	s	e	r	P	h	e	s	e	r	P	r	o	a	g	60
DB	617	A	T	T	C	T	G	T	C	T	A	C	T	A	T	A	G	A	A	A	A	A	A	A	T	T	A	A	C	T	T	G	A	C	T	T	G	A	C	T	T	G	A	C	T	T	G	A	A	A	A	A	A	A	A	A	A									
QY	61	T	h	r	s	e	r	T	r	i	p	a	r	g	i	n	T	r	h	r	V	a	l	e	y	s	a	r	g	h	r	T	r	a	l	a	P	h	e	g	i	g	i	u	l	y	s	i	s	a	p	a	n	80												
DB	677	A	C	C	A	G	T	T	A	C	C	A	G	A	C	A	G	A	C	A	G	A	C	A	G	A	C	T	T	A	A	C	T	T	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A												
QY	81	C	y	e	t	h	r	T	h	a	s	e	r	s	e	r	T	h	e	r	g	i	u	e	n	a	r	g	a	l	a	s	e	r	C	y	s	e	r	P	h	e	s	e	r	P	r	o	a	g	100															
DB	737	T	G	T	A	C	A	C	A	A	A	T	A	G	T	T	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A															
QY	101	I	l	e	t	h	r	i	e	P	r	o	A	s	p	a	n	T	r	i	p	a	r	g	i	n	V	a	l	e	g	i	u	a	l	a	G	i	u	a	s	n	g	i	y	a	s	p	g	i	y	a	l	i	e	120										
DB	797	A	T	A	C	A	T	C	C	A	G	A	T	A	T	T	A	T	A	T	A	C	A	T	T	A	C	A	T	T	A	C	A	T	T	A	C	A	T	T	A	C	A	T	T	A	C	A	T	T	A	C	A	T	T											
QY	121	L	y	s	e	r	I	s	e	r	T	r	i	p	a	r	g	i	u	e	n	a	r	g	a	l	a	s	e	r	T	h	e	r	i	p	r	o	f	i	y	s	i	e	140																					
DB	857	A	A	A	T	C	A	T	A	C	A	T	A	C	A	T	A	C	A	T	A	C	A	T	A	C	A	T	A	C	A	T	A	C	A	T	A	C	A	T	A	C	A	T	A	C	A	T	A	C	A	T	A	C												
QY	141	P	h	e	a	r	g	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	M	e	t	I	e	g	i	n	I	e	g	i	n	I	e	g	i	n	I	e	g	i	n	I	e	g	i	n	I	e	g	i	n	I	e				
DB	917	T	T	C	C	G	T	G	A	A	C	A	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T																
QY	161	G	i	u	l	e	u	a	l	a	P	r	o	V	a	l	e	s	e	r	s	e	r	P	r	o	f	i	y	s	i	e	r	T	r	i	p	a	r	g	i	n	P	h	e	r	g	h	r	V	a	l	e	s	e	r										
DB	977	G	A	G	T	T	G	C	C	T	G	T	T	C	A	T	C	T	A	T	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A																
QY	181	T	h	r	s	e	r	T	r	i	p	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g								
DB	1037	A	C	C	A	G	T	T	A	C	C	A	G	T	T	A	C	C	A	G	T	T	A	C	C	A	G	T	T	A	C	C	A	G	T	T	A	C	C	A	G	T	T	A	C	C	A	G	T	T	A	C	C													
QY	201	L	e	u	t	h	r	G	i	u	e	n	P	r	o	f	h	e	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y						
DB	1097	C	T	C	A	C	G	G	G	C	T	C	A	G	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T																	
QY	221	S	e	r	i	v	e	P	h	e	r	T	r	i	p	a	r	g	i	n	P	r	o	f	h	e	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y									
DB	1157	T	C	A	A	A	T	T	T	G	A	G	T	A	C	T	G	A	C	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A																	
QY	241	C	y	e	g	i	u	e	n	P	r	o	f	h	e	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y									
DB	1217	T	G	T	G	C	T	G	A	C	T	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A	G	A																	
QY	261	A	r	g	i	n	P	r	o	f	h	e	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y	s	a	r	g	i	n	V	a	l	e	y												

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Db      1277 CGGTTGTTATGSAAGAGCAAGAGGCCAGTCTTAGAAGAAAACATTGGCTACAAAC 1336
Oy      281  |||TTP|Y|Y|Y|P|G|L|S|e|A|n|T|h|r|A|n|L|e|u|T|h|r|T|h|r|A|n|G|n| 300
Db      1337 ATATGCTACTATCCAGAAAGCAACATACTCACAGAAACAATGAACCTACTAACAG 1396
Oy      301  G|N|L|e|u|G|L|e|u|H|L|e|u|G|L|V|G|L|S|e|P|h|e|T|P|V|L|S|e|M|L|S|e|T|Y|r|A|n|S|e| 320
Db      1397 CAGCTTGAACTGCATCTGGAGAGCGAGCTTTGGGTGCTATATATTTCTATATATCT 1456
Oy      321  L|e|u|G|L|Y|S|e|P|P|V|A|L|A|T|h|r|e|u|A|r|g|L|P|P|V|A|L|L|e|G|N|L|S|e|S|e|P|h|e|G|n| 340
Db      1457 CTTGGGAAGTCTCCAGTGGCCACCTGAGGATTCAGACTATTCAGAAAAATCATTTGAG 1516
Oy      341  C|y|S|I|e|G|L|V|A|L|M|e|G|L|A|L|A|C|y|S|V|A|L|A|G|L|A|P|G|L|N|L|e|u|V|A|L|V|S|T|P|G|L|S|e| 360
Db      1517 TGCATTGAGGTCATCCAGGCCCTGCTGAGAGCCAGCTAGTGAGTGAAGTGGAAGC 1576
Oy      361  S|e|r|A|L|e|u|A|P|V|A|A|n|T|h|r|T|h|r|P|h|e|I|e|G|U|T|P|h|P|P|P|P|A|P|V|A|A|P|S|e|r|G|L|P|P| 380
Db      1577 TCTGCTCTAGAGAGTGAACCTTGAGATGATGAATGGTTCCGAGTGGACTCAGAGGCC 1636
Oy      381  T|h|r|T|h|r|L|e|u|S|e|r|T|P|G|L|S|e|r|V|A|L|S|e|r|G|L|A|T|h|r|A|n|T|h|r|T|h|r|L|e|G|N|L|A|P|L|S| 400
Db      1637 ACCACCCCTTCTCGGGAATCTGTCTCAGGCCAAGACTGGAACCATCCAGCAAGATATA 1696
Oy      401  L|e|u|Y|P|P|h|e|T|P|C|y|T|Y|r|A|n|L|S|e|r|V|A|L|Y|P|P|h|e|L|e|u|H|A|P|L|Y|V|A|G|L|Y| 420
Db      1697 TTAACACCTTCTGCTGCTATACATCTCTGTGATCCAAATGTCATGACAGCAAAATGGC 1756
Oy      421  G|L|U|P|O|Y|r|S|e|r|L|e|G|N|A|L|Y|r|A|L|Y|S|G|L|V|A|L|P|P|S|e|r|G|L|Y|P|P|G|L|U|T|h|r| 440
Db      1757 GAGCAATATTCATCCAGGCTTATGCCAAAGAGGCGTTCCATCCAGAAAGTCTGAGACC 1816
Oy      441  L|y|S|V|A|G|L|A|n|L|e|G|L|V|A|L|Y|e|T|h|r|V|A|L|T|h|r|L|e|T|h|r|T|P|Y|S|G|L|U|L|e|P|h|Y|S|e|r| 460
Db      1817 AAGGCGAAGACATTTGGCGTGAAGACGCTCAGCATCAGATGGAAGAGATTTCCAGAGCT 1876
Oy      461  G|L|U|A|r|G|L|Y|S|G|L|L|e|L|C|y|A|n|T|Y|r|T|h|r|L|e|P|h|e|Y|r|G|L|N|A|L|G|L|U|G|L|Y|L|Y|S|G|L| 480
Db      1877 GAGAGAAAGGATATCATCTGCACATACACACATCTTTACCAAGCTGAAAGTGAAGAAAGA 1936
Oy      481  P|h|S|e|r|Y|r|T|h|r|V|A|A|n|S|e|r|S|e|r|L|e|u|G|N|T|Y|r|G|L|Y|L|e|u|S|e|r|L|e|u|Y|A|r|G|L|Y|S| 500
Db      1937 TTCTCCAGACAGTCAATTTCCAGACATCTTGACAGTCCGAGTCCCTGAAAGGAAG 1996
Oy      501  T|h|S|e|r|Y|r|L|e|V|A|G|N|V|A|L|M|e|r|A|L|S|e|r|T|h|S|e|r|A|L|G|L|Y|G|L|Y|r|T|h|A|S|G|L|Y|r|T|h|S|e|r| 520
Db      1997 ACCCTTTCATTTGTTCAAGTCAATGCCACACAGCATGCTGGGGGAACCAACCGGACACG 2056
Oy      521  I|L|e|A|n|P|h|e|Y|r|T|h|r|L|e|u|S|e|r|P|h|S|e|r|V|A|L|P|h|e|G|L|U|L|e|L|e|u|L|e|T|h|S|e|r|L|e|u|L|e| 540
Db      2057 ATAAATTTCAAGACATTTGTCATTCAGTCTTTGAGATTATCCCTCAATATCTCTGATTT 2116
Oy      541  G|L|Y|G|L|Y|L|e|u|L|L|e|u|L|L|e|L|e|u|T|h|r|V|A|L|A|T|Y|r|G|L|Y|L|e|u|L|Y|L|e|P|h|S|e|r|A|n| 560
Db      2117 GGTGAGGCGCTTCTTATTTCTCATATTCCTGACAGTGAAGTATGCTCTCAAAAACCCACAC 2176
Oy      561  L|y|S|e|u|T|h|r|H|L|S|e|C|y|T|P|P|h|T|h|r|V|A|L|P|h|S|e|r|P|h|A|L|S|e|r|S|e|r|L|e|A|T|h|r| 580
Db      2177 AATATGATCATCTGTGTTGGCCCACTTCCCAACCTGCTGAAAGTAAGTACCCACA 2236
Oy      581  T|h|r|H|S|G|L|Y|A|P|A|P|h|e|Y|r|A|P|L|Y|S|L|e|u|A|n|L|e|u|Y|S|G|L|S|e|r|A|P|S|e|r|V|A|L|A|n| 600
Db      2237 TGGCATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTCTGATGACTCTGTGAAC 2296
Oy      601  T|h|r|G|L|U|A|P|A|r|G|L|L|e|u|L|Y|P|h|C|y|S|e|r|T|h|r|P|h|S|e|r|A|P|L|Y|L|e|u|V|A|L|L|e|S|P|L|Y|S| 620
Db      2297 ACAGAAAGCAGGATCTTAAACCATGTTCCACCCCACTGACAACTGTGTGATGACAAAG 2356
Oy      621  L|e|u|V|A|L|A|n|P|h|e|G|L|Y|A|n|V|A|L|L|e|u|G|N|L|U|L|e|P|h|T|h|r|A|P|S|G|L|U|A|L|A|r|G|T|h|r|G|L|Y| 640
Db      2357 TTGGTGTGAACCTTTGGGAATGTTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAACGGGT 2416

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Oy      641  G|I|N|G|L|U|A|n|A|n|L|e|u|G|L|V|G|L|U|L|Y|A|n|G|L|Y|r|A|r|G|L|L|e|u|S|e|r|C|y|E|P|h|P|h|r| 660
Db      2417 CAGAAAAACAATTTAAGAGGGGAAAAAGATGGAGCTAGAAATTTCTTCTCCGCCCCAACT 2476
Oy      661  S|e|r|L|e| 662
Db      2477 TCAATA 2482

RESULT 5
ABA93803
ID ABA93803 standard; cDNA: 2529 BP.
XX
AC ABA93803;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human zcytor17 cDNA sequence SEQ ID NO:45.
XX
KW zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; splenic; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
XX
OS Homo sapiens.
XX
PN W0200200721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US020484.
XX
PR 26-JUN-2000; 2000US-0214282P.
PR 29-JUN-2000; 2000US-0214955P.
PR 08-FEB-2001; 2001US-0267963P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
XX Maurer MF;
XX WPI: 2002-090519/12.
XX DR P-PSDB; ABB05738.
XX
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders.
XX
PS Claim 2; Page 190-194; 235p; English.
XX
CC The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,
CC antineumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
CC for stimulating lymphocyte proliferation, such as in the treatment of
CC infections involving immunosuppression, including certain viral
CC infections. They are also useful for inducing cytotoxicity and for
CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05720 to ABB05745 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 2529 BP; 764 A; 530 C; 576 G; 659 T; 0 U; 0 Other;
XX
Alignment scores: 0 Length: 2529
Pred. No.:

```

Score: 3518.00 Matches: 660
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.72% Indels: 0
DB: 6 Gaps: 0
US-10-006-265-17 (1-662) x ABA93803 (1-2529)
QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
DB 129 CTCTCTCCAGCCCTTCATGTGTAACTTGGGGATGTGTGACCTGGGACCTGTGGATG 188
QY 23 LeuProSerLeuCysIysPheSerLeuAlaAlaLeuProAlaIysProGluAsnIleSer 42
DB 189 CTCCTCCATCTCGCAAAATTCAGCCTGGGACGCTCTGCACCTAAAGCTGAGAACATTTCC 248
QY 43 CysValTyrTyrTyrArgIysAsnLeuThrCysThrTrpSerProGlyIysGlyIuThrSer 62
DB 249 TGTGTCTACTACTATAGGAAAAATTTAACTGCACCTGGAGTCCAGGAAAGAACACAGT 308
QY 63 TyrThrGlnTyrThrValIysArgTrpTyrTrpAlaPheGlyGlyIuIysHisAspAsnCyThr 82
DB 309 TATATCCAGTACACGTTAAGAGAACTTACGCTTTTGGAGAAAAACATGATTAATGTACA 368
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102
DB 369 ACCAAATAGTCTTCAAGTGAATAATCGTGTGCTCTTTTTCCTTCCAAAGATTAAG 428
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleIysSer 122
DB 429 ATCCCATATATATATACATTGAGGTGGAAGCTGAAATGAGATGGGTAAATTAATCT 488
QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaIysThrGluProProIysIlePheArg 142
DB 489 CATATGACATCTAGAGATTAAGAACATAGCCAAAACTGAACCACTTAAGATTTTCCGT 548
QY 143 ValIysProValLeuGlyIleIysArgMetIleGlnIleGluTrpIleIysProGluLeu 162
DB 549 GTGAACCAAGTTTGGGCATCAACGAATGATTCAAATTTGAATGAATAAGCCGTGAGTTG 608
QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
DB 609 GCCCGCTGTTCACTGATTTTAAATACACACTTCGATTGAGGACAGCAACAGTACAGC 668
QY 183 TrpMetGluValAsnPheAlaIysAsnArgIysAspIysAsnGlnThrTyrAsnLeuThr 202
DB 669 TGAATGAAATCAACTTCGCTAAGAACCTGAAGATTAACCAACAGTACCAACTCAG 728
QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValIysGluSerIys 222
DB 729 GGGCTGCAGCCTTTTACGAATAATGTATAGTCTGTGAGTGTGGGTCAAGAGTCAAG 788
QY 223 PheTrpSerAspTrpSerGlnGlyIuIysMetGlyMetThrGluGluGluAlaProCysGly 242
DB 789 TTTCTGGAGTACTGAGCCCAAGAAAAATGGAATGACTGAGAGAACGCTCATGTGGC 848
QY 243 LeuGluLeuTrpArgValIleuIysProAlaGluAlaAspGlyArgArgProValArgLeu 262
DB 849 CTGAAGATGTGGAGAGTCTGAAACCAAGCTGAGCGGATGAGAAAGGCCAGTGGCTTG 908
QY 263 LeuTrpIysIysAlaArgGlyAlaProValLeuGluIuIysThrLeuGlyTyrAsnIleTrp 282
DB 909 TTATGGAAGAAAGGAGAGAGAGGCCCACTGCTAGAGAAAAACATTGGCTTCAACATATGG 968
QY 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
DB 969 TACTATCTCAAGAAAGCACTAACTTCACAGAAACATGAACACTAATCAACGACGCTT 1028
QY 303 GluLeuHisLeuGlyGlyIuIysArgPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
DB 1029 GAATCTGATCTGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCTTATTAATTTCTTTGGG 1088
QY 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluIysSerPheGlnCysIle 342

DB 1089 AAGTCTCCAGTGGCCACCCTGAGATTCACGCTATTTCAAGAAAAATCAATTCAGTGCATT 1148
QY 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValIysTrpGlnSerSerAla 362
DB 1149 GAGGTCTAGCAGGCCCTGCGTGTCTGAGGACCAAGCTGATGATGATGGCAAGCTCTGTCT 1208
QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
DB 1209 CTAGACGTACAACATTGATGATGATTTCCGGAATGTGATCTCAGAGCCCAACCAACC 1268
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspIysLeuIys 402
DB 1269 CTTTCTGGGAATCTGTGCTCAGGCCACGAACGTGACATCCACAGATTAATTAATAA 1328
QY 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspIysValGlyIuPro 422
DB 1329 CTTTCTGTGTCTATTAACATCTCTGTATCCAAATGTGCATGACAAAGTTGGCCAGCA 1388
QY 423 TyrSerIleGlnAlaTyrAlaIysGluGlyValProSerGluGlyProGluThrIysVal 442
DB 1389 TATTCATCTCAGGCTTATGCAAGAGAGCCGTTCCATCAGAAAGTCTTGAGACCAAGTG 1448
QY 443 GluAsnIleGlyValIysThrValIleThrTrpIysGluIleProIysSerGluArg 462
DB 1449 GAGAACATTTGGCGTGAAGACGGTCAAGATCATGAGAAAGAAATTTCCCAAGATGAGAGA 1508
QY 463 IysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyIysGlyPheSer 482
DB 1509 AAGGATATCATGTGACATCACATCTTTTACCAAGCTGAAGGTGAGAAAGATTTCTCC 1568
QY 483 IysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuIysArgIysThrSer 502
DB 1569 AAGACAGTCAATTTCCAGCATCTTGCAATGCGGCTGAGATCCCTGAACGAAGACCTT 1628
QY 1629 TACATGTTCAGATGATGCGCCAGCACCAAGTGTGGGGCAACCAAGCGGACAGCATTAAT 1688
QY 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyIysThrAsnGlyThrSerIleAsn 522
DB 1689 TTCAGACATTTTCATCTGATGCTTTGAGATTAATCTCAATCACTCTGATGTGTGGA 1748
QY 523 PheIysThrLeuSerPheSerValPheGluIleIleuIleThrSerLeuIleGlyIys 542
DB 1748 TTTCAAGACATTTTCATCTGATGCTTTGAGATTAATCTCAATCACTCTGATGTGTGGA 1748
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuIysIysProAsnIysLeu 562
DB 1749 GGCCTTCTATTCTCATTTATCTGACAGTGGCATGTGCTCAAAAAACCAAAATTTG 1808
QY 563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
DB 1809 ACTCATCTGTGTTGGCCCAACGTTCCAACTGCTGAAGATGATATGACCACATGGCAT 1868
QY 583 GlyAspAspPheIysAspIysLeuAsnLeuIysGluSerAspAspSerValAsnThrGlu 602
DB 1869 GAGAGATGATTTCAAGGATTAAGCTTAACCTGAAGAGATCTGATGATCTGTGAACACAGAA 1928
QY 603 AspArgIleLeuIysProCysSerThrProSerAspIysLeuValIleAspIysLeuVal 622
DB 1929 GACAGATCTTTAAACCACTTCCACCCCACTGACAAATTTGTGATTAACAAGTTGGTG 1988
QY 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
DB 1989 GTGAATTTGGGAATGTTCTGCAAGAAATTTTCAAGAGTGAAGCCAGAACGGGTCAAGAA 2048
QY 643 AsnAsnLeuGlyGlyIuIysAsnGlyThrArgIleLeuSerSerCysProThrSerIle 662
DB 2049 AACCAATTTAGAGGGGAAAAAGATGGACTAAGATTTGTCTTCTGCCCAACTTCAATA 2108
RESULT 6
ADL26671
ID ADL26671 standard; cDNA; 2529 BP.
XX
AC
XX ADL26671;

DT 20-MAY-2004 (first entry)

XX Human cytokine receptor zcytor17 DNA seqid 108.

DE antiinflammatory; antitumor; dermatological; antiallergic; antipsoriatic;

XX antibacterial; immunosuppressive; cell proliferation inhibitor;

KW immune response inhibitor; inflammatory response inhibitor;

KW multimeric cytokine receptor; heterodimeric cytokine receptor; cancer;

KW cytokine-binding domain; class I cytokine receptor; hematopoietic cell;

KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;

KW hematopoietic progenitor cell; zcytor17lig-induced inflammation;

KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;

KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;

KW septicemia; toxic shock syndrome; zcytor17, human; gene; ss.

OS Homo sapiens.

XX US2003215838-A1.

XX 20-NOV-2003.

PD 21-JAN-2003; 2003US-00351157.

XX 18-JAN-2002; 2002US-0350325P.

PR 14-JUN-2002; 2002US-0389108P.

PR 19-DEC-2002; 2002US-0435361P.

XX (SPRE/) SPRECHER C A.

PA (GAOZ/) GAO Z.

PA (KUIJ/) KUIJPER J L.

PA (DASO/) DASOVICH M M.

PA (GRAN/) GRANT F J.

PA (PRES/) PRESNELL S R.

PA (WHIT/) WHITMORE T E.

PA (HAMM/) HAMMOND A K.

PA (NOVA/) NOVAK J E.

PA (GROS/) GROSS J A.

PA (DILL/) DILLON S R.

XX Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ,

PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;

XX MPI: 2003-876545/81.

DR P-PSDB: ADL26672.

XX Novel multimeric or heterodimeric cytokine receptors useful for treating

PT chronic inflammatory disease such as inflammatory bowel disease,

PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,

PT septicemia.

XX Disclosure; SEQ ID NO 108; 205bp; English.

XX The invention describes an isolated polypeptide having 90 percent sequence

CC identity with a 732 (S1) or 649 (S2) amino acid sequence given in

CC specification, and where (1) binds a ligand comprising a 164 (S3) amino

CC acid sequence, given in specification, or at least one polypeptide

CC comprising residue 20-227 of (S1). (1) is useful for killing cancer cells

CC and producing an antibody to (1) and a cytokine-binding domain of a class

CC I cytokine receptor. A composition (C1) comprising (1) and a cytokine-

CC binding domain of a class I cytokine receptor and a vehicle is useful

CC for: reducing hematopoietic cells and hematopoietic progenitor cells in

CC a mammal; inhibiting zcytor17lig-induced proliferation or differentiation

CC of hematopoietic cells and hematopoietic progenitor cells; reducing

CC zcytor17lig-induced inflammation; treating a mammal afflicted with an

CC inflammatory disease in which zcytor17lig plays a role. The disease is a

CC chronic inflammatory disease such as inflammatory bowel disease,

CC ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and

CC psoriasis. The disease is acute inflammatory disease such as

CC endotoxaemia, septicemia, toxic shock syndrome and infectious disease.

CC An immune response inhibiting composition is useful for inhibiting an

CC immune response in a mammal exposed to an antigen or pathogen. An

CC inflammatory response inhibiting composition is useful for suppressing an

CC inflammatory response in a mammal with inflammation. An antibody that

CC specifically binds to (1) is useful for detecting the presence of a

CC multimeric or heterodimeric cytokine receptor in a biological sample.

CC This sequence encodes a human zcytor17 cytokine receptor that can be used

CC in a comparison with other zcytor17 receptors.

XX SQ Sequence 2529 BP; 764 A; 530 C; 576 G; 659 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Mismatches:	Indels:	Gaps:
Score: 3518.00	2529	660	0	0	0
Percent Similarity: 100.00%					
Best Local Similarity: 100.00%					
Query Match: 99.72%					
DB: 11					

US-10-006-265-17 (1-662) x ADL26671 (1-2529)

QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetThrPheAlaLeuTyrMet 22

DB 129 CTCTCTCCCGACCTTCATGTTTAACTGGGGATGATGAGCTGGGCACTGTGATG 188

QY 23 LeuProSerLeuCybLysPheSerLeuAlaLeuProAlaLysProGluAsnIleSer 42

DB 189 CTCCCTCAGCTCTGCAATTGAGCTGGCAGCTCTGGCAGATTAGCTGAGAACATTTCC 248

QY 43 CysValTyrTyrTyrValGlyAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62

DB 249 TGTGCTACTACTATGAGAAAATTTAACTGCACTTGAGATCCAGGAAGAAACCGT 308

QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysAspAsnCysThr 82

DB 309 TATACCAAGTACAGATTAGAGAACTTACGCTTTGGAGAAAACATGATTAATTTGACA 368

QY 83 ThrAsnSerThrThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThr 102

DB 369 ACCAATGTTCTACAAGGAAATCGTGCTTCGTCCTTTCTTCCCAAGATAACG 428

QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyLysArgValIleLysSer 122

DB 429 ATCCAGATTAATTATACATTGAGGTGAGCTGAAAATGAGATGATTAATTAATCT 488

QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProValIlePheArg 142

DB 489 CATATGACATATCTGAGATTAGAGAACATAGCAAACTGAAACCATTAATTTCCGT 548

QY 143 ValLysProValIleGlyIleLysArgMetIleGlnIleGluTyrIleLysProGluLeu 162

DB 549 GTGAACCAAGTTTGGGCAATCAACGAATGATTAATGATTAAGCTGAGTTG 608

QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182

DB 609 GCGCTGTTTCATCTGATTTAAATATACACTTGATTCAGGACATCAAGATCACAGC 668

QY 183 TrpMetGluValAsnProAlaLysAsnArgLysAspLysAsnGlnTyrAsnLeuThr 202

DB 669 TGGATGAGAGCACTTCGCTCAACACCGTAAGGATTAAGAAACCAACGATCAACCTCAGC 728

QY 203 GlyLeuGlnProPheThrGlnTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222

DB 729 GGGGTGACGCTTTTACGAAATGTCATAGCTCTGGAGTGGCGTCAAGGATTCAAAG 788

QY 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242

DB 789 TTCGAGAGTGACTGAGACCAAGAAAATGGGATGACTGAGGAAGAGCTCATGTGGC 848

QY 243 LeuGluLeuTrpArgValIleLysProAlaGluAlaAspGlyArgProValArgLeu 262

DB 849 CTGGAACGTGGAGAGTCTGAAACCAAGCTGAGGAGTGAAGAGCCAGTGGGTTG 908

QY 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282

DB 909 TTATGGAAGAAAGCAAGAGAGGCCCAAGTCTTAGAAGAAAACCTTGCTCAACATATGG 968

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QY 283 TyrTyrProGlnSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
DB 969 TACTATCCAGAAAGCAACTAACCTACAGAAACAAATGAACTACTAACCGACGACTT 1028
QY 303 GlnLeuHisLeuGlnGlyGlnSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
DB 1029 GAACCTCATCTGGAGCGGAGAGCTTTGGGTCTATGATTTCTTAATAATCTCTTGGG 1088
QY 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGlnLysSerPheGlnCysIle 342
DB 1089 AAGTCTCCAGGTGGCCACCCTGAGAGATTCAGCTATTCAAGAAAAATCATTTGCTCAT 1148
QY 343 GluValMetGlnIaCysValaIaGluAspGlnLeuValValIleTyrTrpGlnSerAla 362
DB 1149 GAGGTATGAGGCGCTCCGTGCTGAGAGACCACTAGTGTGAAGTGGCAAACTCTGCT 1208
QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
DB 1209 CTGACGCTGAACACTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1268
QY 383 LeuSerTrpGlnSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuVal 402
DB 1269 CTTTCCGGGAATCTGTCTCAGGCCACGAACTGACGATCCAGCAAGATTAATTAATA 1328
QY 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro 422
DB 1329 CTTTCTGGGTGCTATACATCTCTGTGTATCCAAATGTGATGATGATGATGATGATG 1388
QY 423 TyrSerIleGlnAlaTyrAlaLysGlnValProSerGlnGlyProGluThrLysVal 442
DB 1389 TATTCATCATCAGGCTTATGCTCAAGAAAGCGTTCATCAAGAAAGTCCCTGAGACCA 1448
QY 443 GluAsnIleGlyValIleLysThrValThrIleThrTrpLysGlnIleProLysSerGlu 462
DB 1449 GAAACATTGGCGGTGAGAGCGTCAAGATCAGATGAAAGATTTCCCAAGATGAGAGA 1508
QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGlnGlyLysGlyPheSer 482
DB 1509 AAGGTATATCTTCGAACTACACCATCTTTTACCAAGCTGAAGTGAAGAAAGATTCTCC 1568
QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysValGlyThrSer 502
DB 1569 AAGACAGTCAATTCAGCATCTTGAGTACGAGTACGCTGAGTCCCTGAAACGAAAGAC 1628
QY 503 TyrIleValGlnIleMetAlaSerThrSerAlaGlyGlyThrLysGlnIleAsn 522
DB 1629 TACATGTTCAGGTCATGCGCAGACCAAGTGGGGGAAACCAACGAGACCATTAAT 1688
QY 523 PheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerLeuIleGlyGly 542
DB 1689 TTCAGACATGTCATTCATGTCATCTTGAGATTAATCTCTCAATCTCTCGATTGGTGA 1748
QY 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
DB 1749 GGCCTTCTTATCTCATTTATCTGACAGTGGCATATGATCTCAAAAAACCAATAATTG 1808
QY 563 ThrHisLeuGlnSerTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrpHis 582
DB 1809 ACTCATCTGTGTGGCCCGCCACCGTCCCAACCTGCTGAAGATGAAGCAACATGGCAT 1868
QY 583 GlyAspAspPheLysAspLysLeuAsnLysGlnSerAspAspSerValAsnThrGlu 602
DB 1869 GAGAGATGATTTCAAGATTAAGTAACTGAAGAGCTGATGATCTGTGGAACACAGAA 1928
QY 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
DB 1929 GACAGGATCTTAACCATGATTTCCACCCAGTGAACAAGTTGGATGATGACAAGTTGG 1988
QY 623 ValAsnPheGlnLysAsnValIleGlnGlnIlePheThrAspGlnAlaGlnThrGlyGlnGlu 642
DB 1989 GTGAATCTTGGGAAATGTTCTGCAAGAAATTTTTCACAGATGAAGCCAGAAAGGCTGAG 2048

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QY 643 AsnAsnLeuGlnGlyGlnLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle 662
DB 2049 AACCAATTTGAGGGGGAAGAAAGATGGAGCTAGAAATTTCTGTCTGCGCCCACTCAATA 2108

RESULT 7
AB083363
ID AB083363 standard; cDNA; 4315 BP.
XX
AC AB083363;
XX
DT 20-JUN-2003 (first entry)
XX
DE Human NR10.3 splicing variant encoding cDNA SEQ ID NO:1.
XX
KW NR10; splicing variant; haematopoietic receptor; immunomodulator;
KW haematopoietic factor; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2052
FT /tag= a
FT /product= "NR10.3"
XX
PN W020027230-A1.
XX
PD 03-OCT-2002.
XX
PF 22-MAR-2002; 2002W0-JP002769.
XX
PR 26-MAR-2001; 2001JP-00087298.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Maeda M, Yaguchi N, Hasegawa M;
XX
DR MPI; 2003-018925/01.
XX
DR P-PSDB; ABP54363.
XX
PT NR10 splicing variants of hematopoietic receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases.
XX
PS Example 2; Fig 1-2; 250pp; Japanese.
XX
CC The present invention describes haematopoietic receptor NR10 splicing
CC variants (1). (1) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietic receptor genes participate
CC in vivo immunomodulation and haematopoietic cell regulation, and in the
CC search for haematopoietic factors capable of functionally binding to the
CC receptors. The present sequence encodes the human NR10.3 protein from the
CC present invention
XX
SQ Sequence 4315 BP; 1187 A; 1008 C; 1061 G; 1059 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 4315
Score: 3518.00 Matches: 660
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.72% Indels: 0
DB: 8 Gaps: 0

US-10-006-265-17 (1-662) x AB083363 (1-4315)
QY 3 LeuSerProGlnProSerCysValAsnLeuGlnMetTrpThrTrpAlaLeuTrpMet 22
DB 70 CTCTCTCCCGAGCTTTCATGTGTAACTGGGAGATGATGAGACTGGGACCTGTGATG 129
QY 23 LeuProSerLeuCysLysPheSerLeuAlaIleLeuProAlaLysProGlnLysSer 42

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Db      130 CTCCCTCACTCTGAAATTGAGCTGGAGCTCTGCCAGCTTAACCTGAGAACCTTTCC 189
Qy      43 CysValTyrTyrTyrArgLysAlaLeuThrCysThrTrpSerProGlyLysGluThrSer 62
Db      190 TGTGCTACTACTATAGAAAAATTTAACTGCACTTGAGAGTCCAGAAAGGAAACCACT 249
Qy      63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnGlyThr 82
Db      250 TATACCCAGTACACAGTTAGAGAACTTACGCTTTTGAGAAAAACATGATTAATGTACA 309
Qy      83 ThrAsnSerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProGlyLeuThr 102
Db      310 ACCAATATTTCTCAAGTGAAGAAATCGTCTGCTCTCTTTTCTCTTCCAGAAATTAACG 369
Qy      103 IleProAspAsnTyrThrIleGluValGluAlaGlnAsnGlyAspGlyValIleLysSer 122
Db      370 ATCCAGATTAATTAATACATTGAGGTGGAAGCTGAAAAATGAGATGATTAATTAATCT 429
Qy      123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
Db      430 CATATGACATCTGAGATTAAGAAACATAGCGAAACCTGAACCACTTAAGATTTTCCGT 489
Qy      143 ValLysProValIleGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
Db      490 GTGAACCAAGTTTGGCATCAACCAAGATGATTCAAAATTGAATGAATTAAGCTGAGTTG 549
Qy      163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
Db      550 GCGCTGTTTCACTGATTTAAATTAACAACCTTCATTGAGGACAGTCAACAGTCCAGC 609
Qy      183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
Db      610 TGGAGGAAAGTCAACTTGCTAAGAACCTGAAGATTAACCAACCTGAACCTCCACG 669
Qy      203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysValIleValIleGluSerLys 222
Db      670 GGGCTGCGACCTTTTACGAATATCTCATAGCTCTGCCATGTGCGGTCAAGAGTCAAG 729
Qy      223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242
Db      730 TTTCGAGTGACTGAGGCCAAGAAAATGGGAAATGACGAGAGAAAGCTCATGTGCG 789
Qy      243 LeuGluLeuTrpArgValIleLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262
Db      790 CTGGAACCTGTGAGAGTCTCTGAACCACTGAGGAGTGAAGAAAGCCAGCTGGGTGG 849
Qy      263 LeuTrpLysLysAlaArgGlyValAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
Db      850 TTATGGAAGAGAGGCAAGAGAGCCCACTGCTTAGAGAAACCTTGCTTACACATATGG 909
Qy      283 TyrTyrProGluSerAsnThrAsnLeuThrArgIleMetAsnThrThrAsnGlnLeu 302
Db      910 TACTATCCAGAAAGCAACCTAACCCTCAAGAAACATAGAACATCACTAACAGAGCTT 969
Qy      303 GluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
Db      970 GAACGTGCACTCTGGGAGGCGAGAGCTTTGGGTGTCTATGATTTCTTATATATCTCTGGG 1029
Qy      323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342
Db      1030 AAGTCTCAAGTGGCCACCTGAGATTCAGCTATTCAAGAAATCACTTTCAGTGCATT 1089
Qy      343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValIleLysTrpGlnSerSerAla 362
Db      1090 GAGGTCAATGCAAGGCTGGTGTCTGAGGACCAAGTGTGTAAGTGGCAAAAGCTGTCT 1149
Qy      363 LeuAspValAsnThrTyrMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db      1150 CTAGACGTGAACACTTGATGATGATTAATGATTTCCGAGTGTGACTCAGAGCCCAAC 1209
Qy      383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpTrpIleGlnAlaAspLysLeuLys 402

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Db      1210 CTTTCCTGGAAATCTGTGTCTCAGGCCACGAATGACATCCAGACATTAATTAATA 1269
Qy      403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro 422
Db      1270 CTTTCTGTGCTCTATACATCTGTGTATCCAAATGTTGACAGCAAAAGTTGGCAGGCA 1329
Qy      423 TyrSerIleGlnAlaTyrAlaLysGluGlyValIleProSerGluGlyProGluThrLysVal 442
Db      1330 TATTCATCCAGGCTTATGCAAGAGAGGCTTTCATCAGAAAGTCTCGAACCAGGTG 1389
Qy      443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 462
Db      1390 GAGAACATTTGCGTGAAGACGCTCAGCATCAACAGAAAGATTTCCCAAGAGTGAAGA 1449
Qy      463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
Db      1450 AAGGTATCATCTGCACTACACCATCTTTTACCAAGCTGAAGTGAAGGATTCCTCC 1509
Qy      483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
Db      1510 AAGACATCAATTCAGCATCTTGACATTCGACGCTGAGTCCCTGAACGAAAGACTCT 1569
Qy      503 TyrIleValGlnValMetAlaSerThrSerAlaGlyTyrThrAsnGlyThrSerIleAsn 522
Db      1570 TACATTTGTCAGTCAATGCGACAGCACAGCTCTGGGGGAAACCAAGGACCATTAAT 1629
Qy      523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
Db      1630 TTCAAGCATTTGATTCAGTCTTGAGATTAATCCATCACTCTCTCATATTTGTGGA 1689
Qy      543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
Db      1680 GGCCTTCTTATCTCATTTATCTTCAACGTGSCATATGTCTCAAAAAACCAAAATTTG 1749
Qy      563 ThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
Db      1750 ACTCATCTGTGTGGCCACCGTCCCAACCTGCTGAAGATGAATGATGACATGTCAT 1809
Qy      583 GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu 602
Db      1810 GGAGATGATTTCAAGATTAACCTTAACCTGAAGAGTCTGATGACTGTGAACACAGAA 1869
Qy      603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db      1870 GACGAGATCTTAACCACTGTTCCACCCCGTACAGATGATGATGATGATGATGATG 1929
Qy      623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db      1930 GTGAACCTTTGGGAATGTTCTCAAGAAATTTTCAAGATGAAGCAAGACGGTCAAGAA 1989
Qy      643 AsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle 662
Db      1990 AACCAATTTAGAGGGGAAAGAAATGAGACTGAATTTCTCTCTGCCCAATTCATA 2049

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RESULT 8
 AAC92337
 ID AAC92337 standard; cdna; 2969 BP.
 AC AAC92337;
 DE 26-MAR-2001 (first entry)
 XX Human haemopoietic receptor protein NR10.1 encoding cdna SEQ ID NO.1.
 XX Human; haemopoietic receptor; NR10.1; NR10.2; NR10.3; NR10;
 KW immunoregulation; haemopoietic cell regulation; transmembrane;
 KW immune disorder; haemopoietic disorder; autoimmune disease; allergy;
 KW metal allergy; pollen allergy; ss.
 OS Homo sapiens.
 XX MO200075314-Al.
 XX

PD 14-DEC-2000.
 XX 01-JUN-2000; 2000MO-JP003556.
 XX 02-JUN-1999; 99JP-00155797.
 PR 30-JUL-1999; 99JP-00217797.
 XX (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.
 PA Maeda M, Yaguchi N;
 XX WPI; 2001-061720/07.
 DR P-PDB; AAB51242.
 XX Hematopoietin receptor protein NR10 for screening potential ligands for
 PT treatment of immune and hematopoietic disorders such as autoimmune
 PS diseases and allergies.
 XX Claim 1; Fig 3-5; 127pp; Japanese.
 CC The present sequence encodes a human haemopoietin receptor protein
 CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
 CC which participates in immunoregulation and haematopoietic cell regulation
 CC in vivo, and is useful in searching for haematopoietic factors capable of
 CC binding to the receptor. NR10 can be used for the identification of
 CC substances for the treatment and prevention of immune and haematopoietic
 CC disorders including autoimmune diseases and allergies such as metal and
 CC pollen allergy
 XX
 SQ Sequence 2969 BP; 939 A; 618 C; 662 G; 750 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 2969
 Score: 3512.00 Matches: 661
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.70% Mismatches: 0
 Query Match: 99.55% Indels: 1
 DB: Gaps: 0
 US-10-006-265-17 (1-662) x AAC92337 (1-2969)
 QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetThrTrpThrPalaleu 20
 DB 523 ATGAAGCTCTCTCCCAAGCTTCATGTGTAACTGGGAGATGATGGACCTGGACATG 582
 QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
 DB 583 TGGATGCTCCCTCACTCTCAAAATTCAGCTGGCAGCTCTGCCAGCTAAAGCTGAGAAC 642
 QY 41 IleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 DB 643 ATTTCCGTGTCTACTACTATAGGAAAAATTAAACCTGCACCTTGGAGTCCAGAAAAAGAA 702
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysIleAspAsn 80
 DB 703 ACCAGTATACCCAGTACAGATTAGAGAACTTACCTTCGAGAAAAAATCATGATTAAT 762
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 DB 763 TGTACCAACCAATAGTCTTACAGTGAAGAAATCGTGTCTCTTTTCTTCCCAAGA 822
 QY 101 IleThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 DB 823 ATAACGATCCCAAGTATATTATACATTGAGTGAAGCTGAATAATGAGATGAGTAAAT 882
 QY 121 LysSerHisMetThrTyrTrpArgLysGluAsnIleAlaLysThrGluProProLysIle 140
 DB 883 AAATTCATATGACATCTGAGATTAGAAACATAGCGAAAACTGAACCACTTAAGATT 942
 QY 141 PheArgValLysProValLysGlyLysValArgMetIleGlnIleGluTyrPylLysPro 160
 DB 943 TTCGGTGTGAACCAAGTTTGGGCATCAACGAATGATTCAAATGATGAATAAAGCCT 1002

QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 DB 1003 GAGTTGGCGCCTGTTCATCTCATTTAAATACACCTTCGATTGAGACAGTCAACAGT 1062
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 DB 1063 ACCAGCTGATGAGTCAACTCTTCAGAACCCGTAAAGATTAATAACCAACCGTAAAC 1122
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
 DB 1123 CTCACGGGCTGAGCTTTTACAGATATGTCTCAATGCTCTGCGATGTCCGTCAAGAG 1182
 QY 221 SerLysPheTrpSerAspTrpSerGlnGlyLysMetCysMetThrGluGluAlaPro 240
 DB 1183 TCAGAGTTCTGGAGTGACCTGAGGCCAAGAAAAATGGAAATGATCGAGGAAGAAGCTCA 1242
 QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
 DB 1243 TGTGGCTGGAACTGTGGAGAGTCTGTAAACAGCTGAGCGGATGGAAGAGCGCAGTG 1302
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
 DB 1303 CGGTGTATGGAAGAGGCAAGAGGCCCAAGTCTTGAAGAAAACCTTGCTTCAAC 1362
 QY 281 IleTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 DB 1363 ATATGATCTATACCAAGAAAGCAACTAACCTCAGAAACATGAACTACTAACCAAG 1422
 QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSer 320
 DB 1423 CAGCTTGAACGTCACTCTGGAGGCGAGAGCTTTGGGTGTATGATATTTCTTAATAATCT 1482
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 DB 1483 CTGGGAAGTCTCCAGTGGCCACCTGAGGATTCAGACGATTCAGAAAAACATTTTCAG 1542
 QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSer 360
 DB 1543 TGCATTGAGTCATGACAGGCTCGGTGTGAGAGCAGACTAGTGGTGAAGTGGCAAGC 1602
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTyrPheProAspValAspSerGluPro 380
 DB 1603 TCTGCTCTAGAGGTGAACCTTGAGATGATGATGATTCGGAATGTGAACCTCAGAGCCC 1662
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
 DB 1663 ACCACCTTTCTGGGAATCTGTCTCAGGCCACGAACTGAGCAATCCAGCAAGTTAA 1722
 QY 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrPrometLeuHisAspLysValGly 420
 DB 1723 TTAAACCTTTCTGGGTATTAACATCTGTGTATCCAAATGTGATGACAAAGTTGAC 1782
 QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
 DB 1783 GAGCCATATTTCCATCCAGGCTTATGCCAAAGAGGGTTCATCCGAAAGCTCTGAGACC 1842
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 DB 1843 AAGGTGGAACATTTGGCGTAAGACGTTCAGATCACATGAAAGAGATTTCCCAAGAT 1902
 QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 DB 1903 GAGAGAAAGGATATCATCTGCAACTACACATCTTTACCAAGCTGAAGTGAAGAAAGGA 1962
 QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
 DB 1963 TTCTCCAGACAGTCAATTCAGCATCTTGCAGTACCGGCTGAGATCCCTGTAAGCAAG 2022
 QY 501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSer 520
 DB 2023 ACCTCTTAATGTTTCAGGTCAATGCGCAACCAAGTGTGGGGGAACCAACGGAGCACAGC 2082

QY 521 ILeaenPhelyThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db 2083 ATAAATTTCAAGACATTTGCTCATTCAGTGTCTTGAGATTATCTCAATAATCTTCTGATT 2142
 QY 541 G1yG1yLeuLeuIleIleIleIleLeuThrValAlaIleYrG1yLeuIleYsPheProaen 560
 Db 2143 GGTGAGGCGCTTCTTATCTCTCATTCATCTGACAGAGGCGATATGCTCTCAAAAACCCCAAC 2202
 QY 561 LysLeuThrHisLeuCysTrpProThrValPheProaenProAlaGluSerSerIleAlaThr 580
 Db 2203 AAATGACTCATCTGTGTGGCCCAACCGTTCACACCTGTGAAAGATATAGTACCCACA 2262
 QY 581 TrpHisG1yAAspPhePheLeuAAspIleLeuLeuIleYsG1ySerAAspAAspSerValaen 600
 Db 2263 TGGCATGAGATGATTTCAAGATTAAGCTTAACCTGAAAGAGCTGTGATGATCTTGTGAC 2322
 QY 601 ThrGluAAspAArgIleLeuIleYsPheCysSerThrProSerAAspIleValIleAAspIle 620
 Db 2323 ACAGAAACAGAGATCTTAAACCATGTTCCACCCCAAGTGAACAAAGTTGATGACAAAG 2382
 QY 621 LeuValValaenPheG1yAAsnValleuG1yIleIlePheThrAAspGluAlaArgThrGly 640
 Db 2383 TTGGTGTGAACCTTGGGAATGTTCTGCAAGAAATTTCAAGATGAAGCCAGAACGGGT 2442
 QY 641 G1yGlu-AAsnAenLeuG1yG1yGluIleAAsnG1yThrAArgIleLeuSerSerCysProTh 660
 Db 2443 CAGGAAACAACTTTAGAGGAGGAGAAAGATGGAGCTGAAATTTCTTCTTCTGCCCCAAC 2502
 QY 660 rSerIle 662
 Db 2503 TTCAATA 2509
 RESULT 9
 ABA93767
 ID ABA93767 standard; cDNA; 2386 BP.
 XX ABA93767;
 AC
 XX 01-MAY-2002 (first entry)
 DT
 XX Human zcytor17 cDNA sequence SEQ ID NO:1.
 -DE
 XX Zcytor17: chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone; disease;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200721-A2.
 PD 03-JAN-2002.
 XX
 PF 26-JUN-2001; 2001WO-US020484.
 PR 26-JUN-2000; 2000US-0214282P.
 PR 29-JUN-2000; 2000US-0214955P.
 PR 08-FEB-2001; 2001US-0267963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JI,
 PI Maurer MF;
 XX WPI: 2002-090519/12.
 DR P-PSDB: ABB05730.
 XX
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders.
 XX

PS Claim 2; Page 161-166; 235pp; English.
 XX
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
 CC zcytor17 antibodies are useful in stimulating cell-mediated immunity
 CC for stimulating lymphocyte proliferation, such as in the treatment of
 CC infections involving immunosuppression, including certain viral
 CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 2386 BP; 711 A; 525 C; 575 G; 575 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,75e-314 Length: 2386
 Score: 3465.50 Matches: 651
 Percent Similarity: 99.24% Conservative: 1
 Best Local Similarity: 99.09% Mismatches: 2
 Query Match: 98.23% Indels: 3
 Gaps: 1
 US-10-006-265-17 (1-662) x ABA93767 (1-2386)
 QY 3 LeuSerProGlnProSerCysValAAsnLeuG1yMetMetTrpThrAlaLeuTrpMet 22
 Db 138 CTCTCTCCCAAGCCCTTATGATGTTAACTGGGAGATGATGGAGCTGGCACTGTGATG 197
 QY 23 LeuProSerLeuCysIlePheSerLeuAlaAlaLeuProAlaIleProGluAAsnIleSer 42
 Db 198 CTCCCTCAGCTTCGAAATTCAGCTGAGCTGCGAGCTGCGAGTAAAGCTGAGAAATTTCC 257
 QY 43 CysValIleYrYrYrAArgIleAAsnLeuThrCysThrTrpSerProG1yIleG1yThrSer 62
 Db 258 TGTGTCTACTACTCTATGAGAAATTTTAACTGCAGCTTGAGATCCAGAGAAAGAAACAGT 317
 QY 63 TyrThrGlnIleYrThrValIleAArgThrTyrAlaPheIleGluIleYsHsaAAspAAspCysThr 82
 Db 318 TATACCCAGTACACAGATTAAGAGAACTTACGCTTTTGAGAAAAAAGATGATATGTGACA 377
 QY 83 ThrAAsnSerSerThrSerGluAAsnAArgAlaSerCysSerPhePheLeuProAArgIleThr 102
 Db 378 ACCAATGATCTACAGATGAGAAATCGTCTTCTGCTCTTTTCTTCCCAAGAAATTAAG 437
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 QY 123 HisMetThrIleYrTrpAArgLeuAAsnIleAlaIleYsThrGluProPheIlePheArg 142
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 QY 143 ValIleProValIleuG1yIleYsAArgMetIleGlnIleGluTrpIleYsProGluLeu 162
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 QY 163 AlaProValSerSerAAspLeuIleYrYrThrLeuAArgPheAArgThrValAAsnSerThrSer 182
 Db 618 GCGCTGTGTTCACTGATGATTTAAATACACACTTGATGAGACAGTCAACAGTACAGC 677
 QY 183 TrpMetGluValaenPheAlaIleAAsnAArgIleAAspIleAAsnGlnIleYrAAsnLeuThr 202
 Db 678 TGGATGAGATGCACTTCGCTTAAGAACCTGTAAGATTAACCAACCAAGTCAACCTCAGC 737
 QY 203 G1yLeuGlnProPheThrGluIleYrValIleAlaLeuAArgCysAlaValIleYsGluSerIle 222

Db 738 GGGCTCAGCGCTTTTACAGAAATATGTCATAGCTCTGCGAGTGTGCGGTCAAGAGTCAAG 797
 Qy 223 PheTrpSerAspTrpSerGlnGluYsMetGlyMetThrGluGluGluAlaProCysGly 242
 Db 798 TTCTGGAGTACCTGGAGCCCAAGAAAAATGGAAATGACTGAGGAAGAGTCCATGTGGC 857
 Qy 243 LeuGluLeuTrpArgValLeuYsProAlaGluAlaAspGlyArgProValArgLeu 262
 Db 858 CTGGAACTGGAGAGTCTCGAAACAGCTGAGGCGGATGAGAAAGGCGAGTGGTGG 917
 Qy 263 LeuTrpLeuValAlaArgGlyAlaProValLeuGluLeuYsThrLeuGlyYsAsnIleTrp 282
 Db 918 TTATGGAAAGAGGCAAGAGAGCCCACTCTAGAGAAAACTGTGCTACCAATATGG 977
 Qy 283 TyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnLeu 302
 Db 978 TACTATCCAGAAAGCAACACTAATCTCAGAAACCAATGAACTACTAATCCAGAGCTT 1037
 Qy 303 GluLeuHileuGlyGlyGlySerPheTrpValSerMetIleSerYsAsnSerLeuGly 322
 Db 1038 GAATCTCATCTGGAGGCGAGAGCTTTGGGTGTCTATGATTCTTATATCTCTTGGG 1097
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 Db 1158 GAGGTATGCAAGGCGCTGCTGCTGAGAGCACTAGTGTGAAATGGCAAGCTCTGCT 1217
 Qy 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
 Db 1218 CTGAGGTGAAACCTTGATGATTGAATGGTTCCGAGTGTGAGCTCAGAGCCCAACACC 1277
 Qy 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspYsLeuYs 402
 Db 1278 CTTTCCGGAACCTGTGTCTCAGGCCACGAACCTGACGATCCAGCAAGATTAATTAATA 1337
 Qy 403 ProPheTrpCysTrpAsnIleSerValYsProMetLeuHileAspYsValGlyGluPro 422
 Db 1338 CTTTCTGGTGTCTATTAACATCTGTGTATCCAAATGTTGATATCAAAAGTGGCGAGCCA 1397
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 Db 1398 TATTCATCCAGGCTTATGCCAAAGAGGCTTCATCAGAAAGTCTCGAGCAAGAGTGG 1457
 Qy 443 GluAsnIleGlyValYsThrValIleThrIleTrpYsGluIleProYsSerGluArg 462
 Db 1458 GAAACAATTTGGCTGGAAGAGGTCAAGATCCACATGAAAGAAAGATTTCCCAAGATGAGA 1517
 Qy 463 YsGlyIleIleCysAsnYsTrpIlePheYsGlnAlaGluGlyGlyYsGlyPheSer 482
 Db 1518 AAGGATATCATCTGCAACTACACCATCTTTACCAAGCTGAGAGTGAAGAAAGATTTCTCC 1577
 Qy 483 YsThrValAsnSerSerIleLeuGlnYsGlyLeuGluSerLeuYsArgYsThrSer 502
 Db 1578 AAGACAGTCAATCCAGCATCTTGACAGTAGGCGCTGGAAGTCCCTGAACCAAGACCTCT 1637
 Qy 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyYsThrAsnGlyYsThrSerIleAsn 522
 Db 1638 TACATTTGTCAGGTCAAGTGGCACACCAAGTGGGGGAACCAACGGGACACACATTAAT 1697
 Qy 523 PheYsThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
 Db 1698 TTCAAGACATTTGATTCAGTGTCTTGAGATTATCTCTCAATACCTCTCTGATTGGTGA 1757
 Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaYsGlyLeuYsYsProAsnYsLeu 562
 Db 1758 GGCCTTCTTATCTCATATTATCTGACAGTGGCATATGTTCTCAAAAAACCAACAATTG 1817
 Qy 563 ThrIleLeuYsTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
 Db 1818 ACTCATCTGTGTGGCCACCGTTCACACCTGTGAAAGTAGTATAGCCACATGGCAT 1877

Qy 583 GLYAspAspPheLeuAspYsLeuAsnLeuYsGluSerAspAspSerValAsnThrGlu 602
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 Qy 603 AspArgIleLeuYsProCysSerThrProSerAspYsLeuValIleAspYsLeuVal 622
 Db 1938 GACAGGATCTTAAACCAATGTTCCACCCCACTGTGCAACTGTGTGATGACAAAGTTGGTG 1997
 Qy 623 ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
 Db 1998 GTGAAGTGTGGAAATGTTCTGCAAGAAATTTTCAAGATGAAGCCGAACGGGTCAAGAA 2057
 Qy 643 AsnAsnLeuGlyGlyGlyYsAsnGlyThrArgIleLeuSerSerCysPro 659
 Db 2058 AACAAATTTAGAGGGGAAAGAAATGGG-----TATGTACCTGCCCC 2099
 RESULT 10
 ADL26673
 ID ADL26673 standard; cDNA; 2402 BP.
 XX
 AC ADL26673;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human cytokine receptor zcytor17 DNA seqid 110.
 KW antiinflammatory; antiulcer; dermatological; antifallergic; antipsoriatic;
 KW antibacterial; immunosuppressive; cell proliferation inhibitor;
 KW immune response inhibitor; inflammatory response inhibitor;
 KW multicentric cytokine receptor; heterodimeric cytokine receptor; cancer;
 KW cytokine-binding domain; class I cytokine receptor; hematopoietic cell;
 KW zcytor17lig-induced proliferation; zcytor17lig-induced differentiation;
 KW hematopoietic progenitor cell; zcytor17lig-induced inflammation;
 KW inflammatory disease; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease; atopic dermatitis; eczema; psoriasis; endotoxaemia;
 KW septicemia; toxic shock syndrome; zcytor17; human; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003215838-A1.
 XX
 PD 20-NOV-2003.
 XX
 XX 21-JAN-2003; 2003US-00351157.
 PR 18-JAN-2002; 2002US-0350325P.
 PR 14-JUN-2002; 2002US-0389108P.
 PR 19-DEC-2002; 2002US-0435361P.
 XX
 XX (SPRE/) SPRECHER C A.
 PA (GAOZ/) GAO Z.
 PA (KUI/) KUIJPER J L.
 PA (DASO/) DASOVICH M M.
 PA (GRAN/) GRANT F J.
 PA (PRES/) PRESNEL S R.
 PA (WHIT/) WHITMORE T E.
 PA (HAMM/) HAMMOND A K.
 PA (NOVA/) NOVAK J E.
 PA (GROS/) GROSS J A.
 PA (DILL/) DILLON S R.
 XX
 PI Sprecher CA, Gao Z, Kuijper JL, Dasovich MM, Grant FJ;
 PI Presnell SR, Whitmore TE, Hammond AK, Novak JE, Gross JA, Dillon SR;
 XX MPI; 2003-876545/81.
 DR P-PSDB; ADL26674.
 XX
 PT Novel multicentric or heterodimeric cytokine receptors useful for treating
 PT chronic inflammatory disease such as inflammatory bowel disease,
 PT ulcerative colitis, acute inflammatory disease such as endotoxaemia,
 PT septicemia.
 XX

PS Disclousure; SEQ ID NO 110; 205pp; English.

XX The invention describes an isolated multimeric or heterodimeric cytokine receptor (I) having at least one polypeptide having 90 percent sequence identity with a 732 (S1) or 649 (S2) amino acid sequence given in specification, and where (I) binds a ligand comprising a 164 (S3) amino acid sequence, given in specification, or at least one polypeptide comprising residue 20-227 of (S1). (I) is useful for killing cancer cells and producing an antibody to (I) and a cytokine-binding domain of a class I cytokine receptor. A composition (CI) comprising (I) and a cytokine-binding domain of a class I cytokine receptor and a vehicle is useful for: reducing haematopoietic cells and hematopoietic progenitor cells in a mammal; inhibiting zcytoir17lig-induced proliferation or differentiation of hematopoietic cells and hematopoietic progenitor cells, reducing zcytoir17lig-induced inflammation; creating a mammal afflicted with an inflammatory disease in which zcytoir17lig plays a role. The disease is a chronic inflammatory disease such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, atopic dermatitis, eczema and endotoxaemia, septicemia, toxic shock syndrome and infectious disease. An immune response inhibiting composition is useful for inhibiting an immune response in a mammal exposed to an antigen or pathogen. An inflammatory response inhibiting composition is useful for suppressing an inflammatory response in a mammal with inflammation. An antibody that specifically binds to (I) is useful for detecting the presence of a multimeric or heterodimeric cytokine receptor in a biological sample. This sequence encodes a human zcytoir17 cytokine receptor that can be used in a comparison with other zcytoir17 receptors.

CC Sequence 2402 BP; 713 A; 532 C; 580 G; 577 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,78e-314 Length: 2402
Score: 3465.50 Matches: 651
Percent Similarity: 99.24% Conservatave: 1
Best Local Similarity: 99.09% Mismatches: 2
Query Match: 98.23% Indels: 3
DB: 11 Gaps: 1

US-10-006-265-17 (1-662) x ADL26673 (1-2402)

Oy 3 LeuSerProGlnProSerCyValAsnLeuGlyMetMetTrpThrTrpAlaLeuTrpMet 22
Db 138 CTCTCTCCCGACCTTCAATGTTTAACTGGGGAATGATGGACCTGGACCTGGATG 197
Oy 23 LeuProSerLeuCyValPheSerLeuAlaLeuProAlaLeuProGluAsnLeuSer 42
Db 198 CTCCTCACTCTGCAAAATTCAGCTGGCAGCTGCCAGCTAAAGCTGAAGAACTTCC 257
Oy 43 CyValAlaLeuTrpTrpTrpAlaLeuAsnLeuTrpCyValTrpSerProGluValGluTrpSer 62
Db 258 TGTGCTCTACTAATAGAAAATTTAACTGACCTGGAGTCCAGAAAGAAACCACT 317
Oy 63 TyrTrpGlnTyrThrValIleAspThrThrTyrAlaPheGlyGluValAspAsnCyThr 82
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Oy 83 ThrAsnSerSerThrSerGluAsnArgIleSerCySerPhePheLeuProArgIleThr 102
Db 378 ACCAATAGCTTCAACAGTGAATGCTGCTGCTCTTTTCTTCCCAAGATAACG 437
Oy 103 IleProAspAsnTyrThrIleGluValIleGluValAsnGlyAspGlyValIleAspSer 122
Db 438 ATCCAGATTAATTAATACATTAAGGTGAAGCTGAATAAGAGAGTGAATTAATCT 497
Oy 123 HisMetTrpTyrTrpArgLeuGluAsnIleAlaValThrGluProProGlyIlePheArg 142
Db 498 CATATGACATCTGAGATTAAGAACTAAGCAAACTGAACCACTTAAGATTTTCCGT 557
Oy 143 ValIleProValLeuGlyIleValArgMetIleGlnIleGluTrpIleValProGluLeu 162
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Oy 163 AlaProValSerSerAspLeuValSerTyrThrLeuArgPheArgThrValAsnSerThrSer 182
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Oy 183 TrpMetGluValAsnPheAlaIleAspAsnArgIleAspValAsnGlnTrpTyrAsnLeuThr 202
Db 678 TGAATGAAAGTCAACTTGGTAAAGACGTTAAGATTAATAAAGCAACGTAACCTCAGC 737
Oy 203 GlyLeuGlnProPheTrpGluTyrValIleAlaLeuArgCyValAlaValGluSerIleAs 222
Db 738 GGGCTGACGCTTTTAAAGAAATGATGATGCTTGGCATTTGGGCTCAAGAGTCAAG 797
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Oy 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluValSerPheGlnCysIle 342
Db 1098 AAGTCTCAGAGGCGACCTGAGGATTCACAGTATTCAGAAATAATCACTTCACTG 1157
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Db 1158 GAGGTCAAGAGGCTGGTGTGCTGAGAGACCAAGCTAGAGTGAAGTGAAGTGAAGT 1217
Oy 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db 1218 CTAGACGTGAACCTTGATGATTAATGATGTTCCGATGTGAGCTCAGAGCCACACACC 1277
Oy 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLeuVal 402
Db 1278 CTTTCTGAGAAATCTGTCTCAGGCCAGCACTGACGATCCAGAAATTAATTAATA 1337
Oy 403 ProPheTrpCyThrAsnIleSerValTyrProMetLeuHisAspValValGlyValPro 422
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Oy 423 TyrSerIleGlnAlaTyrAlaValGluGlyValProSerGluGlyProGluThrIleVal 442
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Oy 443 GluAsnIleGlyValIleThrValThrIleThrTrpValGluIleProValSerGluArg 462
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Db 1518 AAGGTATCACTGCAACTACATCTTTTAACTGAACCTGAAGGTGAAGAAAGATTCCTC 1577
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Db 1578 AAGACATCAATTCACATCTTGCAATACGCGCTGAGAGTCCCTGAAGCAAGAACTCT 1637
Oy 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
Db 1638 TACATTTGTCAGGTCAAGGCGACAGACAGTGGGGAACCAACGAGCAAGCATTAAT 1697
Oy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542

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Db      1698 TTCAGACATTCATTCAGTCCTTGACATTATCCTCATTAACCTTCGATTGGGGA 1757
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Qy      563  ThrHisLeuCytrProThrValProAsnProAlaGluSerSerIleAlaThrTPHis 582
Db      1818 ACTCATCTGTGTGGCCACCGTTCCCAACCTGCTGAAGGTATAGCCACATGGCAT 1877
Qy      583  GlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsnThrGlu 602
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Qy      603  AspArgLysLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db      1938 GACAGGATCTTAAACCATTCACCCCGACGACAAAGTGTGATTTGACAAAGTTGGTG 1997
Qy      623  ValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db      1998 GTTAACTTTGGGATGTCTTCAGAGAAATTTTCACAGATTAAGCCAGAACGGGTACAGAA 2057
Qy      643  AsnAsnLeuGlyGlyGlyLysAsnGlyThrArgIleLeuSerSerCysPro 659
Db      2058 AACAAATTAGAGAGGAGAAAGAAATGGG-----TATGTGACCTGTGCCCC 2099

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RESULT 11
AAB38772 standard; cDNA; 2480 BP.
AC      AAD38772;
XX      23-SEP-2002 (first entry)
DE      Human haematopoietin receptor 1 (HPRI) cDNA.
XX      Human haematopoietin receptor; receptor; HPRI; HPR2; cell proliferation;
KM      pancytopenia; leukopenia; anaemia; thrombocytopaenia; osteoporosis;
KM      neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
KM      cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
KM      ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
KM      osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;
KM      anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
KM      demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
KM      vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
KM      stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
KM      ischaemic disease; gene; ss.
XX      Homo sapiens.
XX      Location/Qualifiers
FH      Key      132..2369
FT      CDS      /tag= a
FT      /product= "Human HPRI protein"
FT      /transl_except= (pos:1680..1682, aa:Asn)
FT      /note= "This region is specifically claimed as SEQ ID NO:
FT      5 in claim 6 of the specification"
FT      sig_peptide 191..227
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FT      mat_peptide 228..2366
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FT      /product= "Human mature HPRI protein"
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FT      variation replace(633, G)
FT      /tag= e
FT      variation replace(691, G)
FT      /tag= f
FT      variation replace(1212, G)
FT      /tag= g
FT      variation replace(1216, G)
FT      /tag= h

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FT      variation replace(1660, G)
FT      /tag= i
FT      variation replace(1680, G)
FT      /tag= j
FT      variation replace(2166, G)
FT      /tag= k
XX      MO200229060-A2.
XX      11-APR-2002.
XX      05-OCT-2001; 2001WO-US031634.
XX      06-OCT-2000; 2000US-0238706P.
XX      13-OCT-2000; 2000US-0240476P.
XX      20-FEB-2001; 2001US-0270282P.
XX      (IMMV ) IMMUNEX CORP.
XX      Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR,
PI      WPI, 2002-330172/36.
DR      P-PSDB; AAE24024.
XX      Human and murine haematopoietin receptor polypeptides HPRI and HPR2,
PT      useful for treating cell proliferation, metabolic, and reproductive
PT      hormone related conditions.
XX      Claim 6; Page 83-84; 136pp; English.
XX      The present invention relates to human and murine haematopoietin receptor
XX      polypeptides HPRI and HPR2. Sequences of the invention are useful for
XX      treating cell proliferation conditions e.g., pancytopenia, leukopenia,
XX      anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis
XX      resulting from a lack of bone-forming cells. They are also useful for
XX      treating cell proliferation conditions such as leukaemia and tumour
XX      metastasis, osteoporosis resulting from an excess of bone-resorbing
XX      cells. HPR sequences are also useful for treating medical conditions and
XX      diseases such as cell proliferation, metabolic and reproductive hormone
XX      related conditions. They are useful for treating various haematologic and
XX      oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
XX      carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
XX      cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
XX      cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
XX      sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
XX      squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
XX      of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
XX      dysplastic syndromes (including refractory anaemia, refractory anaemia
XX      with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
XX      penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
XX      myeloid metaplasia, osteoclast disorders that lead to bone loss such as
XX      osteoporosis including post-menopausal osteoporosis, periodontitis
XX      resulting in tooth loosening or loss, prosthesis loosening after joint
XX      replacement, neurodegenerative conditions (e.g., acute polynuropathy,
XX      Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
XX      dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
XX      Guillain-Barre syndrome, vertebral disc disease, stroke including
XX      myasthenia gravis, chronic neuronal degeneration, Gulf war syndrome,
XX      cerebral ischaemic diseases. HPRI and HPR2 polypeptides are also useful
XX      for treating various other disorders such as osteoporosis, obesity,
XX      deficient mammary development and infertility. The present sequence is
XX      human HPRI cDNA

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Seq Sequence 2480 BP; 722 A; 558 C; 600 G; 600 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.91e-314 Length: 2480
Score: 3465.50 Matches: 651
Percent Similarity: 99.09% Conservative: 2
Best Local Similarity: 98.79% Mismatches: 3
Query Match: 98.23% Indels: 3
DB: 6 Gaps: 1

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Db	1272	ACCAACCTTCTCTGGGAATCTGTCTCTCAGGCCACGAATCGAGATCCAGCAAGATAA	1331
QY	401	LeuIysProPheTrpCysTrpAsnIleSerValTrpProMetLeuHisAspIysValGly	420
Db	1332	TTAAAACTTCTCTGGTCTATACATCTCTGTATCCAAATGTTCATGACAAAGTTGGC	1391
QY	421	GluProTrpSerTrileGlnIleTrpAluIysGluIleValProSerGluIleProGluThr	440
Db	1392	GAGCCATATTCATCTCCAGGCTTATGACCMAAAGAGCGTTCATGAAAGATCTTGAGACC	1451
QY	441	LysValGluAsnIleGlyValIysThrValThrIleThrTrpIysGluIleProIysSer	460
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Db	1512	GAGAGAAAGGCTATCATCTGCATCCACATCCATCTTTATCCAAAGCTGAAGGTGAAAAAGGA	1571
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QY	521	IleAsnPheIysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle	540
Db	1692	ATAAAATTCAGACATCTGTCATGAGTCTTGAAGATTATCCCATPAACCTTCTCTGATT	1751
QY	541	GlyIleGlyIleLeuIleIleIleIleLeuThrValAlaTrpGlyLeuIysIysProAsn	560
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QY	561	LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr	580
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QY	581	TrpHisGlyAspAspPheIysAspIysLeuAsnLeuIysGluSerAspAspSerValAsn	600
Db	1872	TGGCATGTGAGATGATTTCAAGATPAACCTAAACCTGAAGAGGTCTGATGACTCTGTGAAC	1931
QY	601	ThrGluAspArgIleLeuIysProCysSerThrProSerAspIysLeuValIleAspIys	620
Db	1932	ACAGAAAGCAGGATCTTAAACCAATGTTCACCCCAAGTCGACAAATGGTGATTAACAG	1991
QY	621	LeuValValAsnPheGlyAsnValLeuGlnIleIlePheThrAspGluAlaArgThrGly	640
Db	1992	TTGGTGGTGAACCTTTGGGAAGTTCTCTCAAGAAATTTTCCACAGATGAAGCAGAACGGGT	2051
QY	641	GlnGluAsnAsnLeuGlyIleGlyIleIysAsnGlyThrArgIleLeuSerSerCysPro	659
Db	2052	CAGCAAAAAATATTAGAGGGGCAAAAGAAATGGG-----TATGTGACCTGCCCC	2099
RESULT 12			
ACF36434			
ID	ACF36434 standard; cDNA; 2481 BP.		
XX	ACF36434;		
AC	18-DEC-2003 (first entry)		
XX	Human type-1 cytokine receptor, GLM-R encoding cDNA.		
DT	GLM-R; type-1 cytokine receptor; gene therapy; gene mapping; human;		
XX	transgenic; gene; 88.		
KM			


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XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 63..2261
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FT /product= "GLM-R"
FT /note= "type-1 cytokine receptor"
FT sig_peptide 63..119
FT /*tag= b
FT mat_peptide 120..2258
FT /*tag= c
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XX MO2003072740-A2.
XX
XX 04-SEP-2003.
XX
XX 24-FEB-2003; 2003WO-US005616.
XX
XX 25-FEB-2002; 2002US-0359806P.
XX
XX (GETH ) GENENTECH INC.
XX
XX De Sauvage FJ, Ghilardi NP, Goddard A, Godowski PJ, Grimaldi CJ,
XX Gurney AL, Wood WI;
XX
XX WPI; 2003-712721/67.
XX
XX P-PSDB; ABR82790.
XX
XX New isolated nucleic acid molecule encoding a GLM-R polypeptide, useful
XX for treating disorders characterized by the over or under abundance of
XX monocytes or macrophages.
XX
XX Claim 3; Fig 1; 156pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
XX type-1 cytokine receptor GLM-R polypeptide. The nucleic acid molecules,
XX polypeptides, antibodies, agonists or antagonist, and compositions are
XX useful for treating disorders characterized by the over or under
XX abundance of monocytes or macrophages. The nucleic acid molecules are
XX useful as hybridization probes, in chromosome and in gene mapping, and in
XX generating antisense RNA or DNA. The present sequence represents a cDNA
XX encoding a human GLM-R polypeptide
XX
XX Sequence 2481 BP; 729 A; 553 C; 603 G; 596 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,91e-314 Length: 2481
XX Score: 3465.50 Matches: 651
XX Percent Similarity: 99.24% Conservative: 1
XX Best Local Similarity: 99.09% Mismatches: 2
XX Query Match: 98.23% Indels: 3
XX DB: 10 Gaps: 1
XX
XX US-10-006-265-17 (1-662) x ACF36434 (1-2481)
XX
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XX |||
XX 30 CTCCTCCAGAGCTTCATGTGTTAACTGGGATGATGAGACCTGGGCACTGTGGATG 89
XX |||
XX 23 LeuProSerLeuGlyPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
XX |||
XX 90 CTCCTTCACCTGCAAAATTCAGCTGCGAGCTCTGCACTGAAGCTGAGAACATTTCC 149
XX |||
XX 43 CysValIleTyrTyrAlaGlyAsnLeuThrCysThrTrpSerProGlyIleGluThrSer 62
XX |||
XX 150 TGGTGCTACACAAATGAGAAAATTTAACTGCACCTTGAGTCAGGAAAGGAAACCACT 209
XX |||
XX 63 TyrThrGlnIleTyrThrValIleAspArgThrTyrAlaPheGlyGlyIleLysHisAspAsnCysThr 82
XX |||
XX 210 TATTAACCAAGTACAGATTAAAGAACTTACGCTTTGGAGAAAACATGATAATGTACA 269
XX |||
XX 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArgIleThr 102
XX |||
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DB 270 ACCAATAGTTCTACAAAGTGAATAATCGTCTGTCTCTTTTTCCTCCAGAAATTAAG 329
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DB 390 CATATGACATACTGAGATTAAGAAACATGAGAAACCGAACCTTAAGATTTTCGGT 449
DB |||
DB 143 ValLysProValIleuGlyTlleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
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DB 450 GTGAAACCGAGTTTGGGCATCAAAACGAATGATCAAAATGAATGATTAAGCTGAGTTG 509
DB |||
DB 163 AlaProValSerSerPheSerLeuLysTyrThrLeuAspPheArgThrValAsnSerThrSer 182
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DB |||
DB 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
DB |||
DB 570 TGGATGGAAGTCACTTCGCTTAAGAACCTTAAGATTAATAACCAACGTAACCTCAAG 629
DB |||
DB 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
DB |||
DB 630 GGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGCGGTCAAAGAGTCAAG 689
DB |||
DB 223 PheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGlnGluAlaProCysGly 242
DB |||
DB 690 TTCTGGAGTACTCGGAGCCCAAGAAAATGGAATGACTGAGAGAAAGAACCTCAATGTGC 749
DB |||
DB 243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262
DB |||
DB 750 CTGGAACCTGTGAGAGTCTCTGAACCAAGCTGAGGGGAGTGAAGAAAGCCAGTGGGTTG 809
DB |||
DB 263 LeuTrpLysValAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
DB |||
DB 810 TTAATGGAAGAAAGCAAGAGAGACCCCAAGTCATGAGAAAACCTGGCTACAAACATATG 869
DB |||
DB 283 TyrTrpProGlnSerPheAsnThrAsnLeuThrGluTrpMetAsnThrThrAsnGlnIleu 302
DB |||
DB 870 TACTATCCAGAAAGCAACCTAACTCACAGAAACATATACATCTAACCAAGCAGCTT 929
DB |||
DB 303 GluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
DB |||
DB 930 GAACCTCATCTGGAGGCGAGAGCTTTGGGTGTCTATGATTTCTTAATAATCTCTGGG 989
DB |||
DB 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle 342
DB |||
DB 990 AAGTCTCCAGTGGCCACCTGAGGATTCAGCTAATCAAGAAAATCATTTCAAGTGCATT 1049
DB |||
DB 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAla 362
DB |||
DB 1050 GAGGTGATCAGAGCCCTGCTGTCTGAGGACAGCTAGTGTAAGTGGCAAGGCTGTGCT 1109
DB |||
DB 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
DB |||
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DB 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
DB |||
DB 1170 CTTTCTCGGGAATCTGTGCTCAGGCGACGAGACATGAGATCAAGATTAATTAATA 1229
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DB 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro 422
DB |||
DB 1230 CCTTCTGTGTCTATTAACATCTCTGTGTAATCCAAATGTGCATGACAAATTTGGCGAG 1289
DB |||
DB 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal 442
DB |||
DB 1290 TATTCATCAAGCTTTATCCAAAGAGCGTTCCATCGAAGGCTCTGAGACCAAGTG 1349
DB |||
DB 443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 462
DB |||
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Dh 1350 GAGAACATTGGCGTGAAGACGGTCAACATGACATGAGAAAAGAGATTCCCAAGAGTGAGAGA 1409
Qy 463 LygellYIlelleCybaantYrThrllePhetyrGlnalagluYgilyLysGlyPheSer 482
Dh 1410 AAGGGGATCATCTGCATACACCATCTTTTACCAGCTGAAGGTGAGAAAAGATTCTCC 1469
Qy 483 LysrThValaasSerSerlleleuGlnYrGlyleuGlnuSerleuYArGlyrThSer 502
Dh 1470 AAGACAGCAATTCAGACATCTTGACAGTACGGCTGAGGTCCCTGAAAAGAAAGCTCT 1529
Qy 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyYrThraSnglyThrSerlleaSn 522
Dh 1530 TACATGTTGTCAGTCATGTCAGCCAGACCACTGCTGGGGAACCAACGGACCATTAAT 1589
Qy 523 PheYrThrLeuSerPheSerValPheGluIlelleuIleThrSerleuIleGlyGly 542
Dh 1590 TTCAGACATGTCATTCAGTCTTGTGAGATTACCCATTAACCTTCGATTGTGGA 1649
Qy 543 GilyleuLeuIlelleuIlelleuThrValAlaTyrGlyleuYrGlyleuYrGlyleu 562
Dh 1650 GGCTTCTTATTCATTCATTCCTGACAGTGGCATATGCTCAAAAACCCAAACAAATTG 1709
Qy 563 ThrIleleuCyStrProThrValProaAnProAlaGlySerSerlleaIleThrTrpHis 582
Dh 1710 ACTCATCTGTGTGGCCCAACCGTTCCCAACCTGCTGAAGATGATGACCATGGCAT 1769
Qy 583 GilyaPAPheYrAaPlyleuAaSnleuYrGlyuSerAaPAPSerValaSnThrGlu 602
Dh 1770 GGAATGATTCAGATACATTAACCTGAAGAGTGTGATGATCTGTGAACACAGAA 1829
Qy 603 AaPAPGlyleuYrProCySerThrProSerAaPlyleuValIleAaPlyleuVal 622
Dh 1830 GACAGGATCTTAACCAAGTTCACACCCAGTGAACAGTGTGATGACAAAGTGTG 1889
Qy 623 ValaSnPheGlyAaSnValleuGlnIuIlePheThraPAGluAlaArgThrGlyGlnIu 642
Dh 1890 GTGAACCTTGGGAATGTTCTGCAGAAATTTTCAAGATGAAGCAAGACGGGTGAGAA 1949
Qy 643 AaSnleuGlyGlyGlyleuAaSnGlyThraGlyleuSerSerCyPro 659
Dh 1950 AACCAATTAGGAGGAGGAGAAAGATGG-----TATGTGACCTGCCCC 1991
RESULT 13
ID AB083365 standard; cDNA; 2952 BP.
XX AC AB083365;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.4 splicing variant encoding cDNA SEQ ID NO:5.
XX
KW NR10, splicing variant; haematopoietin receptor; immunomodulator;
KW haematopoietic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
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OS Homo sapiens.
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FH Key Location/Qualifiers
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FT /tag= a
FT /product= "NR10.4"
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PN MO30277230-A1.
XX
PD 03-OCT-2002.
XX
PF 22-MAR-2002; 2002MO-JP002769.
XX
PR 26-MAR-2001; 2001JP-00087298.
XX
PA (CHUS) CHUGAI SEIVAKU KK.
XX

PI Maeda M, Yaguchi N, Hasegawa M;
XX
XX WPI; 2003-018925/01.
DR P-PSDB; ABP54365.
XX
XX NR10 splicing variants of hematopoietin receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases.
XX
XX Claim 1; Fig 7-9; 250pp; Japanese.
XX
XX The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (i) have immunomodulator and haematopoietic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietin receptor genes participate in
CC in vivo immunomodulation and haematopoietic cell regulation, and in the
CC search for haematopoietic factors capable of functionally binding to the
CC receptors. The present sequence encodes the human NR10.4 protein from the
CC present invention
XX
SQ Sequence 2952 BP; 821 A; 688 C; 727 G; 716 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3,74e-314 Length: 2952
Score: 3465.50 Matches: 651
Percent Similarity: 99.24% Conservative: 1
Best Local Similarity: 99.09% Mismatches: 2
Query Match: 98.23% Indels: 3
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Qy 23 LeuProSerleuCyLysPheSerleuAlaAlaLeuProAlaLysProGlnAaSnIleSer 42
Dh 130 CTCCTCCCAAGCCTTCATGTTAACTGGGAGATGATGACCTGGGACCTGGATG 189
Qy 43 CyValaTyrTrpTrpArgLysAaSnleuThrCyThrTrpSerProGlyLysGluThrSer 62
Dh 190 TGCTCTACTACTATAGGAAAAATTTAACTGCACTTGAGTCCAGAAAGAAACCAAGT 249
Qy 63 TyrThrGlnYrThrValaLysArgThrTyrAlaPheGlyGlyuYrHisAaPAPSerCyThr 82
Dh 250 TATACCAAGTACACAGTTTAAGAGAACTTACGCTTTGGAGAAAACATGATTAATTGACA 309
Qy 83 ThrAaSerSerThrSerGluAaSnArgAlaSerCySerPhePheLeuProAlaIleThr 102
Dh 310 ACCAATAGTTCTACNACTGAAGAAATCGGTCTGCTCTTTTCCCTTCAAGATTAACG 369
Qy 103 IleProAaSnYrTrpTrpIleGluValGluAlaGluAaSnGlyAaPlyValIleLysSer 122
Dh 370 ATCCAGATTAATTAACATGAGGTGAAGCTGAAGATGAAGATGATTAATTAATCT 429
Qy 123 HisMetThrYrTrpArgLeuGluAaSnIleAlaLysThrGluProProlYsIlePheArg 142
Dh 430 CATATGACATACATGAGATTAAGAGAACATAGCGAAACATGACCACTTAAGATTTCCGT 489
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Qy 163 AlaProValSerSerAaPlyleuYrThrThraPheArgPheArgValaAaSerThrSer 182
Dh 550 GGCCCTGTTCACTGATTTAAATACACACTTCGATTCAGACAGTCAACAGTACACAGC 609
Qy 183 TrpMetGluValaSnPheAlaLysAaSnArgLysAaPlyAaSnGlnIleThrYrAaSnleuThr 202
Dh 610 TGATGAGATGCAACTTCGCTTAAGAACGTAAGATTAAGAAACCAAGTCAACCTCACG 669

QY 203 GYLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValysGlnSerLys 222
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 QY 223 PheTTPSerAspTTPSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly 242
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 DB 850 TTATGGAGAGGAGCAAGAGAGCCCAAGTCTTAGAGAAACACTTGGCTACACATATGG 909
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 DB 1030 AAGTCTCAGATGGCCACCTGAGATTTCCAGTATTTCAAGAAATCATTTGCTGATTCAT 1089
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 DB 1210 CTTTCTGGGAATCTGTGTCTCAGGCCAGAACATGAGCATCCAGCAAGATTAATTAATA 1269
 QY 403 ProPheTTPCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro 422
 DB 1270 CTTTCTGGGTATTAACATCTGTGTATCCAAATGTGCATCAAAAGTTGGCAGACCA 1329
 QY 423 TTTTTPSerIleGlnAlaTyrAlaLysGlnGlyValProSerGlnGlyProGluTTPThrLysVal 442
 DB 1330 TATTCATCCAGGCTTATGCCAAGAGGCTTCCATCAGAGGCTCTGAGACCAAGGTG 1389
 QY 443 GluAsnIleGlyValLysThrValThrIleThrTTPLysGluIleProLysSerGluArg 462
 DB 1390 GAGAACATTTGGCGTGAAGCGTCAAGATCATGAAAGAGATTCCTCAAGAGTGAAGA 1449
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 DB 1450 AAGGGTATCATCTGCAACTACACCATCTTTTCAAGCTGAAAGTGAAGAAAGATTTCTCC 1509
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 QY 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
 DB 1630 TTCAAGACATTTGCATTCAGTGTCTTGAAGATTAATCTCTTAATCTCTGATGGTGGGA 1689
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 DB 1690 GGGCTTCTATTTCTCATATCTGACAGTGGCATATGGTCTCAAAAACCCCAAAATTTG 1749
 QY 563 ThrHisLeuCysTTPProThrValProAsnProAlaGlnSerSerIleAlaThrTTPHis 582

DB 1750 ACTCATCTGTGTGGCCACCCTTCCAACTCTGTCGAAGATGATAGCCACATGGCAT 1809
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 DB 1930 GTGAACCTTGGGAATGTTCTGCAAGAAATTTTCACAGATGAAGCCAGAACGGGTGAGGA 1989
 QY 643 AsnAsnLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysPro 659
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 RESULT 14
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 ID ABO83364 standard; cDNA; 5271 BP.
 AC ABO83364;
 DT 20-JAN-2003 (first entry)
 DX
 DE Human NR10.4 splicing variant encoding cDNA SEQ ID NO:3.
 XX
 KW NR10.4 splicing variant; haematopoietic receptor; immunomodulator;
 KW haemostatic; haematopoietic factor; immunological disease;
 KW haematopoietic disease; haematopoietic cell regulation; gene; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..2301
 FT /*tag= a
 FT /product= "NR10.4"
 XX
 PN WO20027230-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 22-MAR-2002; 2002WO-JP002769.
 XX
 PR 26-MAR-2001; 2001JP-00087298.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Maeda M, Yaguchi N, Hasegawa M;
 XX
 DR WPI; 2003-018925/01.
 DR F-PSDB; ABP54364.
 XX
 PT NR10 splicing variants of hematopoietic receptor proteins and encoded
 PT genes, applicable in searching hematopoietic factors and developing
 PT remedies for immunological and hematopoietic diseases.
 XX
 PS Claim 1; Fig 4-5; 250pp; Japanese.
 XX
 CC The present invention describes haematopoietic receptor NR10 splicing
 CC variants (I). (I) have immunomodulator and haemostatic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietic receptor genes participate in
 CC in vivo immunomodulation and haematopoietic cell regulation, and in the
 CC search for haematopoietic factors capable of functionally binding to the
 CC receptors. The present sequence encodes the human NR10.4 protein from the
 CC present invention
 XX
 SQ Sequence 5271 BP; 1312 A; 1302 C; 1318 G; 1339 T; 0 U; 0 Other;

[illegible]

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Db	310	ACCAATAGTTCTCAACAGTGAATAACGTCGCTCGCTCTTTTTCCTTCCAGAAATACG	369
Oy	103	IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer	122
Db	370	ATCCACATATATTATACCATTTAGCTAGGTGAAGCTGAAATATGAGATGGTATTAATTAATCT	429
Oy	123	HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg	142
Db	430	CATATGACATCTGGAATTAGAGAACATAGCGAAAACCTGAACCACTTAAGATTTCGT	489
Oy	143	ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu	162
Db	490	GTGAACACAGTTTGGGCATCAACACGAATGATTCAAATTGATGATTAAGATTAAGCCTGAGTTG	549
Oy	163	AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer	182
Db	550	GCGCTGTTTCATCTGATTTAAATACACACTTCGATTCAGCACGTCAACACAGTACACGC	609
Oy	183	TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr	202
Db	610	TGATATGAAGCAACTTCGCTTAAGAACCTTAAGATTAATAAACCAACGTCACACTACG	669
Oy	203	GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys	222
Db	670	GGCGTCGACGCTTTTACAGAAATATGATAGTCTCTGGATGCTGGCTCAAGAGATCAAG	729
Oy	223	PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCysGly	242
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Oy	243	LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu	262
Db	790	CTGGAACCTGAGAAAGTCTGAAAACCAAGCTGAGCGGATGGAAGAACGCCAGTGGGTTG	849
Oy	263	LeuTrpLysLysAlaArgGlyAlaProValLeuGlnLysThrLeuGlyTyrAsnIleTrp	282
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Db	910	TACTATCCAGAAACCAACACTAACCTCACAGAAACAATGAACCTAACCCAGACACTT	969
Oy	303	GluLeuHisIleLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeuGly	322
Db	970	GAACCTGATCTGGAGGCGAGAGCTTTGGGTGTATGATTTCTTAAATTCCTTTGGG	1029
Oy	323	LysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIle	342
Db	1030	AAGTCTCCAGTGGCCACCTCGAGATTCACAGCTATTCAAGAAAATCATTTCACTGCATT	1089
Oy	343	GluValMetGlnAlaCysValAlaGluAspGlnLeuValIleLysTrpGlnSerSerAla	362
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Oy	363	LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr	382
Db	1150	CTAAGACGTGAACACTTGATGATGATTAATGATTTCCGATGTGGACTCAGAGCCACACACC	1209
Oy	383	LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys	402
Db	1210	CTTTCCTGGGAATCTGTGCTCAGGCAACGAACTGAGCATCCAGCAAGTAAATTAAAA	1269
Oy	403	ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValIleGlyLysPro	422
Db	1270	CCTTTCTGGTGCATTAACATCTCTGTGTATCCAAATGTGCATGACAAAGTTGGGAGCA	1329
Oy	423	TyrserIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyLysProGluThrLysVal	442

Db 1330 TATTCATCCAGGCTTATGCCAAGAGGCGTTCCATCAGAAAGTCTGAGACCAAGTGG 1389
QY 443 G|u|a|n|i|e|g|y|v|a|l|y|e|t|h|r|t|p|l|y|g|i|u|l|e|p|r|o|l|y|s|e|r|g|u|a|g 462
Db 1390 GAGAACATTTGGCGTAAGACGGTCCAGATCACATGAAAGAGATTCCCAAGAGTGAGAGA 1449
QY 463 L|y|e|g|i|l|e|i|e|C|y|a|s|n|t|r|t|h|r|i|e|p|h|e|t|r|g|i|n|a|l|a|g|i|u|g|i|l|y|e|g|i|y|p|h|e|s|e|r 482
Db 1450 AAGGATCATCTGACATCAACCATCTTTTCCAAAGCTGAAGGTGAAAGAGATTCTCC 1509
QY 483 L|y|e|t|h|r|v|a|l|a|s|e|r|s|e|r|i|l|e|u|g|i|n|t|r|g|i|l|e|u|g|i|u|s|e|r|l|e|u|l|y|a|g|i|y|e|t|h|r|s|e|r 502
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QY 503 T|y|r|i|l|e|v|i|g|i|n|v|i|a|l|e|t|h|r|s|e|r|a|l|a|g|i|y|l|t|h|r|a|e|n|g|i|l|t|h|r|s|e|r|i|l|e|a|n 522
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QY 523 P|h|e|l|y|e|t|h|r|l|e|u|s|e|r|p|h|e|s|e|r|v|a|l|p|h|e|g|i|u|i|e|i|l|e|u|i|e|t|h|r|s|e|r|l|e|i|l|e|g|i|y|l|y 542
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QY 543 G|i|l|e|u|l|e|i|l|e|u|i|e|i|l|e|u|t|h|r|v|a|l|a|t|r|g|i|l|e|u|l|y|e|p|h|o|b|i|l|y|s|e|r|u 562
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QY 563 T|h|r|i|b|l|e|u|C|y|t|r|p|p|r|o|t|h|r|v|a|l|p|r|o|a|n|p|r|o|l|a|g|i|u|s|e|r|i|l|e|i|a|l|t|h|r|t|r|h|i|s 582
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QY 623 V|a|l|a|n|p|h|e|g|i|y|a|s|n|v|a|l|e|u|g|i|n|t|r|l|e|p|h|e|r|a|s|p|g|i|u|a|a|r|g|t|h|r|g|i|y|g|i|n|g|i|u 642
Db 2050 GTGAACCTTTGGGAATGTTCTGCAAGAAATTTTCAACAGATGAAGCCAGAACGGGTCAAGAA 2109
QY 643 A|e|n|a|n|l|e|u|g|i|y|g|i|l|y|a|s|n|g|i|l|t|h|r|a|r|g|i|l|e|u|s|e|r|C|y|a|p|r|o 659
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Job time : 1052.78 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:59:57 / Search time 304.791 Seconds
(without alignments)
3553.966 Million cell updates/sec

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Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	685	19.4	3085	US-09-023-655-1131
3	683	19.4	2754	US-08-825-558-5
4	683	19.4	2754	US-09-312-611-5
5	683	19.4	3085	US-08-795-473B-4
6	683	19.4	3085	US-09-439-856-4
7	678.5	19.2	2369	US-07-797-556-1
8	678.5	19.2	2369	US-08-308-881-1
9	678.5	19.2	2369	US-09-058-263-1
10	678.5	19.2	2369	US-09-059-099-1
11	678.5	19.2	2369	US-09-058-264-1
12	678.5	19.2	2369	US-09-455-962-1

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14	636.5	18.0	1977	2	US-08-825-558-3	Sequence 3, Appli
15	636.5	18.0	1977	3	US-09-312-611-3	Sequence 3, Appli
16	616	17.5	3477	4	US-09-313-942-25	Sequence 25, Appli
17	616	17.5	3507	4	US-09-313-942-23	Sequence 23, Appli
18	508.5	14.4	2943	4	US-07-923-976-3	Sequence 3, Appli
19	508.5	14.4	2943	4	US-09-023-655-1086	Sequence 1086, Ap
20	506.5	14.4	3024	4	US-07-923-976-7	Sequence 7, Appli
21	490	13.9	2563	6	5422248-1	Patent No. 5422248
22	490	13.9	2563	6	5422248-1	Patent No. 5422248
23	465.5	13.2	3293	1	US-07-923-976-1	Sequence 1, Appli
24	464	13.2	2855	1	US-07-923-976-5	Sequence 5, Appli
25	404	11.5	3182	1	US-07-797-556-5	Sequence 5, Appli
26	404	11.5	3182	1	US-07-943-843-1	Sequence 1, Appli
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30	404	11.5	5245	4	US-09-949-016-4210	Sequence 4210, Ap
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ALIGNMENTS

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US-09-700-820C-17
; Sequence 17, Application US/09700820C
; Patent No. 6610485
; GENERAL INFORMATION:
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Saito, Mikiyoshi
; APPLICANT: Ohmoto, Toshihiko
; TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
; FILE REFERENCE: 06501-070001
; CURRENT APPLICATION NUMBER: US/09/700,820C
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/JP99/02341
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: JP 10/138652
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 10/279876
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 17
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) .. (2839)
; US-09-700-820C-17

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Score: 691.00
Percent Similarity: 46.83%
Best Local Similarity: 28.28%
Query Match: 19.59%
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Mismatch: 286
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US-10-006-265-17 (1-662) x US-09-700-820C-17 (1-2395)

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QY      55  TrpSerProGlyLysGluThrSerTyr---ThiGluTyrThrValLysArgThrTyrAla 73
Db      524  TGGGACCCCGAAGGAGACTTACTCTTGAACAACAACTACACTTGTAAATCAGAGTGCGCA 583
QY      74  PheGluGluLysHisAspAsnCysThrThrAsnSerSerThiSerGluAsnAlaSer 93
Db      584  ---ACAGAGAAAGTTCTCTGATTCAGATGCAAGACATGCACT-----TCA 625
QY      94  CysSerPhe---PheLeuProArgIleThrIleProAspAsnTyrThrIleGluValGlu 112
Db      626  TGTATGTGACGTACATACGCCCACTTATATGTC-----AACATTGAAGCTGGGGGAA 679
QY      113  AlaGluAsnGlyAspGlyValIleLysSerHisMetThrTyrTrpArgLeuGluAsnIle 132
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QY      133  AlaLysThrGluProProLysIlePheArgValLysProValLeuGlyIleLysArgMet 152
Db      740  GTGAAACCCACCCCACTATATATTTATCATGATCAGCACTCAGAGAAATTTATCCAGTATA 799
QY      153  IleGluIleGluTrpIleLysProGluLeuAlaProValSerSerAspLeuLysTyrThr 172
Db      800  TTAAACTTATCATGGGTCACTTCAAGGCTGGCGGCTTT---TTAGATCTAAAGTCTTGAC 856
QY      173  LeuArgPheArgThrValAsnSerThrSerTrpMetGluValAsnPheAlaLysAsnArg 192
Db      857  ATCCAAATATATAGACCAAAAGATGCTCAACTTGATCAGAGTCCCTCT---GAAGATACA 913
QY      193  LysAspLysAsnGlnThrTyrAsnLeuThrGlyLeuGluProPheThrGluTyrValIle 212
Db      914  ATGTCCTCTGAACTTCTTCACTGTCAGAGCACTCAAGCCTTTTACAGAAATATGTGTTT 973
QY      213  AlaLeuArgCysAlaValLysGlnSer-----LysPheTrpSerAspTrpSerGlnGlu 230
Db      974  AGGATCCCG---TCCATTAAAGACAGTGGGAAGGCTACTGAGTGTACTGAGTAGAGAG 1030
QY      231  LysMetGlyMetThrGluGluGluAlaProCys---GlyLeuGluLeuThrArgValLeu 249
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QY      250  LysProAlaGluAlaAspGlyArgArgProValArgLeuLeuThrLysLysAlaArgGly 269
Db      1091  AATCCATCCCATGGGAGAAATATAGATCTGTACGGCTCATATGAGGAAGCACTGCCTCTT 1150
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QY      290  AsnLeuThrGluThrMetAsnThrThrAsnGlnGluLeuGluLeuHisIleLeuGlyGlu 309
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QY      370  IleGluTrpPheProAspValLysSerGluProThrThrLeuSerTrpGluSerValSer 389
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Db      1565  ACAGTAACCTCCCGTATTCGCGCAGGGGCGCGGAGCTGTGATCTCTTGAGAGCGTACCTC 1624
QY      430  LysGluGlyValProSerGluGlyProGluTrpLysValGluAsnIleGlyValLysThr 449
Db      1625  AAACAAGCCGCTCTGCGCAAGAGACCACTGTTCCGACAAAGAAAGTGGGAAAAATGAA 1684
QY      450  ValThrIleThrTrpLysGluIleProLysSerGluArgLysGlyIleIleCysAsnTyr 469
Db      1685  GGTGCTTACGCTGGGACCAATTCCTGTGACAGCAGCAAGATGGCTTATTTGAAACTAC 1744
QY      470  ThrIlePheTyrGlnAlaGluGlyLysGlyPheSerLysThrValAsnSerSerIle 489
Db      1745  TCCATATCTTACAGAACCAAGCGTGGAAAGAGATGTTGTGCATGTGATTCCTCTCAC 1804
QY      490  LeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSerTyrIleValGlnValMetAla 509
Db      1805  ACGGAGTACAGCTGTCTCTCTGATGTGATGATGATGATGATGATGATGATGATGATGAT 1864
QY      510  SerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsnPheLysThrLeuSerPheSer 529
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QY      530  ValPheGluIleIleLeuIleThrSerLeuIleGlyGlyLysLeuIleLeuIleIle 549
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QY      550  LeuThrValAlaTyrGlyLeuLysLysProAsnLysLeuThrHisLeuCysThrProThr 569
Db      1985  CTGGCGCTTGTGTCTGCTTTAAACAAGACCTTAATTAATAAAACACATCTGGCTTAAT 2044
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QY      583  GlyAspAspPheLysAspLysLeuAsnLeuLysGlnSerAspAspSer----- 598
Db      2105  AATTTTAATCTCAAAAGATCAAAATG-----TACTGGACGGCAATTTCACTGATGTA 2155
QY      599  -----ValAsnThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeu 616
Db      2156  ACGTGTGTGAAATAGAAAGCAAAACAAGAAAGCTTGT-----CGAGATACCTGAAG 2209
QY      617  ValIleAspLysLeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGlu 636
Db      2210  TCCGTGGAC-----CTGTTCAAGAAAGAG 2233
QY      637  -----AlaArgThrGlyGlnGlnAsnAsnLeuGlyGlyLysLysAsnGlyThrArgIle 654
Db      2234  AAAGTAGATACGAAGAGGAGACAGAGTGCATCGGGGCG----- 2272
QY      655  LeuSerSerCysProThrSer 661
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RESULT 2
US-09-023-655-1131
Sequence 1131, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:

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Oy      35 ProAlaValSerProGluAsnIleSerCysValIlyrTyTrArgIysAsnLeuThrCysThr 54
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Oy      71 ThrTyRAlaPheGlu-----IysHisAsp-----AsnCysThrThrAsn 84
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Oy      124 MetThrTyTrArgLeuGluAsnIleAlaIysThrGluProProIysIlePheArgVal 1434
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Oy      144 LysProValLeuGlyIleLysArgMetIleGlnIleGluIleIleLysProGluVal 163
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Dd	1006	AGTGTTATAATAA---CTAAATAATATACATTCAAATATAGGACCAAGAGCTCCAACCTTGG	1062
Oy	184	MetGluValaAnPheAlaYasnArgLysAspLysAsnGlnThrTYrAsnLeuThrcly	203
Dd	1063	AGCCAGATTTCT---CCTGAAGACACAGCATCCACCCGATCTTCAATTCAGTCTCCAGAC	1119
Oy	204	LeuGlnProPheThrGluTYrValIleAlaLeuArgCysAlaValIleuGluSerIys---	222
Dd	1120	CTTAACCTTTTACAGAAATATGTGTTTTAGATTCGCTGTATGAAGAAAGATGTAAGGA	1179
Oy	223	PheTrpSerAspTrpSerGlnGluIleuIleuArgCysIleuMetThrGlnGluGluAlaProCys---	241
Dd	1180	TACTGGAGTGACTGGAGTGAAGAAAGCAAGTGGAGTACCTTATGAAGATATAGACATCTTAA	1239
Oy	242	GlyLeuGluIleuTrpArgValIleuLysProAlaGluAlaAspGlyArgArgProValArg	261
Dd	1240	GCACCAAGTTTCTGGTTTAAATATAGATCCATCCATACCTCAAGGCTACAGAACTGTCAA	1299
Oy	262	LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTYrAsnIle	281
Dd	1300	CTCGTGGAAAGACATTCCTCCCTTTTGAAGCCAAAGTGAAGAAATCTTGATTAATGAAGTG	1355
Oy	282	TrpTYrTYrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThraAsnGlnGln	301
Dd	1360	ACTCTCACAAATGGAATATCATATTACAATAATACACAGTTAATGCCAC-----AAA	1413
Oy	302	LeuGluLeuHisIleuGlyGlyGluSerPheTrpValSerMetIleSerTYrAsnSerLeu	321
Dd	1414	CTGACAGTAAATCTCACAAATAGATCGGTATATACCAACCCCTAAGACGTAAAGAAATCTTGT	1473
Oy	322	GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys	341
Dd	1474	GGCAATATAGATGACGCTGTTTAACTATCCCTCCCTGTGACTCTTCAAGCTACTCACCTT	1533
Oy	342	IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValIleTrpGlnSerSer	361
Dd	1534	GTAATGATCTTAAGCATTCCTCCCAAGATATACATGCTTTGGGGATGAGCACTATCCA	1593
Oy	362	AlaLeuAspValaAnThrTrpMetIleGluTrpPheProAspValaAspSerGluProThr	381
Dd	1594	AGGCAATCTGTAAGAAATATATATACTGTAGCGTGTGTATATACGATTAAGCAACCTGT	1653
Oy	382	ThreusertTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu	401
Dd	1654	ATCACAGACTGGCAACAAGAGATGTACCGCTGATGCACCTATTTAAGGGGAACCTTA	1713
Oy	402	LysProPheTrpCysTYrAsnIleSerValTYrProMetLeuHisAspLysValGlyGlu	421
Dd	1714	GCAAGAGCAAAATCTATTGTATACAGTTTACTCAAGTATATGCTGATGACACGAGAACG	1773
Oy	422	ProTYrSerIleGlnAlaTYrAlaLysGluGlyValProSerGlnGlyProGluThrLys	441
Dd	1774	CCTGAATCTCAATAAAGCATACCTTAAACAAGCTCACCTTCCAAAGGACCTACGTTCGG	1833
Oy	442	ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu	461
Dd	1834	ACAAAAGAAAGTGAAGGAAAAAGAAAGCTGTCTTAAGTGGGACCAATCTTCTGTGATGTT	1893
Oy	462	ArgLysGlyIleIleCysAsnTYrThrIlePheTYrGlnAlaGluGlyLysGlyPhe	481
Dd	1894	CAGATGATTTTATACAGAAATATATATATTTTATATGAAACATCATTGGAATGAAACT	1953
Oy	482	SerLysThrValaAsnSerSerIleLeuGlnTYrGlyLeuGluSerLeuLysArgLysThr	501
Dd	1954	GCTGTGATGATGATTTCTTCCACACAGAAATATATCATTTGCTCTTTGACATGAGACACA	2013
Oy	502	SerTYrIleValaGlnValMetAlaSerThSerAlaGlyGlyThrAsnGlyThrSerIle	521
Dd	2014	TTGTATATGTGATCAATGCGCATATACAGATGATAGGTGGAGGATGTGTCAGAAATTC	2073

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QY 522 AsnPhelYthrLeuSerPheSerValPheGluIleLeuIleThrSerLeuIleGly 541
DB 2074 ACTTTACTACCCCAAGTTTGCCTCAAGAGAAATGAAACCATAGTCGCTGTTGC 2133
QY 542 GlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuValProAsnLys 561
DB 2134 TTGACATTCCTAATGCAACTCTTGGAGAGCTCTGCTTATTAAGCAGACTTA 2193
QY 562 LeuThrHisLeuGlySerProThrValProAsnProAlaGluSerSerIleAlaThrPro 561
DB 2194 ATTTAAAAACACATCTGGCCTAATGTTCCAGATCTTCAAGAGTCAATATGCGCAGTGG 2253
QY 582 -----HisGlyAspAspPheLeuAspLysLeuAsnLeuLysGlu 594
DB 2254 TCACCTCACACTCCTCCAGGACCAATTTTAATTCAAAGATCAATG-----TAT 2304
QY 595 SerAspAspSer-----ValAsnThrGluAspArgIleLeuLysPro 608
DB 2305 TCAGATGGCAATTTCACTGATGTAGTGTGTGGAAATAGAACCAATGACAAAGCCCT 2364
QY 609 CysSerThrProSerAspLysLeuValIleAspLysLeuValValAsnPheGlyAsnVal 628
DB 2365 -----TTTTCACAGAGATCTGAATCATTTGAC----- 2391
QY 629 LeuGlnGluIlePheThrAspGluAla-----ArgThrGlyGlnGluAsnLeuGly 646
DB 2392 -----CTGTTCAAAAGGAAATAATTAATACGAAAGACACACGACGCTGATTTGG 2442
QY 647 GlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSer 661
DB 2443 GGG-----TCTTCATGATGATGCATCT 2463

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RESULT 3

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US-08-825-558-5
; Sequence 5, Application US/08825558
; Patent No. 5965724
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: GP 130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,558
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623.0530001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2754
US-08-825-558-5

Alignment Scores:
Pred. No.: 4.2e-65 Length: 2754
Score: 683.00 Matches: 187
Percent Similarity: 46.264 Conservative: 116
Best Local Similarity: 28.554 Mismatches: 280
Query Match: 19.368 Indels: 72
DB: 2 Gaps: 20

US-10-006-265-17 (1-662) x US-08-825-558-5 (1-2754)
QY 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
DB 376 CCGAAGAAACCTTAAATTTGAGTTGCATTTGAAACGAGGAGAAAGAAATGAGTGTGAG 435
QY 55 TrpSerProGlyLysGlnThrSerTyr---ThrGlnTyrThrValLys-----Arg 70
DB 436 TGGAGTGGTGAAGGAAACACACTTGAGACAACTTCACTTAAATCTGAATGGCA 495
QY 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
DB 496 ACACACAAAGTTGCTGATTTGCAAGCAAAACGTGACACCCCACTCATGCTGTTGAT 555
QY 85 SerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProArgIleThrIlePro 104
DB 556 TATTTCTACT-----GTGTATTTGTCT----- 576
QY 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer---His 123
DB 577 ---AACATTGAAGTCTGGCTAGAGAGAGATGCTGCTGGAGAGTTATCATCAAGTAT 633
QY 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProLysIlePheArgVal 143
DB 634 ATCAATTTTGATCTGATATATTAAGTG---AAGCCCAATCCGCCCATATTTATCACTG 690
QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
DB 691 ATCAACTCAGAGAACTGTCTAGTATCTTAAATTAATGACATGAGCCAACTCAAGTATTAG 750
QY 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
DB 751 AGGTGTTATATA---CTAAATATTAACATTCATATATGAGACCAAGATCTCTCACTTG 807
QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
DB 808 AGCCAGATTCTCT---CTTGAAAGACACAGCATCCACCCGATCTTCATCTCTCCAAAGAC 864
QY 204 LeuGlnProPheThrGluIleValIleAlaLeuArgCysAlaValLysLeuSer--- 222
DB 865 CTTAACCTTTTACAGAAATATGTGTAGATTCCTGTATATAGAAAGAAATGTAAGGGA 924
QY 223 PheTrpSerAspTrpSerGlnGluLysMetCylMetThrGluGluGluLysProCys--- 241
DB 925 TACTGAGAGTCTGAGTGAAGAGCAAGTGGAGTACCTTAAGATGACATCTAA 984
QY 242 GlyLeuGluLeuThrArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
DB 985 GCACCAAGTTCTGGATTAATAATAGATCCATCTACTCAAGGCTACAGAACTGACAA 1044
QY 262 LeuLeuThrLysLeuAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
DB 1045 CTCGTGTGAAGACATTCCTCTTTTGAAGCCAAATGAAAAATCTTGATTTATAGAGTG 1104
QY 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
DB 1105 ACTCTCAAGATGGAATCAATTTACAAATTTACACAGTTAATGCCCA-----AAA 1158
QY 302 LeuGluLeuIleLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
DB 1158

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Db	1159	CTGACAGTAAATCTCACAATATGCGTATCTTAGCAACCCCTTAACAGTAAGAATCTTGT	121
Oy	332	GLYSSerProValAlaThrLeuArgIleProAlaIleGlnIleuSerPheGlnCys	341
Db	1219	GGCAATACAGATGACAGCTGTTTAACTATCCTGCTGGATCTTCAAGCTTACACCT	1278
Oy	342	IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer	361
Db	1279	GTAATGATCTTAAAGACATTCCTCCCAAGATTAACAATGTTGGGTGAATGACTCTCA	1338
Oy	362	AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr	381
Db	1339	AGGGAATCTGTAAAGAAATATATCTTAGTGCTGTGTCTTATCAGATTAAGACCTCT	1399
Oy	382	ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysIleu	401
Db	1399	ATCAGACAGCTGGCACAAGAGATGTAACCGTACATCGACCTATTTAAGAGAACTTA	1459
Oy	402	LysProPheTrpCysTrpAsnIleSerValTrpProMetLeuHisAspLysValGlyIleu	421
Db	1459	GCAGAGACCAATGCTATTTGTGTAAACAGTTACTCCAGATATATGCTGATGACCAAGAC	1519
Oy	422	ProTrpSerIleGlnAlaTrpAlaLysGlnGlyValProSerGlnGlyProGlnThrLys	441
Db	1519	CCTGAATCATTAAGCAGATCCTTAAACAAGCTCCACTTCAAAAGACCTACTGCTGG	1579
Oy	442	ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu	461
Db	1579	ACAAAAGAAAGTAAAGGAAAAAGCAACCTGCTTAGAGTGGACCAACTTCTTGATGTT	1639
Oy	462	ArgLysGlyIleIleCysAsnTrpThrIlePheTrpGlnAlaGluGlyGlyLysPhe	481
Db	1639	CAGATGATTTATCAGAAATATATCTATATTTATAGAACCATATGGAATGAACACT	1699
Oy	482	SerLysTrpValAsnSerSerIleLeuGlnTrpGlyLeuGluSerLeuLysArgLysPhe	501
Db	1699	GCTGTGAATGTGGATCTTCTCCACACAGAAATATCAATGTTCTCTTTGATCAGACACA	1759
Oy	502	SerTrpIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle	521
Db	1759	TTGTTACATGTTACGAATGGCAGCATACACAGATGAAGGTGGAAAGATGGTCCAAATTC	1819
Oy	522	AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly	541
Db	1819	ACTTTTACTACCCCAAGATTGCTCAAGAGAAATTGAAGCCATATGCTGCTGTTGTC	1879
Oy	542	GlyIleLeuLeuIleLeuIleIleLeuThrValAlaTrpGlyLeuLysLysProAsnLys	561
Db	1879	TTAGCAATCTTAATGACAACCTCTTGGGAGTGGCTGTTCTGTTAATTAAGGAACCTA	1939
Oy	562	LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp	581
Db	1939	ATTAAAAAACACATGTGGCTTAATGTTCCAGATCTTCAAAAGTCATATTTGCCAGTGG	1999
Oy	582	HisGlyAspAspPheLysAspLysLeuAsnLeuLysGlu	594
Db	1999	TCACCTCACACTCTCTCAAGGACACATTTTATTAACAAAAGATCAAAATG-----TAT	2049
Oy	595	SerAspAspSer-----ValAsnThrGluAspArgIleLeuLysPro	608
Db	2050	TCAGATGGCAATTTTCACTGATGTAAAGTGTGGGAAATAGAAAGCAATAGCAAAAAGCCT	2109
Oy	609	CysSerThrProSerAspLysLeuValIleAspLysLeuValValAsnPheGlyAsnVal	628
Db	2110	-----TTTCCGAAGATCTGAATCATTTGAC-----	2139
Oy	629	LeuGlnGlnIlePheThrAspGluAla-----ArgThrGlyGlnGluAsnAsnLeuGly	646
Db	2137	-----CTGTTCAAAAAGAAAAAATTAACTAGGAAGGACACAGCATGTATTGGG	2189
Oy	647	GlyIleLysAsnGlyThrArgIleLeuSerSerCysProThrSer	661
Db	2188	GGG-----TCCTTCATCATCATGTCTATCT	2208

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US-09-312-611-5
/ Sequence 5, Application US/09312611
/ Patent No. 6380160
/ GENERAL INFORMATION:
/ APPLICANT: SHARKEY, ANDREW
/ APPLICANT: SMITH, STEPHEN K.
/ APPLICANT: DELOW, KIMBERLY A.
/ TITLE OF INVENTION: Gpi30 Lacking the Transmembrane Domain
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
/ STREET: 1100 NEW YORK AVENUE
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/312,611
/ FILING DATE: 17-MAY-1999
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ESMOND, ROBERT W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0623.0530002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)371-2600
/ TELEFAX: (202)371-2540
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2754 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..2754
US-09-312-611-5

Alignment Scores:
Pred. No.: 4.2e-65 Length: 2754
Score: 683.00 Matches: 187
Percent Similarity: 46.26% Conservative: 116
Best Local Similarity: 28.55% Mismatch: 280
Query Match: 19.36% Indels: 72
DB: 3 Gaps: 20

US-10-006-265-17 (1-662) x US-09-312-611-5 (1-2754)

QY 35 ProbabalyserprobiunseilseSerCySeValTyrrTyrrArglyAsenleuthrCyeThr 54
Db 376 CCAGAAAACCTVAAAAATTTGAGTTCATTGTGAACGAGGGAAAGAAAAATGAGGTGAG 433
QY 55 TrpSerProGlylsgluthrSertyr---ThrglnTrhThvallys-----Arg 70
Db 436 TCGGATGCTGGAAGGGAACAACACTTGAGAGCAACAACTTCATTAATAATCGAATGGCA 495
QY 71 ThrTrAlaPhelGlylu-----LysHIsAp-----AenCyEThThAsn 84
Db 496 ACACACACAGTTTCCTGATTGCACAAGCAAAACGTGACACCCACCCTCATGACGTGGAT 555
QY 85 SerSerSerSerclunamArghalaserCySerPhePheLeuProArgIleThrllePro 104
Db 556 TATTTCTCT-----GCTGATTTTTC----- 576
QY 105 AspAsnTyrrThrIleGlValgluAluaglunenglyAspGlyValIleTySer--His 1233

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Db 577 ---ACATTGAAGCTGGGTAGAGAGCAAGAAATGCCCTTGGGAAGGTATCATCATGATCAT 633
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Db 634 ATCAATTTGATCTCTGATATTAAGTG--AAGCCCAATCCGCACTTAATTTATCAAG 690
Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 691 ATCAACTCAGAGAACTGCTAGATCTTAAATTTGATGACCAACCAAGATTAAG 750
Qy 164 ProValSerSerLeuLysIleValThrLeuArgPheArgThrValAsnSerThr 183
Db 751 AGGTATATATA---CTAAATATTAACATTCAATATATGACCAAAAGTGCCTCAACTGG 807
Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnIleThrLysLeuThrGly 203
Db 808 AGCCAGATTCT--CCTGAAGACACAGCATCCACCCGATCTTCATTCTACTGTCAGAAC 864
Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys-- 222
Db 865 CTAAACCTTTTACAGATATGTGTTTAGGATTGCGTGTATGAAGAAATGGTAAAGGA 924
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaProCys-- 241
Db 925 TACTGAGTGACTGAGTGAGAAAGCAAGTGGATCATCTATGAGATAGACCATCTAA 984
Qy 242 GlyLeuGluLeuThrArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
Db 985 GCACCAAGTTCTGCTGATTAATAATGATCCATCCATATCTCAAGGCTACACAACTGACAA 1044
Qy 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
Db 1045 CTCGTGTGGAAGACATTCCTCTTTTGAAGCAATGAAATACTTGATTTAGAAAGTG 1104
Qy 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGln 301
Db 1105 ACTCTCAAGATGGAATCAATCAATTAACAAATTAACAGTTAATGCCACA-----AAA 1158
Qy 302 LeuGluLeuIleAsnGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
Db 1159 CTACAGTAATCTTCAAAATGATCGCTATCTAGCAACCTTAACAGTAAGAAATCTTGTT 1218
Qy 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnLysLysSerPheGlnCys 341
Db 1219 GCGAAATCAAGATGACAGTGTATTAACATCCCTGCGTGTGATCTTCAAGTACTCAACCT 1278
Qy 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSerSer 361
Db 1279 GTATGATCTTAAAGCATTCCTCCCAAGATACATGCTTTGGGTGAGATGCACTACTCCA 1338
Qy 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
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Db 1399 ATCAGACTGCGCAACAAGATGGTACCGTGACCGCACTTAATTTAAAGGAAGAACTTA 1458
Qy 402 LysProPheTrpCysTrpAsnIleSerValTyrProMetLeuIleAspLysValGlyGlu 421
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Qy 422 ProTyrSerIleGlnIleTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
Db 1519 CTGGAATCCATTAAGGATATCTTAACAGCTCCACCTTCCAAAGAGACTTACTGTGG 1578
Qy 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db 1579 ACAAAAAAGTAGGAAAAAGCAAGCTGCTTGAAGTGGAGCAACTCTCTGTGATGTT 1638
Qy 462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyGlyPhe 481

Db 1639 CAGAAATGATTTATCAAGAAATTAATCTATATTTTATAGAACATCATTCGAAATGAAC 1698
Qy 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
Db 1699 GCTGGAATGTGATGATCTTCCACACAGAAATATATCTTCTCTTTGATGATGACACA 1758
Qy 502 SerTyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
Db 1759 TTGTATCATGTATGATGACATACATACAGATGAAAGTGGAGAGATGTCAGAAATTC 1818
Qy 522 AsnPheLysThrLeuSerSerValPheGluIleLeuIleIleThrSerLeuIleGly 541
Db 1819 ACTTTTACTATCCCAAGTTCTCTCAAGAGAAATTAAGCAATAGTCTGCTGTTTC 1878
Qy 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
Db 1879 TTAGCATCTCTATGACAACTCTTCGGAGAGTGCCTTGTGCTTAATTAAGGAGACCTA 1938
Qy 562 LeuThrIleLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
Db 1939 ATTAATAAACATCATGCGCTAATGTTCCAGATCTTCAAAAGATCATATTCGCCAGTGG 1998
Qy 582 -----HisGlyAspAspPheLysAspLysLeuAsnLeuLysGlu 594
Db 1999 TCACCTCACATCTCTCAAGGACACATTTTAATTCAAAAGATCAAAATG-----TAT 2049
Qy 595 SerAspAspSer-----ValAsnThrGluAspArgIleLeuLysPro 608
Db 2050 TCGATGCGCAATTTCTCATGATGTAAGTGTGTTGGAATTAAGAAATGACAAATAAGCCT 2109
Qy 609 CysSerThrProSerAspLysLeuValIleAspLysLeuValValAsnPheGlyAsnVal 628
Db 2110 -----TTTCCAGAAAGATCTGAATCATATGAC----- 2136
Qy 629 LeuGlnGluIlePheThrAspGluAla-----ArgThrGlyGlnLysAsnLeuGly 646
Db 2137 -----CTGTCAAAAAGAAATAATTAATCTGAAGGACACAGCATGTGATTTGGG 2187
Qy 647 GlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSer 661
Db 2188 GGG-----TCTTATGATCATCT 2208

RESULT 5
US-08-795-473B-4
; Sequence 4, Application US/08795473B
; Patent No. 6217858
; GENERAL INFORMATION:
; APPLICANT: Galun, Elchan
; APPLICANT: Nahot, Orit
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,473B
; FILING DATE: 11-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963.1007

Db 2392 -----CTGTTCAAAAAGCAAAAATTATATCTGAAGCACAGACAGTGTGATTGGGGG 2445
Qy 648 GtLysAsnGlyThrArgIleLeuSerCysProThrSer 661
Db 2446 -----TCTTCATGCATGTCATCT 2463
RESULT 6
US-09-439-856-4
Sequence 4, Application US/09439856
Patent No. 641009
GENERAL INFORMATION:
APPLICANT: Galun, Etchan
APPLICANT: Nahot, Orit
APPLICANT: Blum, Herbert E.
TITLE OF INVENTION: A Pharmaceutical Composition for Treating
TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Davidson, Davidson and Kappel, LLC
STREET: 1140 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS EDITOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,856
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,473
FILING DATE: 11-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Davidson, Clifford M.
REGISTRATION NUMBER: 32,728
REFERENCE/DOCKET NUMBER: 963.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-997-1028
TELEFAX: (212)-997-1037
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3085 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-439-856-4
Alignment Scores:
Pred. No.: 5.08e-65 Length: 3085
Score: 683.00 Matches: 186
Percent Similarity: 46.48% Conservative: 118
Best Local Similarity: 28.44% Mismatches: 280
Query Match: 19.36% Indels: 70
Gaps: 21
US-10-006-265-17 (1-662) x US-09-439-856-4 (1-3085)
Qy 35 ProAlaIysProGluAsnIleSerCysValIyTrTyTrArgIysAsnLeuThrCysThr 54
Db 631 CCGAAGAAACCTTAATAATTGAGTTGATGTCGACACAGGGGAGAAAGAAATGAGGTGAG 650
Qy 55 TrpSerProGlyIysGluThrSerTyTr---ThrGlnTyThrValIys-----Arg 70
Db 691 TGGATGCTGGAAGGAAACACACTTGAGACAACTTCACTTAAATCGATGGCA 750
Qy 71 ThrTyAlaIheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
Db 751 ACACACAAAGTTGCTGATTCGCAAGCAAAACGTGACACCCCACTCATGCACTGTGAT 810

Qy 85 SerSerThrSerGluAsnArgIaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 811 TATTCACCT-----GTGATATTGTG----- 831
Qy 105 AspAsnTyThrIleGluValGluAsnGlyAspGlyValIleIysSer---His 123
Db 832 ---AACATTGAAGTCGGGTGAGACAGAAATGCCCTGGAGAGGTTACATCAGATCAT 888
Qy 124 MetThrTyTrpArgLeuGluAsnIleAlaIysThrGluProProIysIlePheArgVal 143
Db 889 ATCAATTGATGCTGATATATAAGTG---AAGCCCAATCCGCACATATATTATCAGTG 945
Qy 144 LysProValIleGlyIleIysArgMetIleGlnIleGluTrpIleIysProGluLeuAla 163
Db 946 ATCAACTGACGAGAACTGCTAGTATCTTAATAATTGACATGACACCAAGTATTAAG 1005
Qy 164 ProValSerSerAspLeuIysTyThrIleAspPheArgThrValAsnSerThrSerTrp 183
Db 1006 AGTGTTATATAA---CTAATAATATAACATTCATATAGGACCAAGATCCCTCACTTG 1062
Qy 184 MetGluValAsnPheAlaIysAsnArgIysAspIysAsnGlnThrTyTrAsnLeuThrGly 203
Db 1063 AGCCAGATTCT---CTGAAGACACAGCATCCACCCGATCTTCATCTGTCAGAC 1119
Qy 204 LeuGlnProPheThrGluTyTrValIleAlaLeuArgCysAlaValIysGluSerIys--- 222
Db 1120 CTTAACCTTTACAGAAATATGTTAGATTCGCTGATAGAGAAAGATGTAAGGA 1179
Qy 223 PheTrpSerAspTrpSerGlnGluIysMetGlyMetThrGluGluGluAlaProCys--- 241
Db 1180 TACTGGATGACTGGGAGTGAGAACAGCAAGTGAGATCACCCTAAGATAGACTATATAA 1239
Qy 242 GlyLeuGluLeuThrArgValIleIysProAlaGluAlaAspGlyArgArgProValArg 261
Db 1240 GCACCAAGTTCTGGATATAATAGATCCATCCATATCTCAAGGCTACAGAACTGTACA 1299
Qy 262 LeuLeuTrpLysLysAlaArgGlyAlaProValIleGluIysThrIleGlyTyTrAsnIle 281
Db 1300 CTGCTGTGAGAGACATGCTCCTCTTGAAGCAATGCAAAAATCTGGATATATGAAGG 1359
Qy 282 TrpTyTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
Db 1360 ACTCTCAAGATGGAAATCACATTTACAAATTTACACAGTTAATGCCACA-----AAA 1413
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Db 1414 CTGACAGTAATCTCAAAATATGCTATGTAGCAACCTTAACGTAAGAAATCTTGT 1473
Qy 322 GlyLysSerProValAlaThrIleuArgIleProAlaIleGlnGluIysSerPheGlnCys 341
Db 1474 GCGAATTCAGATGCAAGCTGTTTAACATCCCTGCTGATGATTCACACTACCCCT 1533
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Db 1714 GCAGAGACAAATGCTATTTGATTAACAGTTACTCCAGTATATGCTGATGACACAGAGAC 1773
Qy 422 ProTySerIleGlnAlaTyTrAlaIysGluGlyValProSerGlnGlyProGluThrIys 441
Db 1774 CCGAATCCATTAAGGATACCTTAACAGCTCCACCTTCCAAAGGACCTTACTGTTCGG 1833

QY 184 MetGluValAsnPhenAlaValAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
 Db 1051 AGCCAGATTCTCT---CCTGAAGACACAGCATCCACCAGCTTCATCTCACTGCTCCAGAC 1107
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 QY 223 PheTyrSerAspThrSerGlnGlnLysMetGlyMetThrGlnGlnGlnAlaProCys--- 241
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 QY 242 GlyLeuGlnLeuThrArgValIleLysProAlaGlnAlaAspGlyArgProValArg 261
 Db 1228 GCACCAAGTTCTGCTATTAATAATAGATCCATCCCATATCAAGGCTACAGAACTGACAA 1287
 QY 262 LeuLeuThrLysLysAlaArgGlyAlaProValLeuGlnLysThrLeuGlyTyrAsnIle 281
 Db 1288 CTCGTGTGAAGACATTGCTCTCTTTGAAGCCAAATGAAAATCTTGATTTGAAGTG 1347
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 QY 382 ThrLeuSerTyrGlnSerValSerGlnAlaThrAsnTyrThrIleGlnIleAspLysLeu 401
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 QY 402 LysProPheThrPyrAsnIleSerValTyrProMetLeuThrAspLysValGlyGln 421
 Db 1702 GCAGAGAGCAAAATGCTATTTGATTAACGTTATCTCAATATATGATGACCAAGAAC 1761
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 QY 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuLysSerLysArgLysThr 501
 Db 1942 GCTGTGAATGTGATTTCTCCACACAGAAATATACATTTGCTCTTTGACTAGTACACA 2001
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QY 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
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 QY 562 LeuThrHisLeuCysTyrProThrValProAsnProAlaGlnSerSerIleAlaThrTyr 581
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 RESULT 8
 US-08-308-881-1
 Sequence 1, Application US/08308881
 Patent No. 5783672
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESSES:
 ADDRESSES: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1
 SOFTWARE: Microsoft Word, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/308, 881
 FILING DATE: 12-SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/249,553
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seeze, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2369 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 TISSUE TYPE: human placenta
 IMMEDIATE SOURCE:
 CLONE: B10G/pDC303
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 244..2369
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 310..2369
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 244..309
 US-08-308-881-1

Alignment Scores:

Pred. No.: 1,03e-64 Length: 2369
 Score: 678.50 Matches: 169
 Percent Similarity: 48.44% Conservative: 110
 Best Local Similarity: 29.34% Mismatches: 258
 Query Match: 19.23% Indels: 39
 DB: 1 Gaps: 14

US-10-006-265-17 (1-662) x US-08-308-881-1 (1-2369)

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Qy 55 TrpSerProGlyLysGluThrSerTyTyThrGlnTyThrValLys-----Arg 70
Db 679 TGGGATGGTGAGAGGAAACACACTTGGAGACAACTTCATTAAATCTGAATGGGCA 738
Qy 71 ThrTyAlaPheGlyGlu-----LysHisAsp-----AsnCyseThrThrAsn 84
Db 739 ACACACAGTTTCTGCTGATTGCAACGAAACCTGACACCCCACTCATGCACTGTGAT 798
Qy 85 SerSerThrSerGluAsnArgAlaSerCyseSerPheLeuProArgIleThrIlePro 104
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Qy 105 AspAsnTyTrpThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer--His 123
Db 820 --AACATTGAAGTCTGGTAGAGACAGAGATGCCCTTGGAGAGTTACATCAGATCAT 876
Qy 124 MetThrTyTrpArgLysGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
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Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 934 ATCAACTCAGAGGAACCTCTAGATATCTTAAATTGATGATGACCAACCAAGTATTAG 993
Qy 164 ProValSerSerAspLeuLysTyTrpLeuArgPheArgThrValAsnSerThrSerTrp 183
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Qy 204 LeuGlnProPheThrGluTyTrpValIleAlaLeuArgCysAlaValLysGluSerLys-- 222
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Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys-- 241
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Db 1348 ACTCTCACAAAGATGAAATCACATTACAAATATTCACAGTTAATGCAACA-----AAA 1401
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Db 1402 CTGACAGTAAATCTTACAAATAGATCGTATCTAGCAACCCCTAACAGTAAGAAATCTTGT 1461
Qy 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
Db 1462 GGCAGATCATGATGCAAGCTGTTTAACATATCCCTGCTGTGACTTTCAAGCATACACCT 1521
  
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Qy 342 ILeuGluValMetGlnAlaCysValAlaGluAsnGlnLeuValValLysTrpGlnSerSer 361
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Qy 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
Db 1582 AGGGAATCTGTAAGAAATATATATCTTACAGTGGTGTGTGTTATCAGTAAGAACCCCTGT 1641
Qy 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeu 401
Db 1642 ATCAACAGCTGCAACAAGAAAGATGTAACCTGTGATCGCACCTTATTAAAGAGGAACCTA 1701
Qy 402 LysProPheTrpCyseTyTrpAsnIleSerValTyTrpPheMetLeuHisAspLysValGly 421
Db 1702 GCAGAGACAAATCTTATTTGATTAACGTTACTCCAGATATAGCTGTGATGAGACCAAGAAC 1761
Qy 422 ProTySerIleGlnAlaTyAlaLysGluGlyAlaProSerGluGlyProGluThrLys 441
Db 1762 CTTGAATCATTAAGCATACCTTAACAGCTCCACCTTCAAGAGACTTACTGTTCCG 1821
Qy 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db 1822 ACAAAAAAGTAGGGAAGAAACGAGCTGTCTTGAAGTGGACCAACTTCTGTGATGTT 1881
Qy 462 ArgLysGlyIleIleCyseAsnTyTrpThrIlePheTyGlnAlaGluGlyLysGlyPhe 481
Db 1882 CAGATGATTTATACAGAAATTAATATATATTTATATGAAACCATCATTTGAAATGAAACT 1941
Qy 482 SerLysThrValAsnSerSerIleLeuGlnIleTyGlyLeuGlnSerLeuLysArgLysThr 501
Db 1942 GCTGTGAATGTGATGATTTCTCCACACAGAAATATCATTTGCTCTTTGACTAGTACACA 2001
Qy 502 SerTyIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyTyThrSerIle 521
Db 2002 TTGTATCATGTAGCAATGAGACATGACATGACATGAGATGGGAGATGCTCCAGAAATTC 2061
Qy 522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
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Qy 542 GlyLysLeuLeuIleLeuIleLeuThrValAlaTyArgLysLeuLysProAsnLys 561
Db 2122 TTACATTTCTTATTAACAACCTTTCTGGAGTCTGTTGCTTTAATTAAGCGAGACTTA 2181
Qy 562 LeuThrHisLeuCyseTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
Db 2182 ATTAATAAAACATCTGGCTTAATGTTCCAGATCTTCAAAAGACTCATATTGCCAGTGG 2241
Qy 582 -----HisGlyAspAspPheLysAspLysLeu 590
Db 2242 TCACCTCACACTCTCCAAAGGCACAAATTTTAATTAACAAGATCAAAATG 2289
  
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RESULT 9

US-09-058-263-1
 Sequence 1, Application US/09058263
 Patent No. 5891997
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple 7.1

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SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,263
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta
IMMEDIATE SOURCE:
CLONE: B10G/PDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-09-058-263-1
Alignment Scores:
Pred. No.: 1,03e-64 Length: 2369
Score: 678.50 Matches: 169
Percent Similarity: 48.44% Conservative: 110
Best Local Similarity: 29.34% Mismatches: 258
Query Match: 19.23% Indels: 39
DB: 2 Gaps: 14
US-10-006-265-17 (1-662) x US-09-058-263-1 (1-2369)
QY 35 ProAlaIaYbProGluAenIleSerCyValTYrTYrAlaGlybAenLeuThrCySerThr 54
DB 619 CCGAAGAAACCTTAAGTAATTTGAGTTCATGTGAACGAGGGGAAGAAATGAGAGTGTAG 678
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DB 679 TGGGATGCTGGAGGGAACACACTTGGAGACAAACTTCATTAAATGTGAATGGCA 738
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QY 85 SerSerThrSerGluAenAlaSerCySerPhePheLeuProArgIleThrIlePro 104
DB 799 TATTCTACT-----GTGATTTTCTC----- 819
QY 105 AspAsnTYrThrIleGluValaGluAenGlyAspGlyValIleIleYbSer---His 123
DB 820 ---AACTTGAAGTCTGGGTAGAAAGACAGAAATGCCCTTGGGAAGTTACATCATCAT 876

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DB 1582 AGGGAATCTGTAAAGAAATATATATCTTGAAGTGTGTGTATCAGATTAAGCACCCCTGT 1641
QY 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspYbSer 401
DB 1642 ATCAAGACTGGCAACAAAGAGATGTCAGTCACTGACCACTTATTAAGAGGAACCTTA 1701
QY 402 LysProPheTrpCySerTYrAsnIleSerValTYrProMetLeuHIAbAspYbValaGly 421
DB 1702 GCAGAGAGCAAAATGCTATTTGATTAACAGTACTCCAGTATATGCTGATGAGACCAAGAAC 1761
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DB 1762 CCTGAATCATTAAGGCAATACCTTAACAAGCTCCACCTTCAAGAGCACTTACTGTTCGG 1821
QY 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
DB 1822 ACAGAAAGAGTGGGAAAAACAGAGCTGTCTTAAGGTGGACCAACTTCTGTGATGTT 1881
QY 462 ArgLysGlyIleIleCyAsnTYrThrIlePheTYrGluAlaGluGlyLysLysPhe 481
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Db 2002 TTGTTCATGAGTACGATGCGATACATACAGATGAGGAGGAGATGCTCAGAAATTC 2061
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 522 AsnPheLysThrLaserPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2062 ACTTTACTACCCCAAGTTGCTCAGAGAAATGGAAGCCATAGTCTGCTGTTGC 2121
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 542 GlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysPheProAsnLys 561
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2122 TTAGCATTCCTATTCACAACTCTCTGGAGTCTGTTCTGTTAATATAGGACACCTA 2181
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 562 LeuThrHisLeuCysTyrProThrValProAsnProAlaGluSerSerIleAlaThrTyr 581
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2182 ATTAATAAACATCATCTGCTATATGTTCAGATCTTCMAAGATCATATTCGCCAGTGG 2241
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Qy 582 -----HisGlyAspAspPheLysAspLysLeu 590
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2242 TCACCTCACACTCTCCAGGACAAATTTAATTCAAAGATCAATG 2289
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RESULT 10
US-09-059-099-1
Sequence 1, Application US/09059099
Patent No. 5925740
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059, 099
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308, 881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249, 553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
TISSUE TYPE: human placenta

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IMMEDIATE SOURCE:
CLONE: B106/pDC303
FEATURE:
NAME/KEY: CDS
LOCATION: 244..2369
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 310..2369
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 244..309
US-09-059-099-1

Alignment Scores:
Pred. No.: 1,03e-64 Length: 2369
Score: 678.50 Matches: 169
Percent Similarity: 48.44% Conservative: 110
Best Local Similarity: 29.34% Mismatches: 258
Query Match: 19.23% Indels: 39
DB: Gaps: 14

US-10-006-265-17 (1-662) x US-09-059-099-1 (1-2369)
Qy 35 ProAlaLysProGluAsnIleSerCysValTyrTyrArgLysAsnLeuThrCysThr 54
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Db 679 TGGGATGTGGAAGGAAACACACTTGGAGACAAACTTAAATTCGAATGGGCA 738
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Qy 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCysThrThrAsn 84
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Db 739 ACACACAGATTGCTGATGTAACAAACAAAGTACACACCCCACTCATGACGTGTAT 798
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Qy 85 SerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArgIleThrIlePro 104
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Db 799 TATTTCTACT-----GTGATTTTGTTC----- 819
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Qy 105 AspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer--His 123
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 820 --AACATTGAAGCTGGGTGAGAGAGAAATGCCCTTGGAGGATTAATCATCATGAT 876
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Qy 124 MetThrTyrTyrPheGluGluAsnIleAlaLysThrGluProPheLysIlePheArgVal 143
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 877 ATCAATTTTGAATCCGTATATATAAAGTG--AAGCCCAATCCGCACATATTTATCAGTG 933
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Qy 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTyrPheLysProGluLeuAla 163
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 934 ATCAACTCAGAGAACTGTCTAGTATCTTAAATTTGACATGACCAACCAAGTATTAG 993
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Qy 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTyr 183
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 994 AGTGTTATATAA---CTAAATATATACATTCATATATAGACCAAGATGCTCAACTGG 1050
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      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1051 AGCCAGATTCCT--CCTGAAGACACAGACATCCACCGATCTTATTCATGCTCAAGAC 1107
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Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
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Db 1108 CTTAAACCTTTTACAGATATATGTCTTTAGGATTTGCTGTATGAAGAGATGTAAGGA 1167
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 223 PheTyrSerAspTyrSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1168 TACTGAGTGTGCTGAGTGAAGAGCAAGTGGGATCTCATATGAATAGCATCTTAA 1227
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 242 GlyLeuGluLeuTyrPheValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Qy 262 LeuLeuTyrLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
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Db      1288 CTCGTGTGAGAGACATGCTCCTTTTGAAGCAATGAGAAAACTTGATTAAGAGTG 1347
Qy      282 TrrpTyTrProgluSerAenThraenLeuThrGluThrMetAenThraenGlnIn 301
Db      1348 ACTCTCAACAAGATGGAATACATTTACAAATAATACACAGTTAAATGCCACA-----AAA 1401
Qy      302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyraenSerLeu 321
Db      1402 CTGACAGTAAATCTCACAATGATCGTATCTAGCAACCTTAACAGTAAGAAATCTTGTT 1461
Qy      322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnIleLysSerPheGlnCys 341
Db      1462 GGCAAATCGAGTACAGTCTGTTTAACTATCCCTGCTGACCTTGAAGTAACTCAACCT 1521
Qy      342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValIlySTpGlnSerSer 361
Db      1522 GTAAATGATCTTAAAGATATCCCAAGATACATGCTTTGGGTGAATGAGTACTCCA 1581
Qy      362 AlaLeuAspValAenThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
Db      1582 AGGGAATCTGTAAAGAAATATATATAGTGTGTGTATCAAGTAAAGCACCTGT 1641
Qy      382 ThrLeuSerTrpGluSerValSerGlnAlaThrAenTrpThrIleGlnIleAspLysLeu 401
Db      1642 ATCAGAGACTGGCAGCAAGAGATGTATCCGTGCATCGCACTTATTTAAGAGGAACTTA 1701
Qy      402 LysProPheTrpCysTyraenIleSerValTyraenMetLeuHisAspLysValGlyGlu 421
Db      1702 GCGAGAGCAATGCTTTTGTATACAGTTACTCCAGTATATCTGATGAGACAGGAAGC 1761
Qy      422 ProTySerIleGlnIleAlaTyraenGlyValProSerGluGlyProGluThrLys 441
Db      1762 CTGAATCCATAAAGCATACCTTAAACAAGCTCCCAAGACCTTCAAGAGACTGATCGG 1821
Qy      442 ValGluAsnIleGlyValIlyThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db      1822 ACAAAAAGATGAGAAAAAGAAAGCTGTCTAGAGGAGCAACCTCTGTGATGTT 1881
Qy      462 ArgLysGlyIleIleCysAenTyraenIlePheTyraenIleGluGlyGlyLysPhe 481
Db      1882 CAGAAATGATTTATCAGAAATTTATCTATTTTATTAAGAACATCATGGAATGAAACT 1941
Qy      482 SerLysThrValAsnSerSerIleLeuGlnTyraenGlyLeuGlnSerLeuLysArgLysThr 501
Db      1942 GCTGTAATGTGATCTTCTCCACACAGATATACATGCTCTTGACTAGTACACA 2001
Qy      502 SerTyIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIle 521
Db      2002 TTGTACATGTGTACGAATGCGACATACAGATGAAGGTGGGAAGATGTCCAGAAATTC 2061
Qy      522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
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Qy      542 GlyGlyLeuLeuLeuLeuIleLeuThrValAlaIleTyraenGlyLysProAsnLys 561
Db      2122 TTAGCATTTCTTATGACAACCTTCTGAGGTGTCTGCTTTAATAAGCGAGACTTA 2181
Qy      562 LeuThrHisLeuGlySTpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
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Qy      582 -----HisGlyAspAspPheLysAspLysLeu 590
Db      2242 TCACCTCACCTCCTCCAAGGCAATTTTAAATTCAAAAGATCAAAATG 2289

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RESULT 11
US-09-058-264-1
; Sequence 1, Application US/09058264
; Patent No. 6010886
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.

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; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,264
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,881
; FILING DATE: 12-SEP-1994
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seebe, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; TISSUE TYPE: human placenta
; IMMEDIATE SOURCE:
; CLONE: B10G/pDC303
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 244..2369
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 310..2369
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 244..309
; US-09-058-264-1
; Alignment Scores:
; Pred. No.: 1,03e-64 Length: 2369
; Score: 678.50 Matches: 169
; Percent Similarity: 48.44% Conservative: 110
; Best Local Similarity: 29.34% Mismatches: 258
; Query Match: 19.23% Indels: 39
; DB: 3 Gaps: 14

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US-10-006-265-17 (1-662) x US-09-058-264-1 (1-2369)
Qy      35 ProAlaLysProGluAsnIleSerCysValTyTyTrArgLysAsnLeuThrCysThr 54
Db      619 CCAGAAAACCTTAAATTTGAGTTGTCGTAACGAGGGAAGAAATGAGGTGTAG 678
Qy      55 TrpSerProGlyLysGluThrSerTyraenGlnTyraenValLys-----Arg 70
Db      679 TGGGATGTGTGAAGGGAACACACTTGAGACAACTTGAATCTGAATGGGCA 738

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Qy 71 ThrTyrAlaPheGlyGlu-----LysHisAsp-----AsnCyserThrHisen 84
Db 739 ACACAAAGATTGCTGATGTCACAAAGCAAACTGACACCCCACTTCACGACTGTTGAT 798
Qy 85 SerSerThrSerGluAsnArgAlaSerCyserPheLeuProArgIleThrIlePro 104
Db 799 TATTCTACT-----GTCGATTTTGTG----- 819
Qy 105 AsparTyrThrIleGluValAlaGluAsnGlyAspGlyValIleLysSer---His 123
Db 820 ---AACATTGAAGCTGGGTAGACAGAGATGCCCTTGGAAGGTTACATCATCAT 876
Qy 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
Db 877 ATCAATTTTGATCTGTTATATTAAGTG---AAGCCCAATCCGCACATTAATTATTCAGTG 933
Qy 144 LysProValIleGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 934 ATCAACTCAGAGGAAGTCTGATGATCTTAAATGACATGACAGCAACCCAGATTTAG 993
Qy 164 ProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 994 AGTGTATTATATTA---CTAAATATATTAACATTCATATAGGACCAAGATGCTCAACTGG 1050
Qy 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThrGly 203
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Qy 204 LeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys--- 222
Db 1108 CTTAAACCTTTTACGAATATGTGTTAGAGATTCCTGATGACAGAAAGATGTTAAGGA 1167
Qy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaProCys--- 241
Db 1168 TACTGAGTGAAGTGAAGAGAACCAAGTGGATCAGCTATGAGATGACATCTTAA 1227
Qy 242 GlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
Db 1228 GCACCAAGTTCTGTATTAATAATATACATTCCTCACTCAAGGCTTACAGAACTGTA 1287
Qy 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIle 281
Db 1288 CTCGCTGGAAGACATTCGCTCTTTGAAGCCAAATGGAATTTGATTTAAGTG 1347
Qy 282 TrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 301
Db 1348 ACTCTCAAGATGGAATACATTCATTAACAAATTAACAGTTAATGCCACA-----AAA 1401
Qy 302 LeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
Db 1402 CTGACAGTAACTCTCAAAATGATGCTATTCAGCAACCTCAAGTAAGAAATCTTGT 1461
Qy 322 GlyLysSerProValAlaThrIleuArgIleProAlaIleGlnLysSerPheGlnCys 341
Db 1462 GGCAATATAGATGCGCTGTTTAACTATCCCTGCTGCTGACTTCAAGCTACTACCT 1521
Qy 342 IleGluValMetGlnAlaCysValAlaGluAsnGluValLysTrpGlnSerSer 361
Db 1522 GTAATGATCTTAAAGCATTCCTCCAAAGATAACATGCTTGGGTGGAATGACTCTCA 1581
Qy 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
Db 1582 AGGGAATCTGTAAGAAATATATCTTGAAGTGCTGTGTATTCAGATTAAGCAACCTGT 1641
Qy 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
Db 1642 ATCACAAGCTGGCAACAAAGATGATGACCGGCACTCCATTTAAGAGGAACCTTA 1701
Qy 402 LysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
Db 1702 GCAAGAGCAAAATGCTATTTGATTAACAGTACTCCAGATATATGCTATGACAGCAAGAC 1761

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Qy 422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
Db 1762 CTTGATATCATTAAGGCACTACTTAAACAGCTCCACTTCAAGAGCACTACTGTCGG 1821
Qy 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db 1822 ACAAAAAAGTAAAGGAAAAAGAGAGCTGCTTAGAGTGGAACCAACTTCCTGTTGATGT 1881
Qy 462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481
Db 1882 CAGATGATTTATTCAGAAATTAATCTATTTATTAAGAACCATCATTCAGAAATGAACT 1941
Qy 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgSerThr 501
Db 1942 GCTGGAATGTGATCTTCCACACAGAAATATACATTTCTCTTTACATGACACCA 2001
Qy 502 SerTyrIleValAlaGlnValMetAlaSerThrSerAlaGlyTyrAsnGlyThrSerIle 521
Db 2002 TTGTACATGATGATGAGATGAGAGCATACAGATGAGGTGGGAAGATGTCAGAAATTC 2061
Qy 522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
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Db 2182 ATTAATAAAACACATGCGCTATATGTTCCATCTTCAAAAGATCAATATGGCCAGTG 2241
Qy 582 -----HisGlyAspAspPheLysAspLysLeu 590
Db 2242 TCACCTCACACTCTCCAGGACACAATTTTATTCAAAGATCAATG 2289

RESULT 12
US-09-455-962-1
; Sequence 1, Application US/09455962
; Patent No. 6524817
; GENERAL INFORMATION:
; APPLICANT: Mosley, Bruce
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Receptor for Oncostatin M
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/455,962
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,264
; FILING DATE:
; APPLICATION NUMBER: US 08/249,553
; FILING DATE: 26-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2614-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644

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/ TELEEX: 756822
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2369 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ TISSUE TYPE: human placenta
/ IMMEDIATE SOURCE:
/ CLONE: B10G/PDC303
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 244..2369
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 310..2369
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 244..309
/ US-09-455-962-1

```

Alignment Scores:

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Pred. No.: 1,03e-64 Length: 2369
Score: 678.50 Matches: 169
Percent Similarity: 48.44% Conservative: 110
Best Local Similarity: 29.34% Mismatches: 258
Query Match: 19.23% Indels: 39
DB: 4 Gaps: 14

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US-10-006-265-17 (1-662) x US-09-455-962-1 (1-2369)

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QY 35 ProAlaLysProGluAsnIleSerCysValTyrTyrTyrArgLysAsnLeuThrCysThr 54
Db 619 CCGAATAAACTTAATAATTTGAGTTGTCATGTGAACGAGGAAAGAAATGAGGTGTGAG 678
QY 55 TTPSerProGluLysGluThrSerTyr--ThrGlnTyrThyValLys-----Arg 70
Db 679 TGGAGTGTGGAGGAAACACCTTGGAGACAACTTCACTTAAATCTGAATGGGCA 738
QY 71 ThrTyrAlaPheGluGlu-----LysHisASP-----AsnCysThrThrAsn 84
Db 739 ACAACACAGTTTCTGATTCGAAAGCAAAACGTCACACCCCACTCATGCTGTGGAT 798
QY 85 SerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgIleThrIlePro 104
Db 799 TATTCTACT-----GTGATTTTGTCT----- 819
QY 105 AspAsnTyrThrIleGluValIleGluIleAsnGlyAspGlyValIleLysSer---His 123
Db 820 ---AACATTGAACTCTGGGTGAAGACAGAAATGCCCTTGGGAAGGTTCATCATGATCAT 876
QY 124 MetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArgVal 143
Db 877 ATCAATTTGATCTCTGATATAAGTG--AAAGCCCAATCCGCACTAATTTATCATGAG 933
QY 144 LysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
Db 934 ATCAACTCAGAGAACTGTGATGATCTTAAATTTGATGACGCAACCAAGATATTAAAG 993
QY 164 ProValSerSerAspLeuLysIleTyrIleLeuArgPheArgThrValAsnSerThrSerTrp 183
Db 994 AGTGTATATATA---CTAAATATTAACATTCAATATATGACCAAAAGATGCTCAACTGG 1050
QY 184 MetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnIleThrIleLeuThrGly 203
Db 1051 AGCCAGATTCTCT---CTGAAGACACAGCATCCACCCGATCTTCATCTGCTCAAGAC 1107
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Db 1108 CTTAAACCTTTACAGAAATATGTTAGATTCGCTGATGAGAGAAATGTGAAGGA 1167
QY 223 PheTTPSerAspTTPSerGlnGluLysMetGlyMetThrGlnGluLysProCys--- 241
Db 1168 TACTGAGTACTGAGTGAAGCAAGCAAGTGGATCATCTATGAAGATGACCATTA 1227
QY 242 GlyLeuGluLeuThrArgValIleLysPProAlaGluAlaAspGlyLysArgProValArg 261
Db 1228 GCACCAAGTTTCTGTATATAAATAGATCCATCCATACCAAGCTACAGAACTGACAA 1287
QY 262 LeuLeuTrpLysLysAlaArgLysAlaProValIleGluLysThrLeuGlyTyrAsnIle 281
Db 1288 CTCGTGTGAAACATTTGCCCTCTTTGAAGCCAATGAGAAATCTTGATTAAGAAGTG 1347
QY 282 TTPTrpTyrProGluSerAsnThrAsnLeuThrGlnIleThrMetAspThrThrAsnGln 301
Db 1348 ACTCTCAAGATGGAATCACTTAACAAATTAACACAGTTAATGCCACA-----AAA 1401
QY 302 LeuGluLeuHisLeuGlyLysGluSerPheTrpValSerMetIleSerTyrAsnSerLeu 321
Db 1402 CTGACAGTAAATCTCAAAATGATGCGCTATCTAGCAACCCCTAAGATAAATCTGTT 1461
QY 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
Db 1462 GCGAATCAGATGACGCTGTTTAACTATCCCTGCTGATCTTCACACTCAACCTG 1521
QY 342 IleGluValMetGlnAlaCysValAlaGluAsnArgIleLeuValValLysTrpGlnSerSer 361
Db 1522 GTTAATGATCTTAAGACATCTCCCAAGAAATACATGCTTTGGATGAATGAACTATCCA 1581
QY 362 AlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThr 381
Db 1582 AGGGAATCTGTAAGAAATATATATCTAGTGTGTGTGTGTATACATGAAGACCCCTGT 1641
QY 382 ThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIleAspLysLeu 401
Db 1642 ATCACAGACTGGACACAAAGATGGTACCGTCATCCGACCTATTAAGAGGAACCTTA 1701
QY 402 LysProPheTrpCysThrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
Db 1702 GCGAGAGCAAAATGCTATTGTGAATACAGTTACTCCAGTATATGCTGATGACCAAGAAC 1761
QY 422 ProTyrSerIleGlnIleTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
Db 1762 CCTGAATCATAAAGCATACCTTAACAAGCTCCACTTCCAAAGCATCTACTGTCCG 1821
QY 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
Db 1822 ACNAAAAAGTAGGGAATAAAGACGCTGTCTAGAGTGGACCAACTTCTGTGATGTT 1881
QY 462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481
Db 1882 CAGATAGATTTATACGAATATATCTATATTTTAAGAACATCATCTGGAATGAACACT 1941
QY 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
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QY 522 AsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
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QY 542 GlyGlyLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLysProAsnLys 561
Db 2122 TTAGCATCTCTATGCAACTCTTCTGAGAGTGTCTGTCTTAAATGAAGACACTA 2181
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Db 2182 ATTAACAAACATCTGCGCTAATGTTCAGATCCTTCAAGAGATCATATGCCAGTGG 2241
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RESULT 13
 PCT-US95-06530-1
 Sequence 1, Application PC/TUS9506530
 GENERAL INFORMATION:
 APPLICANT: Mosley, Bruce
 APPLICANT: Cosman, David J.
 TITLE OF INVENTION: Receptor for Oncostatin M
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06530
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/308,881
 FILING DATE: 09-SEP-1994
 APPLICATION NUMBER: US 08/249,553
 FILING DATE: 26-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Anderson, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2614-MO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2369 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 TISSUE TYPE: human placenta
 IMMEDIATE SOURCE:
 CLONE: B10G/pDC303

FEATURE:
 NAME/KEY: CDS
 LOCATION: 244..2369
 FEATURE:
 NAME/KEY: mac_peptide
 LOCATION: 310..2369
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 244..309
 PCT-US95-06530-1

Alignment Scores:
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 Percent Similarity: 48.44% Conservative: 110
 Best Local Similarity: 29.34% Mismatches: 258

Query Match: 19.23% Indels: 39
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Oy 55 TrpSerProGlyIysGluThrSerTrp--ThrGlnTrpValIys-----Arg 70
 Db 679 TGGATGGTGAAGGAAACACACTGGAGCAAACTTCACTTAATCTGAATGGGCA 738

Oy 71 ThrTrpAlaPheGlyGlu-----LysHisAsp-----AsnCysThrAsn 84
 Db 739 ACACACAGTTTGCTGATTCGAAACCAAGTAACACCCACCCTCGACGTGAT 798

Oy 85 SerSerThrSerGluAsnArgAlaSerCysSerPheLeuProArgIleThrIlePro 104
 Db 799 TATCTACT-----GTGATTTTGTG----- 819

Oy 105 AspAsnTrpThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer--His 123
 Db 820 --AACATTTGAAGCTGGGTGAAGCAGAGATCCCTTGGAGAGGTACATCAT 876

Oy 124 MetThrTrpTrpArgGluGluAsnIleAlaLysThrGluProPheLysIlePheArgVal 143
 Db 877 ATCAATTTTGATCCGTGATATATTAAGTG--AAGCCCAATCGCCACATATTTATCATGTG 933

Oy 144 LysProValIleGluGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeuAla 163
 Db 934 ATCAACTCAGAGAACTGTAGTATCTTAATATGATGACCAACCAAGATTTAAG 993

Oy 164 ProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSerThrSerTrp 183
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Oy 223 PheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaProCys-- 241
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Oy 242 GlyLeuGluLeuTrpArgValIleLeuLysProAlaGluAlaAspGlyArgArgProValArg 261
 Db 1228 GCACCAAGTTTCTGTATTAATATAGATCCATCCCATCTCAAGGCTTCAGAGATGTCA 1287

Oy 262 LeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTrpAsnIle 281
 Db 1288 CTGTGTGAAGACATTCCTCTTTGAAGCCAAAGAAATCTTGATTAAGAAATG 1347

Oy 282 TrpTrpTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGlnGln 301
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Oy 302 LeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTrpAsnSerLeu 321
 Db 1402 CTGACAGTAAATCTCACAAATGATGCTATCTTACCAACCTTCAGTAAGAAATCTTGT 1461

Oy 322 GlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCys 341
 Db 1462 GGCAAATCAAGTGAAGCTGTTTAACTTATCCCTGCTGACTTCAAGTCACTACACCT 1521

Oy 342 IleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSerSer 361
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OY 262 LeuLeuTyrPylValAlaArgLysAlaProValLeuGluLysThrLeuGlyLysAsnLe 281
DB 1045 CTCGGTGGAGACATGGCTCTTTTGAAGCCATGCAAAATCTGGATTAATGAAGTG 1104
OY 282 TrrPylTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGln 301
DB 1105 ACTCTCACAAGATGGAATTCACATTATTAACAAATTCACAGATTAAAGCCACA-----AAA 1158
OY 302 LeuGluLeuHisLeuGlyLysLeuSerPheThrPylAsnSerMetLysSerThrAsnSerLeu 321
DB 1159 CTGACAGTAACTCAAAATGATGCTATCTAGCAACCCCTAAGCAAGTAAGAAATCTTGT 1218
OY 322 GlyLysSerProValAlaThrLeuArgLysProAlaIleGlnGluLysSerPheGlnCys 341
DB 1219 GGCAAATCAGATGCAAGCTGTTTAACTATCCCTGCTGAGACTTCAAGCTACCACTCCT 1278
OY 342 IleGluValMetGluAlaCysValAlaGluAspGlnLeuValValLysTyrGlnSerSer 361
DB 1279 GTAAATGATCTTAAAGCATTCCTCCCAAGATTAACATGCTTGGGGAATGAGACTCTCA 1338
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DB 1339 AGGGAATCTGAAGAAATTAATTAAGTGTGTGTGTATTCAGATTAAGCACTCTGT 1398
OY 382 ThrLeuSerTyrGluSerValSerGlnAlaThrAsnTrrPylIleGlnIleAspLysLeu 401
DB 1399 ATCAAGACTGGCAAGAGATGTAACCGTCACTCCCACTATTAAGAGGAACTTA 1458
OY 402 LysPheProThrTyrTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGlu 421
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OY 422 ProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLys 441
DB 1519 CCTGAATCATTAAGCAATCACTTAACAGACTCCCACTCAAGCACTCACTGTTGG 1578
OY 442 ValGluAsnIleGlyValLysThrValThrIleThrTrrPylGluIleProLysSerGlu 461
DB 1579 ACAAATAAGATGGAAGAAACCAAGCTGCTTAAGTGGGCAACTCTCTTATGTT 1638
OY 462 ArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPhe 481
DB 1639 CAGAAATGATTTATCAGAAATTAATTAATTAATTAAGAACATCATTTGAATGAAC 1698
OY 482 SerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThr 501
DB 1699 GCTGTGAATGTGGATTTCTCCACACAGAAATATACATTGTCTCTTATCACTAGTACCA 1758
OY 502 SerTyrIleValAlaIleValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSerIle 521
DB 1759 TTGTAATCATGTAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1818
OY 522 AsnPheLysThrLysSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
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OY 542 GlyLysLeuLeuIleLeuIleLeuThrValAlaTyrGlyLeuLysLeuPheAsnLys 561
DB 1840 -----GAA 1842
OY 562 LeuThrHisLeuCysTrrProThrValProAsnProAlaGluSerSerIleAlaThrTrr 581
DB 1843 TTTAAAAAACAC-ATGTGCTTAATTTCTCAATCTTCAAAAGTCAATATTTGCCAGTGG 1901
OY 582 -----HisGlyAspAspPheLysAspLysLeu 590
DB 1902 TCACCTCACACTCTCCAAAGCACAATTTTAATTCAAAAGATCAAAATG 1949

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RESULT 15
US-09-312-611-3
; Sequence 3, Application US/09312611
; Patent No. 6380160
; GENERAL INFORMATION:
; APPLICANT: SHARKEY, ANDREW
; APPLICANT: SMITH, STEPHEN K.
; APPLICANT: DELLOW, KIMBERLEY A.
; TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,611
; FILING DATE: 17-MAY-1999
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0623_0530002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1974
; US-09-312-611-3

Alignment Scores:
Pred. No.: 3,596-60 Length: 1977
Score: 636.50 Matches: 163
Percent Similarity: 46.53% Conservative: 105
Best Local Similarity: 28.30% Mismatches: 237
Query Match: 18.04% Indels: 72
DB: 3 Gaps: 15

US-10-006-265-17 (1-662) x US-09-312-611-3 (1-1977)
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 Db 1843 TTAAAAAACAC-ATCTGGCTTATGTTCCAGATCTCTTCAAGAGTCAATATTTGCCCATGG 1901
 QY 582 -----HisGlyAspAspPheLysAspLysLeu 590
 Db 1902 TCACTCACACTCTTCAAGGCAAAATTTTAAATTCAAAAGATCAAAATG 1949

Search completed: February 23, 2005, 19:36:50
 Job time : 349.791 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 09:15:27 ; Search time 1030.62 Seconds
(without alignments) 3796.488 Million cell updates/sec

Title: US-10-006-265-17

Perfect score: 3528
Sequence: 1 MKLSBPQSCVNLGMWMTWL.....NNLGEKXKXTRILLSCPTSI 662

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
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Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -IOBEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=plowm62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTENT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10006265_@CGN 1.1 1175 @runat_18022005_094659_22236
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3528	100.0	2119	15	US-10-006-265-16
2	3528	100.0	2903	15	US-09-892-949-53
3	3528	100.0	2903	17	US-10-351-157-4
4	3528	100.0	2903	17	US-10-352-554-4
5	3528	100.0	2903	18	US-10-772-531-53
6	3518	99.7	2529	10	US-09-892-949-45
7	3518	99.7	2529	17	US-10-351-157-108
8	3518	99.7	2529	18	US-10-772-531-45
9	3512	99.5	2969	15	US-10-006-265-1
10	3465.5	98.2	2238	10	US-09-972-708-5
11	3465.5	98.2	2238	18	US-10-715-667-5
12	3465.5	98.2	2402	10	US-09-892-949-1
13	3465.5	98.2	2402	17	US-10-351-157-110
14	3465.5	98.2	2402	18	US-10-772-531-1
15	3465.5	98.2	2480	10	US-09-972-708-3
16	3465.5	98.2	2480	18	US-10-715-667-3
17	2888	81.9	1986	10	US-09-892-949-55
18	2888	81.9	1986	17	US-10-351-157-122
19	2888	81.9	1986	18	US-10-772-531-55
20	2853	80.9	2295	10	US-09-892-949-68
21	2853	80.9	2295	17	US-10-351-157-38
22	2853	80.9	2295	17	US-10-352-554-28
23	2853	80.9	2295	18	US-10-772-531-68
24	2836	80.4	1947	10	US-09-892-949-47
25	2836	80.4	1947	17	US-10-351-157-121
26	2836	80.4	1947	18	US-10-351-157-47
27	2806.5	79.5	2196	10	US-09-892-949-4
28	2806.5	79.5	2196	17	US-10-351-157-120
29	2806.5	79.5	2196	18	US-10-772-531-4
30	2782	78.9	1557	17	US-10-351-157-70
31	2782	78.9	1557	17	US-10-352-554-70
32	2606	73.9	2445	14	US-10-227-884-91
33	2606	73.9	2445	14	US-10-230-163-91
34	2606	73.9	2445	14	US-10-230-338-91
35	2606	73.9	2445	14	US-10-218-631-91
36	2606	73.9	2445	14	US-10-210-414-91
37	2606	73.9	2445	14	US-10-212-224-91
38	2606	73.9	2445	14	US-10-212-159A-91
39	2606	73.9	2445	14	US-10-218-849-91
40	2606	73.9	2445	14	US-10-227-873-91
41	2606	73.9	2445	14	US-10-227-883-91
42	2606	73.9	2445	14	US-10-219-076-91
43	2606	73.9	2445	14	US-10-230-434-91
44	2606	73.9	2445	14	US-10-219-003-91
45	2606	73.9	2445	14	US-10-219-075-91

ALIGNMENTS

RESULT 1
US-10-006-265-16
; Sequence 16, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, NO. US20030125520A1:ko
; TITLE OF INVENTION: NOVEL HEMOPHILIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006, 265
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16

; LENGTH: 2119
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (11) ... (1996)
 ; US-10-006-265-16

Alignment Scores:

Pred. No.:	0	Length:	2119
Score:	3528.00	Matches:	662
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-10-006-265-17 (1-662) x US-10-006-265-16 (1-2119)

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QY      1 MetLysLeuSerProGlnProSerCybValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
DB      11 ATGAAGCTCTCTCCAGCCTTCATGTGTTAACTGGGGATGATGTGACCTGGGCACTG 70

QY      21 TrpMetLeuProSerLeuCybLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
DB      71 TGGATCCTCCCTCCACTGTCGAAATTCAGCCTGCGACTCTGCGAGCTAAGCCTGGAAC 130

QY      41 LLeSerCybValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB      131 ATTTCCTGTGCTACTACTACTAGAAAAATTTAACTTGACCTTGAGTCCAGAAAGGAA 190

QY      61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
DB      191 ACAGATTATATCCAGTACACAGATTAAAGAACTTAAGCTTTGAGAAAAAACAATGATAAT 250

QY      81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB      251 TGTACAAACCAATAGTCTCAAGTGAATAATCGGCTCGCTCTTTTTCCTTCCAAAG 310

QY      101 LLeThrLLeProAspAsnTyrThrLLeGluValGlnAlaGluAsnGlyAspGlyValLLe 120
DB      311 ATACACATCCCAATATTTATACATTGAGCTGAAAGCTGAAATGAGATGAGTGAAT 370

QY      121 LysSerHisMetThrTyrTrpArgLeuGluAsnLLeAlaLysThrGluProProLysLLe 140
DB      371 AAATCATATATGACATATGAGATTAAGAAACATAGCGAAACCTGAACCACTTAAGATT 430

QY      141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
DB      431 TTCCTGGTGAACCAAGTCTTGGGCATCAACGATGATTCAAAATTGATGATGAAGAAAGCCT 490

QY      161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
DB      491 GAGTTGGCCCTTTTCATCTGATTTAAATTAACAACCTTCGATTTCAGAGACATCAACAGT 550

QY      181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
DB      551 ACCAGCTGATGAGATGCAACTTCGCTAAGAACCGTAAGATTAACCAACCAAGTCAAC 610

QY      201 LeuThrGlyLeuGlnProPheThrGluTyrValLLeAlaLeuArgCysAlaValLysGlu 220
DB      611 CTCACGGGGCTGAGAGCTTTTACAGAAATGTGATAGCTCTGCGAGTGGGGTCAAGGAG 670

QY      221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
DB      671 TCAAAATTTCTGAGATGACTGAGACCCAAAGAAAAATGGAAATGACTGAGAGAAAGCTCCA 730

QY      241 CysGlyLeuGluLeuTrpArgValLLeLysProAlaGlnAlaAspGlyArgArgProVal 260
DB      731 TGTGGCTGGAACCTGAGAGAGTCTGAAACCAAGCTGAGGCGGATGGAAGAAAGCCAGTG 790

QY      261 ArgLeuLeuTrpLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
DB      791 CGGTGTGTATGGAAGAGCCAAAGAGAGCCCAAGTCTTAGAGAAAAACACTTGGCTCAAC 850
  
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QY      281 LLeTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
DB      851 ATATGCTACTATCCAGAAAGCAACCTAACCTCAAGAAACAATGAACACTACTAACCAAG 910

QY      301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetLLeSerTyrAsnSer 320
DB      911 CAGCTTGAACGTGATCTGGAGGCGGAGAGCTTTTGGGTGTATGATTTCTTATATTC 970

QY      321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
DB      971 CTTGGGAAGTCTCCAGTGGCCACCCCTGAGGATTCACGCTATTCAGAAAAATCATTTTCAG 1030

QY      341 CysLLeGluValMetGlnAlaCysValAlaGluAspGluLeuValValLysTrpGlnSer 360
DB      1031 TGCATTGAGGTCAATGAGGCTCGCTGCTGAGACCACTAGCTGTAAGTGGCAAGC 1090

QY      361 SerAlaLeuAspValAsnThrTrpMetLLeGluTrpPheProAspValAspSerGluPro 380
DB      1091 TCTGCTCTAGAGGTGAACCTTGATGATTTGAATGATTTCCGGAATGTGACTCAGAGCCC 1150

QY      381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrLLeGlnGluAspLys 400
DB      1151 ACCACCTTTCCTGGGAATCTGTCTCAGGCCACCAACTGACAGATCCAGCAAGATAAA 1210

QY      401 LeuLysProPheTrpCysTyrAsnLLeSerValTyrProMetLeuHisAspLysValGly 420
DB      1211 TTTAAACCTTTCTGAGCTATTAACATCTGTGTATCCAAATGTGATGATACAAAGTTGGC 1270

QY      421 GluProTyrSerLLeGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThr 440
DB      1271 GAGCCATATTCATCCAGGCTTATGCAAAAGGGGTTCATCAAGAAAGTCCCTGAGACC 1330

QY      441 LysValGluAsnLLeGlyValLysThrValLLeThrLLeTrpLysGluLLeProLysSer 460
DB      1331 AAGGTGAGAAACATTTGGCGTGAAGACGTACAGATCACATGAAAGATTTCCCAAGAT 1390

QY      461 GluArgLysGlyLLeLLeCysAsnTyrThrLLePheTyrGlnAlaGluGlyLysGly 480
DB      1391 GAGAGAAAGGTATCATCTGCAACTACACACTTTTACCAAGCTGAAAGTGAAGAAAGCA 1450

QY      481 PheSerLysThrValAsnSerSerLLeLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
DB      1451 TTCTCCAAAGACATCATTCAGACATCTTGACAGTACGGCTGGAGTCCCTGAAACCAAG 1510

QY      501 ThrSerTyrLLeValGlnAlaMetLLeSerThrSerAlaGlyGlyThrAsnGlyThrSer 520
DB      1511 ACCTCTTACATTTTCAGGTCAATGGCCAGCACCAAGTGTGGGGGAAACCAACGGGACCCAGC 1570

QY      521 LLeAsnPheLysThrLeuSerPheSerValPheGluLLeLLeLeuLLeThrSerLeuLLe 540
DB      1571 ATTAATTTCAAGACATTTGATTCATCACTGCTTGGAGATTTATCTCTCAATCTTCTGATT 1630

QY      541 GlyGlyGlyLeuLeuLLeLeuLLeLLeLeuThrValAlaTyrGlyLeuLysLysProAsn 560
DB      1631 GGTGAGGCTCTTATATCTCATTTCTGATATCTGACAGTGCATATGTGTCAAAAAACCAAC 1690

QY      561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerLLeAlaThr 580
DB      1691 AAATTGACTCATCTGTGTGGCCACCGTTCCCAACCTGTGAAAGTGTATGACCA 1750

QY      581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGlyLLeSerAspAspSerValAsn 600
DB      1751 TGGCATGAGATGATTTCAAGATTAAGCTTAACCTGAAGAGATCTGATACCTGTGAAC 1810

QY      601 ThrGluAspArgLLeLeuLysProCysSerThrProSerAspLysLeuValLLeAspLys 620
DB      1811 ACAGAAAGACAGATCTTAACCAATGTTCCACCCCAAGTGAACAAGTTGTGATTGCAAG 1870

QY      621 LeuValValAsnPheGlyAsnValLeuGlnGluLLePheThrAspGluLLeArgThrArg 640
DB      1871 TTGGTGTGTAACTTTGGGATGTTCGCAAGAAATTTTTCACAGATGAACCCAGAAAGGGGT 1930
  
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QY 641 GINGUAENASnLeuG1YQ1YGLuYbAenG1YThrArg1LeuSerSerCySPProThr 660
DB 1931 CAGGAAACAAATTTAGAGGAGGAAAGAAATGGGACTAGAAATTCCTCTCCGCCCACT 1990
QY 661 Serile 662
DB 1991 TCAATA 1996

RESULT 2
US-09-892-949-53
; Sequence 53, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kujper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 2903
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497)...(2482)
US-09-892-949-53

Alignment Scores:
Pred. No.: 0 Length: 2903
Score: 3528.00 Matches: 662
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 10

US-10-006-265-17 (1-662) x US-09-892-949-53 (1-2903)

QY 1 MetLysLeuSerProGlnProSerCybValAsnLeuGlyMetMetTrpThrTyrAlaLeu 20
DB 497 ATGAAGCTCTCTCCACCCCTTCATGTGTAACTGGGAGATGATGTGACCTGGGACACTG 556
QY 21 TrpMetLeuProSerLeuCybValbPheSerLeuAlaLeuProAlaLeuProGln 40
DB 557 TGGATGCTCCCTTCACTGCAATTCAGCCCTGGAGCTCTGCGACTGAAGCTGAGAAC 616
QY 41 lIleSerCybValYrTYrTYrArgLYbAsnLeuThrCybThrTrpSerProGlyLYbGlu 60
DB 617 ATTTCCTGTGTCTACTACTATAGGAAAAATTTAACTGCACCTTGAGCTCGAGAAAGAA 676
QY 61 ThreSerYrThrGlnTYrTYrValLYbArgThryAlaPheGlyGLuLYbHISAspAsn 80
DB 677 ACCAGTTTACCCAGTACACAGTTAAAGAACTTACGCTTTGGAGAAAAATCATGATAT 736
QY 81 CysThrTrpAsnSerSerThreSerGluAsnArgAlaSerCybSerPhePheLeuProArg 100
DB 737 TGTACACCAATAGTTCTACAGTGAAGAAATGCTGTGTGTCTTTTTCCTTCACAGA 796
QY 101 lIleThrIleProAspAsnTYrThrylIleGluValGluAlaGluAsnGlyAspGlyValIle 120
DB 797 ATAAGATCCCAAGATTAATATACATTGAGGTGAGAGCTGAAGAAATGAGAGTGTATTT 856

QY 121 LysSerHISmetThrTYrTrpArgLeuGluAsnIleAlaLYbThrGluProProValIle 140
DB 857 AAATCTCATATGACATCTAGAGATTAAGAAACATAGGAAAAATGACCACTTAAGATT 916
QY 141 PheArgValLYbProValLeuGlyYlIeLYbArgMetIleGlnIleGluTrpIleLYbPro 160
DB 917 TTCCTGTGAACCAAGTTTGGGCACTCAAGAAATGATTTCAAAATTTGAATGAATAAGCT 976
QY 161 GluLeuAlaProValSerSerAspLeuLYbTYrThrLeuArgPheArgThryAlaAsnSer 180
DB 977 GAGTTGGCGCGCTGTTTCATCTGATTTAAATACACACTTCATTCAGGACAGTCAACAGT 1036
QY 181 ThrSerTrpMetGluValAsnPheAlaLYbAsnArgLYbAspLYbAsnGluThrTYrAsn 200
DB 1037 ACCAGCTGATGAAGTAACTGCTGTAAGAACGTAAAGATTAAGAAACCAACGTACAAAC 1096
QY 201 LeuThrGlyLeuGlnProPheThrGluTYrValIleAlaLeuArgCybAlaValLYbGlu 220
DB 1097 CTCACGGGGCTGCACCTTTTACAGAAATATGTCATAGCTCTGCCATGTGCCGTCAAGAG 1156
QY 221 SerLYbPheTrpSerAspTrpSerGlnGluLYbMetGlyMetThryGluGluAlaPro 240
DB 1157 TCAAAATTCTGAGAGTACTGAGCCAAAGAAAAATGGGAATGACTGAGGAAGAGCTCCA 1216
QY 241 CysGlyLeuGluLeuTrpArgValLeuLYbProAlaGluAlaAspGlyArgArgProVal 260
DB 1217 TGTGGCTGGAACTGTGAAGAGTCTTGAAACAGCTGAGGCGGAGTGAAGAAAGCCAGTG 1276
QY 261 ArgLeuLeuTrpLYbLYbAlaArgGlyValaProValLeuGluLYbThryLeuGlyTYrAsn 280
DB 1277 CGGTTGTTATGGAAGAAAGCAAGAGAGCCCAAGTCCATAGAAACACTTGGCTACAAAC 1336
QY 281 lIleTrpTYrTYrProGluSerAsnThryAsnLeuThryGluThrMetAsnThrThryAsnGln 300
DB 1337 ATATGTACTATCCAGAAAGCAACACTTAACCTCAGAAACAAATGAACATACTAAACAG 1396
QY 301 GluLeuGluLeuHISLeuGlyGLuSerPheTrpValSerMetIleSerTYrAsnSer 320
DB 1397 CAGCTTGAACGTCACTGGAGAGCGAGAGCTTTGGGTGTGTATGATTTCTTAATAATCT 1456
QY 321 LeuGlyLYbSerProValAlaThrLeuArgIleProAlaIleGlnGluLYbSerPheGln 340
DB 1457 CTGGGAAGTCTCCAGTGGCCACCTGAGAGTTCCAGTATTTCAAGAAAAATCATTTGAG 1516
QY 341 CysIleGluValMetGlnAlaCybValAlaGluAspGlnLeuValLYbTrpGlnSer 360
DB 1517 TGCATTGAGGTCAATGACAGGCTGCGTTGCTGAGGACCAAGTATGTGTAAGTGGCAAGC 1576
QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
DB 1577 TCTGTCTTACAGCGTGAACACTTGATGATTAAGGTTTCCGGAATGTGGACTCAGAGCC 1636
QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpTrpIleGlnIleAspLYb 400
DB 1637 ACCACCTTTCTGGAAATCTGTCTCAGGCCAGAACTGAGATCCAGACCAAGATTA 1696
QY 401 LeuLYbProPheTrpCYbTYrAsnIleSerValTYrProMetLeuHISAspLYbValGly 420
DB 1697 TTTAAACCTTTCTGTGTCTATTAATCATCTGTGATCAATGTTGATGACAAAGTTGGC 1756
QY 421 GluProTYrSerIleGlnAlaTYrAlaLYbGluGlyValProSerGluGlyProGluThr 440
DB 1757 GAGGCATATTCATCCAGGCTTAATGCAAAAGAGCGTTTCATAGAAAGTCTGAGAGCC 1816
QY 441 LysValIleGluAsnIleGlyValLYbThryValThrylIleThryTrpLYbGluIleProLYbSer 460
DB 1817 AAGGTGAGAAACATTTGGCGTGAACAGCTCACATCACTGAGAAAGATTTCCCAAGAGT 1876
QY 461 GluArgLYbGlyIleIleCYbAsnTYrThrylIlePheThryGlnAlaGluGlyLYbGly 480
DB 1877 GAGAGAAAGGATATCATCTGCACTACACCATTTTAAACCAAGTGAAGGTGAAGAAAGGA 1936

Qy	481	PheSerYsThrValaAsnSerSerIleuengInYrGlyLeuGlyUserLeuYsAryls	500
Db	1937	TTCTCCAGACAGATCAATTCACGACATCTTGACAGTACGGCTCGAGATCCTTAACGAAAG	1996
Qy	501	ThsSerYrIleValaGlnValMetAlaSerThrsEraIagIyGlyThrAsnGlyThrSer	520
Db	1997	ACCTCTTACATGTTTCAAGGTCAATGGCCAGCACCAAGTGTGGGGGACCAACGGGACCAAG	2056
Qy	521	IleAsnPhelYsThrLeuSerPhsSerValpHeGulIleIleuIleThrSerIleuIle	540
Db	2057	ATAAATTTCAAGACATGTCAATTCAGTGTCTTTGAGATTATCCATMACTTCTCGATT	2116
Qy	541	GIYGIYGIYLeuLeuIleuIleIleIleuThrValaIaYrGlyLeuYsValpAsn	560
Db	2117	GGTGAAGCCCTTCTTATTCATTAATCTGACAGTGGGATVGGTCTCAAAAAACCCCAAC	2176
Qy	561	LysLeuThrHisLeuCystrProThrValpProAsnProIaGlySerSerIleAlaThr	580
Db	2177	AAATTGACTACTGTGTGTGGCCCAACCTTCCCAACCTGCTGAAGTAGTATGACCA	2236
Qy	581	TrpHisGlyAspAspPhelYsAspYsLeuAsnLeuYsGlyUserAspAspSerValAsn	600
Db	2237	TGGCATGGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGTGTGAATGACTGTGTGAC	2296
Qy	601	ThrGlnAspAryIleLeuYsProCySerThrProSerAspYsIleValIleAspYs	620
Db	2297	ACAGAAAGCAGAGATCTTAACCAATGTTCCACCCCACTGACCAAGTGTGATTAAGACAG	2356
Qy	621	LeuValValaAsnPhelYsAsnValLeuGlnGlnIlePheThrAspGluAlaArgThrGly	640
Db	2357	TTGGTGTGGAACTTTGGGAATGTTCTGCAAGAAATTTTCAAGATGAAGCCAGAACGGGT	2416
Qy	641	GlnGlnAsnAsnLeuGlyGlyIYgIuYsAsnGlyThrArgIleLeuSerSerCystrProThr	660
Db	2417	CAGAAAAACAATTTAGAGGGGAAAAAGATGGACTAGAAATTCGTCTTCCGCCCAACT	2476
Qy	661	SerIle 662	
Db	2477	TCAATA 2482	
RESULT 3			
US-10-351-157-4			
Sequence 4, Application US/10351157			
Publication No. US20030215838A1			
GENERAL INFORMATION:			
APPLICANT: Sprecher, Cindy A.			
APPLICANT: Gao, Zeren			
APPLICANT: Kuijper, Joseph L.			
APPLICANT: Dasovich, Maria M.			
APPLICANT: Grant, Francis J.			
APPLICANT: Presnell, Scott R.			
APPLICANT: Whitmore, Theodore E.			
APPLICANT: Hammond, Angela K.			
APPLICANT: NO. US20030215838A1ak, Julia E.			
APPLICANT: Gross, Jane A.			
APPLICANT: Dillon, Stacey R.			
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS			
FILE REFERENCE: 02-02			
CURRENT APPLICATION NUMBER: US/10/351,157			
CURRENT FILING DATE: 2003-01-21			
PRIOR APPLICATION NUMBER: US 60/435,361			
PRIOR FILING DATE: 2002-12-19			
PRIOR APPLICATION NUMBER: US 60/389,108			
PRIOR FILING DATE: 2002-06-14			
PRIOR APPLICATION NUMBER: US 60/350,325			
PRIOR FILING DATE: 2002-01-18			
NUMBER OF SEQ ID NOS: 183			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 4			
LENGTH: 2903			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			

1	NAME/KEY	CDS	...	(2482)
1	LOCATION:	(497)	...	US-10-351-157-4
Alignment Scores:				
Pred. No.:	0	Length:	2903	
Score:	3528.00	Matches:	662	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatch:	0	
Query Match:	100.00%	Indels:	0	
DB:	17	Gaps:	0	
US-10-006-265-17 (1-662) x US-10-351-157-4 (1-2903)				
QY	1	MetIysLeuSerProGlnProSerCysValAsnLeuGlyMetThrTPaAlaLeu	20	
Db	497	ATGAAGCTCTCTCCCGCAGCTTCATGTGTTAACTGGAGATGATGTGAAGCTGGGCACTG	556	
QY	21	TrypMetLeuProSerLeuCysIysPheSerLeuAlaAlaLeuProAlaIysProGluAsn	40	
Db	557	TGATGTCTCCCTTCACCTGCAAAATTCAGCTGGACCTGCGACGTAAAGCCTGAAGAC	616	
QY	41	IlSerCysValTYrTYrTYrAglYAsnLeuThrCysThrTPSerProGlyLYsGlu	60	
Db	617	ATTTCCTGTCTCTACTATAGAAAAATTAACTGCACCTTGAGCTCCAGAAAGAA	676	
QY	61	ThiSerTYrThrgInTYrThrValLYsArgThrTYrAlaPheGlyGluYshAspAsn	80	
Db	677	ACCAAGTATACCCAGTACACAGTTAAGAAAGAACTTACGCTTTTGAGAAAGAAACATGATAT	736	
QY	81	CysThrThrAnserSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg	100	
Db	737	TGTAACAACAATAGTCTTACAAAGTAAAAATCGGCTTCGCTCTTTTTCCTTCCAGA	796	
QY	101	IlleThrIlleProAspAsnTYrThrIlleGluValGluAlaGluAsnGlyAspGlyValIlle	120	
Db	797	ATTAACATCCCAATATATTATACCATTTGAGCTGAGACTGAAAAATGAGATGGCTATATT	856	
QY	121	LysSerHisMetThrTYrTPaGLeuGluAsnIlleAlaIysThrGluProProYshIle	140	
Db	857	AAATCTCATATGACATATCTGAGATTTAGAAACATACGAAACCTGAACCACTTAAGATT	916	
QY	141	PheArgValIysProValLeuGlyIlleLYsArgMetIlleGlnIlleGluTPrIlleYsPro	160	
Db	917	TYCCGTGTGAACACAGATTTGGGCGATCAACGATGATCAAAATTGAATGATTAACCT	976	
QY	161	GluLeuAlaProValSerSerAspLeuLYsTYrThreunrPheArgThrValAsnSer	180	
Db	977	GAGTTGGCGCTGTTTATCTGATTTAAATATACACCTTGATTCAGAGACGTCAACAGT	1036	
QY	181	ThiSerTPMetGluValAsnPheAlaLYsAsnArgLYsAspLYsAsnGlnThrTYrAsn	200	
Db	1037	ACCAAGCTGAGTGAAGCAACTTCGCTTAAGAACCGTAAAGATTAACCAACCTACAC	1096	
QY	201	LeuThrGlyLeuGlnProPheThrGluTYrValIlleAlaLeuArgCysAlaValLYsGlu	220	
Db	1097	CTACGGGGGCTGCAGCTTTTACAGAAATATGCTACATCTCTGCGATGCGGTCAAGAG	1156	
QY	221	SerIysPheThrTPSerAspTPSerGlnGluLYsMetGlyMetThrGluGluGluAlaPro	240	
Db	1157	TCAAAAGTTCTGGAGTGCTGGAAGCAAGAAAAATGGAAATGACTGGAAGAAAGCTTCA	1216	
QY	241	CysGlyLYsGluLeuLeuTPaCysValLeuLYsProAlaGluAlaAspGlyLYsArgProVal	260	
Db	1217	TGTGGCTTGAACCTGTGGAAGTCTGAAACCAAGCTAGAGCGGATGGAAGAGCCAGTG	1276	
QY	261	ArgLeuLeuTPYsLYsAlaArgLYsAlaProValLeuGluIlybTYrThreunrTYrAsn	280	
Db	1277	CGGTTGTTTAAGAAAGCAAGCAAGGAGGCCCAAGTCTTAAGAAACACATTGGCTTAAAC	1336	
QY	281	IlleTPYrTYrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln	300	
Db	1337	ATATGTATCATATCCAGAAACAACATCACTCAAGAAACAATGAACAATCACTTAACAG	1396	


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Db      857 AAATCATATGACATATGAGATTAGAGAAATAGCGAAACCTGAACTTAAGATT 916
Qy      141 PhaaArgVallySerProAlLeuGlyIlelyAsArgMetIleGlnIleGlnTTPpIlelyPro 160
Db      917 TTCGGTGTGAACACAGTTTGGGCTATCAACGAATGATTCMAATGATGATAAGAGCCCT 976
Qy      161 GluLeuAlaProValSerSerAspLeuLeuTyThrLeuArgPheArgThrValIAsnSer 180
Db      977 GAGTTGGCGCTCTTTCATCTGATGATTTAAATACACACTTCGATTCAGAGAACGTCACAGT 1036
Qy      181 ThrSerTrpMetGluValAsnPheAlaIlyAsnArgIlyAspIlyAsnGlnThrTyraAsn 200
Db      1037 ACCAGCTGATGATGAATCACTTCGCTAAGAACCGTAAGATGATAAAACCAAGTCAAC 1096
Qy      201 LeuThrGlyLeuGlnInProPheThrGluTyrrValIleAlaIleuArgCysAlaValIlySerGlu 220
Db      1097 CTCACGGGGCTGAGCCCTTTTACAGAAATGTCATAGCTTCGCAATGTGCGTCAAGAG 1156
Qy      221 SerIlyPheTrpSerAspTrpSerGlnGluIlyMetIlyThrGluGluGluAlaPro 240
Db      1157 TCBAATTTCTCGAGTACTGAGACCAAGAAAATGGGAATGACTGAGAGAAAGAGCTCCA 1216
Qy      241 CysGlyLeuGluLeuTrpArgValIleuIlyProAlaIleuAlaAspGlyArgArgProVal 260
Db      1217 TGTGGCCTGGAACCTGAGAGAGTCTGAACACAGCTGAGCGGATGGAAGAGCCAGT 1276
Qy      261 ArgLeuLeuTrpIlySerAlaArgGlyAlaProValLeuGluIlySerThrLeuGlyTyrrAsn 280
Db      1277 CGGTGTGTATGAGAAGAGCAAGAGAGGCCAGTCCCTAGAGAAAACACTGTGCTCAAC 1336
Qy      281 IleTrpTyrrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGln 300
Db      1337 ATATGATATCATCCAGAAAGCAACACTAATCTCAAGAAACATGAACACTACTAATCCAG 1396
Qy      301 GlnLeuGluLeuHileuGlyIlyGluSerPheTrpValSerMetIleSerTyraAsnSer 320
Db      1397 CAGCTTGAACCTGCATCGGAGGCGAGAGCTTTGGGTGTCTATGATTTCTTAATTC 1456
Qy      321 LeuGlyIlySerProAlaAlaThrLeuArgIleProAlaIleGlnIlySerSerPheGln 340
Db      1457 CTGGGAAGGCTCCAGTGGCCACCTGAGAGATTCCAGCTATTTCAAGAAAAATCATTTCCAG 1516
Qy      341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValIlyValIlySer 360
Db      1517 TGCATTGAGGTCTAGAGGCTCTGCTGCTGAGAGAACAGTATGCTGAAGTGGCAAAGC 1576
Qy      361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db      1577 TCTGCTCTAGACGTGAACCTTGATGATTGAATGATTTCCGATGTCGAGCTCAGAGCC 1636
Qy      381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnIlyAsnAspIly 400
Db      1637 ACCACCCCTTCCGGGAATCTGTCTCAGGCCACAGAACAGTCCAGCAAGATTA 1696
Qy      401 LeuIlyProPheTrpCysTyrrAsnIleSerValTyrrProMetLeuIlyAspIlyValIly 420
Db      1697 TTAAACCTTTCGTGGCTATACATCTCTGTGTATCCAAATGTTGATGACAAAGTTGGC 1756
Qy      421 GluProTyrrSerIleGlnAlaTyrrAlaIlyGluIlyValIlyProSerGluIlyProGluThr 440
Db      1757 GAGCCATATTCATCCACAGGCTTATGCCAAAGAGCGTTTCATCAGAGGCTCGAGACC 1816
Qy      441 IlyValIlyAsnIleGlyValIlySerThrValIleThrTrpIlySerGluIleProIlySer 460
Db      1817 AAGGTGAAGAACTTGGCGTGAAGACGGTCACATCACAAGAAAGATTTCCCAAGAGT 1876
Qy      461 GluArgIlyGlyIleIleCysAsnTyrrIlePheTyrrGlnAlaGluIlyGlyIlyGly 480
Db      1877 GAGAGAAAGGATATCATCTGCACTACACCATCTTTTACCAAGCTGAAGGTGAAAGGA 1936
Qy      481 PheSerIlyThrValAsnSerSerIleLeuGlnTyrrGlyLeuGluSerLeuIlySerGly 500

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Db      1937 TTCCTCAAGACAGTCAATTCAGACATCTTGACATCGGCTGGAGTCCCTGAAACGAAAG 1996
Qy      501 ThrSerTrpIleValGlnValMetIlyAsnThrSerAlaGlyIlyThrAsnGlyThrSer 520
Db      1997 ACCTCTTACATTTGTCAGGTCAAGGACAGACAGGCTGGAGGAAACCAAGGAGCAGC 2056
Qy      521 IleAsnPheIlyThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db      2057 ATTAATTTCAAGACATTTGTCATTCAGTGTCTTGAGATTAATCTCTGATTC 2116
Qy      541 GlyIlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrrGlyLeuIlyIlyProAsn 560
Db      2117 GGTGGAGGCTCTTATTCATTTCTGATTCCTGACAGTGGCTATGCTTCAAAAAACCCAA 2176
Qy      561 IlyLeuThrHileuCysTrpProThrValIleProAsnProAlaGluSerSerIleAlaThr 580
Db      2177 AAATGATCACTGTGTGTGGCCACCGTCCCAACCTTGCTGAAGTGTATGACCA 2236
Qy      581 TrpHileGlyAspAspPheIlyAspIlyIleuAsnLeuIlyGluSerAspAspSerValAsn 600
Db      2237 TGGCATGAGAGATTTTCAAGATTAAGCTAAACCTGAAGAGATCTGATGATGCAAC 2296
Qy      601 ThrGluAspArgIleLeuIlyProCysSerThrProSerAspIlyIlyValIleAspIly 620
Db      2297 ACAGAAAGACAGATCTTAACCAATGTTCCACCCAGTGAAGAAAGTTGGTGAATTGCAAG 2356
Qy      621 LeuValIlyAsnPheGlyAsnValIleuGlnIlyIlePheThrAspGluAlaArgThrGly 640
Db      2357 TTGGTGTGTAACCTTGGGAATTTCTGCAAGAAATTTTCAAGATGAACCGAGAGGGGT 2416
Qy      641 GlnIlyAsnAsnLeuGlyIlyGlyIlyIlyAsnGlyThrArgIleLeuSerSerCysProThr 660
Db      2417 CAGGAAAACAATTTGAGAGGAGGAAAGAAATGGAGCTAGAAATCTGTCTTGCCCACT 2476
Qy      661 SerIle 662
Db      2477 TCATA 2482

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RESULT 5

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US-10-772-531-53
/ Sequence 53, Application US/10772531
/ Publication No. US20040142422A1
/ GENERAL INFORMATION:
/ APPLICANT: Sprecher, Cindy A.
/ APPLICANT: Preenell, Scott R.
/ APPLICANT: Gao, Zeren
/ APPLICANT: Whitmore, Theodore E.
/ APPLICANT: Kujiper, Joseph L.
/ APPLICANT: Maurer, Mark F.
/ TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
/ FILE REFERENCE: 00-42
/ CURRENT APPLICATION NUMBER: US/10/772, 531
/ CURRENT FILING DATE: 2004-02-05
/ PRIOR APPLICATION NUMBER: US/09/892, 949
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: US 60/214, 282
/ PRIOR FILING DATE: 2000-06-26
/ PRIOR APPLICATION NUMBER: US 60/214, 955
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: US 60/267, 963
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: PaateSeq for Windows Version 3.0
/ SEQ ID NO 53
/ LENGTH: 2903
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (497) ... (2482)
US-10-772-531-53
Alignment Scores:

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Pred. No. : 0 Length: 2903
 Score: 3528.00 Matches: 662
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-10-006-265-17 (1-662) x US-10-772-531-53 (1-2903)

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
 Db 497 ATGAAGCTCTCCACAGCCTTCATGTGTAACTGGGGATGATGTGACCTGGGCACACTG 556
 QY 21 TrpMetLeuProSerLeuCysLeysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
 Db 557 TGGATGCTCCCTTCACTCTGCAAAATTCAGCCCTGGAGCTTGGCAGCTTAAGCTTAGAAC 616
 QY 41 LLeSerCysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
 Db 617 ATTTCCTGTGTACTACTATAGAAAATTTAACTTGCACTTGAGAGTCCAGAAAGAA 676
 QY 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsn 80
 Db 677 ACCAGTTATACCCAGTACAGCAGTTAAGAACTTACGCTTTGGAGAAAACATGATATAT 736
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgLaserCysSerPhePheLeuProArg 100
 Db 737 TGTACAAACAAATAGTCTACAAAGTAAATCGTGTGTCTCTTTTTCCTTCAAGA 796
 QY 101 LLeThrIleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 Db 797 ATTAAGATCCCAAGATTAATTAATTCATTTGAGTGGAGCTGAAAATGGAGATGCTTAATT 856
 QY 121 LysSerHisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGluProLysIle 140
 Db 857 AAATCTCATATGACACTACTGAGATTAGAAACATAGGAAAACGAAACCACTAAGATT 916
 QY 141 PheArgValLysProValLeuGlyLleLysArgMetIleGlnIleGluTrpLleLysPro 160
 Db 917 TTCCTGTGAAACCGATTGCGCATCAACCAATGATTCAAATTTGATGATAAAGCCT 976
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
 Db 977 GAGTTGGCGCTGTTTCACTGATTTAAATACACACTTCGATTCAGGACGTCACAGCT 1036
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
 Db 1037 ACCAGCTGATGGAAGTCAACTTGGCTAAGAACCTTAAGATTAABAAACCAACGTAACAC 1096
 QY 201 LeuThrGlyLeuGlnProPheThrGlyTyrValIleAlaLeuArgCysAlaValLysGlu 220
 Db 1097 CTCACGGGGCTGACGCTTTTAAAGAAATATGTCATAGCTCGCATGTGCGGCTCAAGCAG 1156
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaPro 240
 Db 1157 TCAGAGTCTGAGTGAAGTGAAGCTGAAACCAAGTGAAGGAGTGAAGAGAGCTCA 1216
 QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
 Db 1217 TGTGGCCTGGAAGCTGGAAGTCTCTGAAACCAAGTGAAGGAGTGAAGAGGCAATG 1276
 QY 261 ArgLeuLeuTrpLysValAlaArgGlyValaProValLeuGluLysThrLeuGlyTyrAsn 280
 Db 1277 CGGTGTATATGAGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1336
 QY 281 LLeTrpTyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 Db 1337 ATATGGTACTATCCAGAAAGCAACTAATCCACAGAAACAAATGAACACTAATCAAG 1396
 QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetLLeSerTyrAsnSer 320
 Db 1397 CAGCTTGAATCGCATCTGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1456

QY 321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaIleGlnGluLysSerPheGln 340
 Db 1457 CTGGGAAGTCTCCAGTGGCCACCTGAGATTCAGCTATTCAGAAATATCATTTTCAG 1516
 QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValLysTrpGlnSer 360
 Db 1517 TGCATTTGAGTCAATGCAAGCCCTGGCTGCTAGAGACAGCTAGTGTGATGAGGCAAGC 1576
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 Db 1577 TCTGCTCTAGACGAGTGAACACTTGAATGATTAATGTTCCGAGATGTGAGCTCAGAGCC 1636
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGluAspLys 400
 Db 1637 ACCACCTTCTCTGGAAATGTGTCTGAGGCACAGAACTGAGATCAGACAGATTA 1696
 QY 401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
 Db 1697 TTTAAACCTTCTGTGTCTATTAACATCTCTGTGATTCAAATGTTGACAGAAAGTTGGC 1756
 QY 421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGlyGlyProGluThr 440
 Db 1757 GAGCCATATTCATTCAGGCTTATGCCAAAGAGCCGTTCCATCAGAAAGTCTGAGAAC 1816
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 Db 1817 AAGGTGGAACATTTGGGTGAAGACGCTACGATCAATGAAAGATTTCCCAAGAGT 1876
 QY 461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
 Db 1877 GAGAGAAAGGATATCATCTGCACTACACACTTTTAAACAGCTGAAGGAGGAAAGAA 1936
 QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLys 500
 Db 1937 TTTCTCAAGACAGTCAATTCAGACATCTTGACAGTACGCGCTGAGAGTCCCTGAAGCAAG 1996
 QY 501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSer 520
 Db 1997 ACCCTTACATTTGTCAGCTATGCGCAGACCCAGCTGCGGAGAACCAACGGAACAGC 2056
 QY 521 LLeAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 Db 2057 ATTAATTTCAAGACATTTCTCATTCAGTGTCTTTAGATTAATCCCTCATTACTTCTGATT 2116
 QY 541 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
 Db 2117 GGTGAGGCGCTTTTATTTCTCATTTATCTGACAGTGGCATGTGCTCAAAAACCCAAC 2176
 QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
 Db 2177 AAATTTGACTCATCTGTGTGTGGCCACCGTTCCCAACCTGTGAAAGTATAGCCACA 2236
 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 Db 2237 TGGCATGGAATGATTTTCAAGATTAACCTTAAGAGAGTGTGACTCTGTGAAC 2296
 QY 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
 Db 2297 ACAGAAAGCAGGATCTTAAACCATGTTCCACCCCAAGTGAAGAGTGTGATGAGCAAG 2356
 QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
 Db 2357 TTGGTGTGAACTTTGGGAAATGTTTCCAGAAATTTTTCACAGTGAAGCCAGAACGGGT 2416
 QY 641 GlnGluAsnAsnLeuGlyGlyLysAsnGlyThrArgIleLeuSerSerCysProThr 660
 Db 2417 CAGAAACAAATTTAGAGAGGAGAAAGAAATGGAGACTGAATTTCTTCTTCCGCCAACT 2476
 QY 661 SerIle 662
 Db 2477 TCATA 2482

RESULT 6

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US-09-892-949-45
; Sequence 45, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; PRIORITY FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)...(2108)
US-09-892-949-45

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Alignment Scores:

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Pred. No.: 0 Length: 2529
Score: 3518.00 Matches: 660
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.72% Indels: 0
DB: 10 Gaps: 0

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US-10-006-265-17 (1-662) x US-09-892-949-45 (1-2529)

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QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeuTTPMet 22
DB 129 CTCCTCCGCCAGCCTTCATGCTGTTAACTGGGATGATGGACCTGGGCACCTGGTGAATG 188
QY 23 LeuProSerLeuCysLysPheSerLeuAlaLeuProAlaLysProGluLysAsnLysSer 42
DB 189 CTCCTCCCTGACTGCAAAATTCAGCTGGCAGCTCTGCAAGCTAAGCCTGAGAACATTTCC 248
QY 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGluLysGluThrSer 62
DB 249 TGTGTCTACTACTATGAGAAATTTTAACCTGCACTTGGAGTCCAGGAAAGAAACCAAGT 308
QY 63 TyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGluLysHisAspAsnCysThr 82
DB 309 TATAACCAGTACAGATTAAAGAACTTACGCTTTTGGAGAAATAACATGATTAATTGACA 368
QY 83 ThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArgLysLeu 102
DB 369 ACCAAATGTTCTCAAGTGAATAATCGGCTTCGCTCTTTTCCCTCCAAAGATTAACG 428
QY 103 IleProAspAsnTyrThrIleGluValGluAlaGluAsnGlyAspGlyValIleLysSer 122
DB 429 ATCCGAGTAAATTAATACCATTTGAGCTGGAGCTGGAATAAGAGATGCTGTAATTAATC 488
QY 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaLysThrGlnProProLysIlePheArg 142
DB 489 CATATACATACATGAGATTAGAGAAACATAGCAAAACCTAACCACTTAAGATTTCCGT 548
QY 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
DB 549 GTGAAACCAATTTGGGCATCAACGAAATGATTCAAATTAATGAATGAATGAAGCTGAGTTG 608

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QY 163 AlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSerThrSer 182
DB 609 GCGCCGTTCATCTGATTTAAATACACACTTCATTCAGGACGTCACAGTACCAAGC 668
QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsnLeuThr 202
DB 669 TGGATGGAAGTCAACTTCGCTTAAGAACCTTAAGATGAATAAACCAACGTAACCTCACG 728
QY 203 GlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGluSerLys 222
DB 729 GGGCTGCACCTTTTACAGAAATATGTCTAGCTCTGCATGCGCGCTCAAGAGTCAAAAG 788
QY 223 PheTrpSerAspTrpSerGlnGluLysMetThrGluGluAlaProCysGly 242
DB 789 TTCTGAGAGTACTGGAGCCAAAGAAAATGGAAATGACTGAGGAAGAGCTCATGTGCGC 848
QY 243 LeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProValArgLeu 262
DB 849 CTGGAACGTGTGAGAGTCTGAAACCACTGAGGCGGATGGAAGAGGCACTGCGGTTG 908
QY 263 LeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsnIleTrp 282
DB 909 TTATGAGAGAGGCAAGAGAGCCCAAGTCTTAAGAAAACCTTGCTACAACTATGG 968
QY 283 TyrTyrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnLeu 302
DB 969 TACTATCCAGAAAGCAACTAATCTCAAGAAACATGAACATTAACCAAGCAGCTT 1028
QY 303 GluLeuHisLeuGlyGlyLysPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
DB 1029 GAACGCACTGGGAGGCGAGGAGCTTTGGGTCTATGATTTCTTAATATCTCTTGCG 1088
QY 323 LysSerProValAlaThrLeuArgLysPheProAlaIleGlnGluLysSerPheGlnCysIle 342
DB 1089 AAGCTCCAGTGGCCACCTTGAAGATTCAGCTATTAAGAAAATCAATTAAGTGCATT 1148
QY 343 GluValMetGlnAlaCysValAlaGluAspGluLeuValValLysTrpGlnSerSerAla 362
DB 1149 GAGGTATACGAGCCCTGCGTCTGAGGACCAAGTATGTGTAATGGCAAGCTCTGCT 1208
QY 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
DB 1209 CTAGACGTGAACACTGATGATTAATGATTTCCGATGTGAGCTCAAGAGCCACAC 1268
QY 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLysLeuLys 402
DB 1269 CTTTCTGGGAAATCTGTGCTCAGGCCACGAATGAGCATGACAGATTAATTAATA 1328
QY 403 ProPheTrpCysTyrAsnLysSerValTyrProMetLeuHisAspLysValGlyLysPro 422
DB 1329 CTTTCTGGTGTATTAACATCTCTGTATCCAAATGTTGCATGACAAAGTTGGCAGCCA 1388
QY 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrLysVal 442
DB 1389 TATTCATCCAGCTTATGCCAAAGAGCGTTTCATCAAGAGGCTCTGAAGCAAGGTG 1448
QY 443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGluLysProLysSerGluArg 462
DB 1449 GAGACATTTGGCTGAAGCGCTCAGATCAATGGAAGAAATTTCCCAAGGTGAGAGA 1508
QY 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyGlyLysGlyPheSer 482
DB 1509 AAGGGTATCATCTGCAACTACACATCTTTTACCAAGCTGAAGGTGGAAGAAAGATTCTCC 1568
QY 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
DB 1569 AAGACAGTCAATTCAGCACTTTCAGTACGTACGCTCGAGTCCCTGAAGCAAGAGCTCT 1628
QY 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyGlyThrAsnGlyThrSerIleAsn 522
DB 1629 TACATTTGTCAGTCTGCGCAGCAACAGTGTGGGGGAACCAAGGACGACATTAAT 1688
QY 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542

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Db 729 GGGCTGACAGCTTTTACAGAAATATGTCATAGCTCTGCAGTGTGGGTCAAGAGTCAAG 788
Qy 223 PheTTPSerAspTPTrSerGlnGlnIuIyMetGlyMetThrGlnGlnIuIaProCysGly 242
Db 789 TTCGTGAGTGACTGGAGCCAGAGAAAAAAGGGAATGACGAGAGAAAGAAAGCTCAATGTGCG 848
Qy 243 LeuGluLeuTPArValLeuAspProAlaGluAlaAspGlyArgArgProValArgLeu 262
Db 849 CTGGAACGTGGAGAGTCTCTGAACCAAGCTGAGCGGATGAGAGAGAGCCAGTGGCGTTG 908
Qy 263 LeuTPArgValArgGlyValArgProValLeuGlnIuIySerThrLeuGlyTyrAsnIleTP 282
Db 909 TTATGAGAGAGAGGCAAGAGAGAGCCCAAGTCTTGAAGAAAAACCTTGGCTACAACTATAG 968
Qy 283 TyrTPProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
Db 969 TACTATCCAGAAAGCACTAACTCAACAGAAACATGACATCACTAAACAGAGCTT 1028
Qy 303 GluLeuHleuGlyGlySerPheTPValSerMetIleSerTyrAsnSerLeuGly 322
Db 1029 GAATGTCATCTGGAGGCGAGAGCTTTGGTGTCTATGATTTCTTATATTTCTTGTGG 1088
Qy 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGlnLysSerPheGlnCysIle 342
Db 1089 AAGTCTCCAGTGGCCACCTGAGATTCAGCTTATCAAGAAAAATCAATTCAGTGCATT 1148
Qy 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTPGlnSerSerAla 362
Db 1149 GAGGTCAAGCAGGCGCTGGCTGTGCTAGAGCAACGCTAGTGTGTAAGTGGCAAGCTCTCT 1208
Qy 363 LeuAspValAsnThrTPMetIleGluTPPheProAspValAspSerGluProThrThr 382
Db 1209 CTAGACGTGAACCTTGAGATGATTAATGTTTCCGATGTGGACTTCAGAGCCCAACCC 1268
Qy 383 LeuSerTPGluSerValSerGlnAlaThrAsnTPThrIleGlnGlnAspLysLeuLys 402
Db 1269 CTTTCTCGGAATCTGTGTCTCAGGCCAAGAACTGAGATTCACAGATTAATTAATAA 1328
Qy 403 ProPheTPCyETyrAsnIleSerValTyrProMetLeuHleAspLysValGlyGluPro 422
Db 1329 CTTTCTGTGTGTAATACATCTCTGTATCCAAAGTTGCAAGAAAGTTGGCCAGAGCA 1388
Qy 423 TyrSerIleGlnAlaTyrAlaLysGlnGlyValProSerGlnGlyProGluThrThrVal 442
Db 1389 TATTCATTCAGGCTTATGCAAGAGAGCGTTCATCAAGAAAGCTCTGAGCCCAAGGTG 1448
Qy 443 GluAsnIleGlyValLysThrValThrIleThrTPArgGluIleProLysSerGluArg 462
Db 1449 GAGAAACATTTGGCGTGAAGACGCTCAGATCACTGAAAGAGATTCCCAAGAGTGAAGA 1508
Qy 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
Db 1509 AAGGTATACATCTGCACTACACCATCTTTTACCAAGCTGAAGGGGAGAAAGATTCCTC 1568
Qy 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLysThrSer 502
Db 1569 AAGACAGTCAATTCAGAGATCTGCAATGAGCGCTGAGAGTCCCTGAAAGCAAGACCTCT 1628
Qy 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyIleThrAsnGlyThrSerIleAsn 522
Db 1629 TACATTTGTTACAGGTATGCGCAGACCAAGTGTGGGGAGAACCAAGGAGCAAGTAAAT 1688
Qy 523 PheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGly 542
Db 1689 TTCAGAGACATTTGCTCATGAGTCTTTGAGATTATCCATTAACCTCTCTGATTTGTGGA 1748
Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsnLysLeu 562
Db 1749 GGCCTTTTATTTCTATTTCTGACAGTGGCATATGGTCTCAAAAAACCCCAACAATTTG 1808
Qy 563 ThrHisLeuCyETPProThrValProAsnProAlaGluSerSerIleAlaThrTPHis 582
Db 1809 ACTATCTGTGTGGCCACCGTTCCAAACCTGTGTGAAGATGATAGTCCCACTGAGCAT 1868

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Qy 583 GluAspAspPheLysAspLysLeuAsnLeuLysGluIuIySerAspAspSerValAsnThrGlu 602
Db 1869 GAGATGATTTTCAAGAGATTAACCTTGAAGAGTGTATGACTCTGTGAACACAGAA 1928
Qy 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db 1929 GACAGATCTTAAACATGTTCCACCCCGAGTACAAAGTTGGTGAATGACAAAGTTGGTG 1988
Qy 623 ValAsnPheGlyAsnValLeuGlnGlnIlePheThrAspGluAlaArgThrGlyGlnGlu 642
Db 1989 GTGAATCTTGGGAATGTCTCTCAAGAAATTTTCAAGATGAAGCAGAAACGGGTACAGAA 2048
Qy 643 AsnLeuLeuGlyGlyGluLysAsnGlyThrArgIleLeuSerSerCysProThrSerIle 662
Db 2049 AACATTTTGAAGAGGAGAAAGAAATGAGACTGAATTTCTGTCTCTGCCCAATTCATTA 2108

RESULT 9
US-10-006-265-1
; Sequence 1, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOLYMERIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006,265
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (523) ... (2478)
US-10-006-265-1

Alignment Scores:
Pred. No.: 0
Score: 3512.00
Percent Similarity: 99.85%
Best Local Similarity: 99.70%
Query Match: 99.55%
Length: 2969
Matches: 661
Conservative: 1
Mismatch: 0
Indels: 1
Gaps: 0

US-10-006-265-17 (1-662) x US-10-006-265-1 (1-2969)
Qy 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetThrTPThrAlaLeu 20
Db 523 ATGAAGCTCTCTCCCGAGCTTCAATGTTAACTGGGAGATGAGTGAAGCTGGGCACTG 582
Qy 21 TrpMetLeuProSerLeuAspLysPheSerLeuAlaLeuProAlaLysProGluAsn 40
Db 583 TGAATGCTCCCTTACTCTGCAATTCAGGCTGCACTCTGCAAGCTTAAAGCTGAGAAC 642
Qy 41 IleSerCysValTyrTyrArgLysAsnLeuThrCysThrTPSerProGlyLysGlu 60
Db 643 ATTTCTGTGTCTACTACTATTAAGAAATTTTAACTGCACTTGAAGTCCAGAGAAAGAA 702
Qy 61 ThrSerTyrThrGlnTyrThrValLysArgThrTyrAlaPheGlyGlyLysAspAsn 80
Db 703 ACCAGTTATACCCAGTACAGAGATTAAAGAACTTACGCTTTCGAGAAAAACATGATTAAT 762
Qy 81 CysThrThrAsnSerSerThrSerGluAsnArgLysSerCysSerPhePheLeuProArg 100

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Db      763 TGTACAAACCAATAGTCTACAGTGAATAATCGTCTGCTCTTTTCTTCCACAGA 822
Qy      101 ILeThrIleProAspAsnThrIleGluValAlaGluAsnGlyAspGlyValIle 120
Db      823 ATACACATCCCAATATTTATACATTTGAGGTGGAAGCTGAAAATGGAGATGTGTAAAT 882
Qy      121 LysSerHisMetThrTyrTrpArgGluAsnIleAlaLysThrGluProProlYsIle 140
Db      883 AATTCATATGACATACATGAGATTAGAAACATGACGAAACCTGAACCACTTAAGATT 942
Qy      141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
Db      943 TTCGGTGTAAACACAGTTTGGCGATCAACGAAATGATTCAAATGAAATGAAAGCCCT 1002
Qy      161 GluLeuAlaProValSerSerAspLeuLysTyrThrLeuArgPheArgThrValAsnSer 180
Db      1003 GAGTTGGCGCTTTTCATCTGATTTTAAATACACACTTGCATTCAGAGACGTCACACAGT 1062
Qy      181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrAsn 200
Db      1063 ACACAGCTGATGAGATGCAACTTCGCTAAGAACCGTAAAGATTAACCAACGATCAAC 1122
Qy      201 LeuThrGlyLeuGlnProPheThrGluTyrValIleAlaLeuArgCysAlaValLysGlu 220
Db      1123 CTCACGGCGCTGACGCTTTTACAGAAATGTATGATAGCTCTGGATGTGGCTCAAGAG 1182
Qy      221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluAlaPro 240
Db      1183 TCAAAGTTCCTGAGTGAATGACCGCAAGAAAATGGGAATGACTGAGAGAAAGCTCCA 1242
Qy      241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
Db      1243 TGTGGCTGGAACTGTGAGAGAGTCTGAACACAGCTGAGGCGGATGAAAGGCGCAGT 1302
Qy      261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrAsn 280
Db      1303 CGGTGTGTATGAGAAAGGAGGAGAGAGCCCGAGCTCTAAGAAACACCTGTGCTCAAC 1362
Qy      281 IleTrpTyrTrpProGluSerAsnThrAsnLeuThrGluThrMetAsnThrTrpAsnGln 300
Db      1363 ATATGTGATCATATCAGAAAGCAACATACCTACAGAAACAAATGAACACTTAACACAG 1422
Qy      301 GlnLeuGluLeuHisLeuGlyGlyGluSerPheTrpValSerMetIleSerTyrAsnSer 320
Db      1423 CAGCTTGAATGATCTGGAGGCGAGAGCTTTGGGTGTCATGATTTCTTAATAATCT 1482
Qy      321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
Db      1483 CTGGGAAAGTCTCCAGTGGCCACCTGAGGATTCAGCTAATTCAGAAAATCATTTCCAG 1542
Qy      341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
Db      1543 TGCATTTGAGGTATGACAGGCTCTGCTGCTGAGAGACAGCTAATGTGAAAGTGGCAAGC 1602
Qy      361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
Db      1603 TCTGCTCTAGACGTGAACCTTGATGATGATGATGTTTCCGATGTGAGCTCAGAGCCC 1662
Qy      381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
Db      1663 ACCACCTTTTCCCTGGGAATCTGTGCTCAGAGCCACAGACGATCCCGCAAGATAA 1722
Qy      401 LeuLysProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGly 420
Db      1723 TTTAAACCTTTCTGGTGTCTAATACATCTCTGTGTATCCAAATGTTCATGACAAAGTTGGC 1782
Qy      421 GluProTyrSerIleGlnAlaTyrAlaLysGluGlyValAlaProSerGluGlyProGluThr 440
Db      1783 GAGCCATATTCATCCAGCCTTATGCCAAGAAAGGCGTTCCATCAGAGAGTCTCGAGACC 1842
Qy      441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluLysProlYsSer 460
Db      1843 AAGGTGAGAAATTTGGCGTGAAGACGCTCAGATCAGATGAGAAAGATTTCCCAAGAGT 1902

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Qy      461 GluArgLysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGly 480
Db      1903 GAGAGAAAGGTATATCATCTGCAACATACACATCTTTTACCAAGCTGGAAGTGAAGAA 1962
Qy      481 PheSerLysThrValAsnSerSerIleLeuGlnTyrGlyLeuGluSerLeuLysArgLys 500
Db      1963 TTCTCCAGACAGTCAATTCACGATCTTGCAAGTACGGCTGTGAAGTCCCTGAAAGCAAG 2022
Qy      501 ThrSerTyrIleValGlnValMetAlaSerThrSerAlaGlyIleValAsnGlyThrSer 520
Db      2023 ACCTCTTACATTTGTCAGGTCAATGGCCACACACAGTCTGGGAGAACCAAGGACAC 2082
Qy      521 IleAsnPheLysThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
Db      2083 ATTAATTTCAAGACATTTGTCATTCAGTGTCTTGAGATTATCCTATACCTTCGTGATT 2142
Qy      541 GlyGlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysLysProAsn 560
Db      2143 GGTGGAGGCGCTTCTTAATCTCATTTCTGACAGAGTGGCATATGTGCTCAAAAAACCAAC 2202
Qy      561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
Db      2203 AATTTGACTCATCTGTGTGGCCACCGTTCCCAACCTGCTGAAGATGTATAGCCACA 2262
Qy      581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
Db      2263 TGGCATGAGATGATTTCAAGATTAAGCTAAACGTAAGAGATCTGATGATCTGTGAAC 2322
Qy      601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
Db      2323 ACAGAAAGACGAGATCTTAAACCATATGTTCCACCCAGAGACAAATGTGTGATTCAGAG 2382
Qy      621 LeuValValAsnPheGlyAsnValLeuGlnGlnIlePheThrAspGluAlaArgThrGly 640
Db      2383 TTGGTGTAACTTTGGGATGTCTGCAAGAAATTTTCACAGATGAACCGAAGCGGT 2442
Qy      641 GlnGlu-AsnAsnLeuGlyGlyLysAsnGlyThrArgIleLeuSerSerCysProThr 660
Db      2443 CAGGAAAAACATTTTAAAGAGGAGGAAAAAGATGGAGCTGAATTCGTCTTCTGCCAAC 2502
Qy      660 rSerIle 662
Db      2503 TTCAATA 2509

RESULT 10
US-09-972-708-5
; Sequence 5, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: DuBoise, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-972-708-5

Alignment Scores:
Score: No.: 0 Length: 2238
Percent Similarity: 3465.50 Matches: 651
Percent Similarity: 99.09% Conservative: 2
Percent Similarity: 98.79% Mismatches: 3

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Query Match: 98.23% Indels: 3
 DB: 10 Gaps: 1
 US-10-006-265-17 (1-662) x US-09-972-708-5 (1-2238)

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyMetMetTrpThrTrpAlaLeu 20
 DB 1 ATGAAGCTCTCTCCCAAGCTTCACTGTGTAACTGGGGATGATGTGGACCTGGGCACTG 60
 QY 21 TrpMetLeuProSerLeuCysAlaPheSerLeuAlaAlaLeuProAlaLysProGln 40
 DB 61 TGGATGCTCCCTTCACTCTGCAAAATTCAGCCCTGCAGCTCTCCAGCTTAAGCTGAGA 120
 QY 41 IleSerCysValTyrrTyrrTyrrArgLysAsnLeuTrpCysThrTrpSerProGlyLysGlu 60
 DB 121 ATTTCCTGTGCTACTACTATAGGAAAAATTAACTCCTCACTTGAAGTCCAGAAAGGAA 180
 QY 61 ThrSerTyrrGlnTyrrThrValLysArgThrTyrrAlaPheGlyLysPheHisAspAsn 80
 DB 181 ACCAGTTATACCACTACACAGCTTAAGAACTTACGCTTTGGAGAAAACATGATATAT 240
 QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
 DB 241 TGTACAAACCAATAGTTCTACAAAGTAAATCGTCTCTGCTCTTTTCTCTTCCCAAGA 300
 QY 101 IleThrIleProAspAsnTyrrThrIleGluValGluAlaGluAsnGlyAspGlyValIle 120
 DB 301 ATAAAGATCCAGATAATTAATACATTAAGGTGAAGTGAATAATGAGATGTGTAAAT 360
 QY 121 LysSerHisMetThrTyrrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIle 140
 DB 361 AAAATCTCATATGACTACTGAGATTAAGAACTATAGGAAAACGAAACCACTTAAGATT 420
 QY 141 PheArgValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysPro 160
 DB 421 TTCCGTGGAACACGATTTTGCGCATCAACGAATGATTCAAAATGAAATGATAAGCT 480
 QY 161 GluLeuAlaProValSerSerAspLeuLysTyrrThrLeuArgPheArgThrValAsnSer 180
 DB 481 GAGTGGGCGCTGTTTCATCTGATTTAAATACACACTTCATCAGACAGTCAACGCT 540
 QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnIleThrTyrrAsn 200
 DB 541 ACCAGCTGATGAGAGTCACTTCCCTTAAGAACCTTAAGATTAATAACCAACGATCAAC 600
 QY 201 LeuThrGlyLeuGlnProPheThrGluTyrrValIleAlaLeuArgCysAlaValLysGlu 220
 DB 601 CTCACGGGGCTGCAGCCTTTTACAGAAATATGTCATAGCTCTGCGATGTGCGGTCAAGAG 660
 QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyMetThrGluGluGluAlaPro 240
 DB 661 TCAAGATTCGTGAGAGTCAAGAGCCMAAAAAAGGAAATGATCAGAGAAAGAGCTCA 720
 QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
 DB 721 TGTGGCTGGAACTGTGAGAGTCTTGAACCAAGCTGAGCGGATGAGAAAGGCCAATG 780
 QY 261 ArgLeuLeuTrpLysLysAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrrAsn 280
 DB 781 CGGTGTTATAGAAAGAGCAAGAGAGCCCAAGCTTCAAGAGAAAAACCTTGGCTACAC 840
 QY 281 IleTrpTyrrTyrrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGln 300
 DB 841 ATAAAGTACTATCAAGAAAGACACATTAACCTCAAGAAACAAATGAACACTTAACAG 900
 QY 301 GlnLeuGluLeuHisLeuGlyGlyLysSerPheTrpValSerMetIleSerTyrrAsnSer 320
 DB 901 CAGCTTGACATGCACTTGGAGGCGAAGCTTTTGGGTGTCTATGATTTCTTAATATCT 960
 QY 321 LeuGlyLysSerProValAlaThrLeuArgIleProAlaIleGlnGluLysSerPheGln 340
 DB 961 CTGGGAAGTCTCCAGTGGCCACCTGAGATTCACAGCTATTCAAGAAATAATCAATTCAG 1020

QY 341 CysIleGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
 DB 1021 TGCATTGAGTCAATGCAAGCGCTTGCCTGAGAACCGCTAGTGTGTAAAGTGGCAAGC 1080
 QY 361 SerAlaLeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluPro 380
 DB 1081 CCGCTGTAGACGTAACACTTGGATGATTAATGTTTCCGATGTGTGACTCAGAGGCC 1140
 QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrIleGlnGlnAspLys 400
 DB 1141 ACCACCTTCTCTGGAACTGTGTCTCAGGCCACGAATGAGAGATCCACCAAGATTA 1200
 QY 401 LeuLysProPheTrpCysTyrrAsnIleSerValTyrrProMetLeuHisAspLysValGly 420
 DB 1201 TTAAACCTTTCTGTGCTATTAACATCTCTGTATCCAAATGTTGATGACAAAGTTGGC 1260
 QY 421 GluProTyrrSerIleGlnAlaTyrrAlaLysGluGlyValProSerGluGlyProGluThr 440
 DB 1261 GAGCATATTCATCCAGGCTTATGCCAAAGAGCGCTTCATCAGAAAGTCTGAGAGC 1320
 QY 441 LysValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSer 460
 DB 1321 AAGGTGGAACATTTGGCGGTGAAGACGGTCAAGATCAATGGAAGAGATCCCAAGAT 1380
 QY 461 GluArgLysGlyIleIleCysAsnTyrrThrIlePheTyrrGlnAlaGluGlyLysGly 480
 DB 1381 GAGGAAAGGATATCATCTGCACTACCACTTTTACCAAGCTGAAGGTGAAGAAAGCA 1440
 QY 481 PheSerLysThrValAsnSerSerIleLeuGlnTyrrGlyLeuGlnSerLeuLysArgLys 500
 DB 1441 TTCTCCAAGACAGTCATTTCCAGATCTTGAGATACCGCTCGAGTCCCTAAGCAAG 1500
 QY 501 ThrSerTyrrIleValGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSer 520
 DB 1501 ACCCTTACATTTGTCAGTGTATGCGCAGACCGATGCGGGGAAACCGAGCGGACAGC 1560
 QY 521 IleAsnPheLysThrLysSerPheSerValPheGluIleIleLeuIleThrSerLeuIle 540
 DB 1561 ATAAATTCCAAGACATTTGTCATCAAGTCTTTAAGATATCCATTAATCTTCTGAT 1620
 QY 541 GlyIleGlyLeuLeuIleIleLeuThrValAlaTyrrGlyLysLysLysProAsn 560
 DB 1621 GGTGAGGCGCTTCTTATTCATTAATCTGACAGATGCAATGTCTCAAAAACCCCAAC 1680
 QY 561 LysLeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThr 580
 DB 1681 AAATTTGACTCATCTGTGTGCGCCACCGTCCCAACCTGCTGAAGATGATAGCCACA 1740
 QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluSerAspAspSerValAsn 600
 DB 1741 TGGCATGAGATGATTTCAAGATTAAGTAACTGAAGAGATGTGATGACTCTGTGAAC 1800
 QY 601 ThrGluAspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLys 620
 DB 1801 ACAGAAAGACAGACTTAAACATTTCCACCCTCCAGTGAACAAGTGTGATGACAG 1860
 QY 621 LeuValValAsnPheGlyAsnValLeuGlnGluIlePheThrAspGluAlaArgThrGly 640
 DB 1861 TTGGTGTGAACCTTGGGAAATGTTCTCAAGAAATTTTCAAGATGAAGCAGAAACGGGT 1920
 QY 641 GlnGluAsnAsnLeuGlyGlyLysLysAsnGlyThrArgIleLeuSerSerCysPro 659
 DB 1921 CAGGAAACCAATTTAGAGAGGGGAAAGAAATGGG-----TATGTGACTGTGCC 1968

RESULT 11
 US-10-715-667-5
 ; Sequence 5, Application US/10715667
 ; Publication No. US20040152161A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Immunex Corporation
 ; APPLICANT: Cosman, David J.
 ; APPLICANT: Mosley, Bruce A.
 ; APPLICANT: Bird, Timothy A.

APPLICANT: DuBoise, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/10/715,667
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US/09/972,708
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 2238
TYPE: DNA
ORGANISM: Homo sapiens
US-10-715-667-5

Alignment Scores:
Pred. No.: 0 Length: 2238
Score: 3465.50 Matches: 651
Percent Similarity: 99.09% Conservative: 2
Best Local Similarity: 98.79% Mismatches: 3
Query Match: 98.23% Indels: 3
DB: 18 Gaps: 1

US-10-006-265-17 (1-662) x US-10-715-667-5 (1-2238)

QY 1 MetLysLeuSerProGlnProSerCysValAsnLeuGlyWMeMetTrpThrTrpAlaLeu 20
DB 1 ATAAAGCTCTCTCCCGACCTTCATGTGTAACTGGGAGATGTGGACCTGGGACCTG 60
QY 21 TrpMetLeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsn 40
DB 61 TGGATGCTCCTTCACCTGCAATTCAGCTGGACGCTGCGACGTAAAGCTGGAAC 120
QY 41 LLeSerCysValLysTrpValArgLysAsnLeuThrCysThrTrpSerProGlyLysGlu 60
DB 122 ATTTCTGTGTCTACCTACATAGAAAAATTAACTGCACTTGAGTCCAGAGAAAGAA 180
QY 61 ThrSerTrpThrGlnTrpThrValLysArgThrTrpAlaPheGlyGluLysHisAspAsn 80
DB 181 AACAGTTATACCAAGTACACAGTTAAAGAACTTACGCTTTTGGAGAAACATGATAT 240
QY 81 CysThrThrAsnSerSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProArg 100
DB 241 TGTACACCAATAGTCTTCAAGTGAATAATCGTCTTCGCTCTTTTCCCTCCAAAG 300
QY 101 LLeThrLLeProAspAsnTrpThrLLeGluValGluAlaGluAsnGlyAspGlyValLLe 120
DB 301 ATTAACGATCCCAATATAATTATACCATTTGAGTGAAGCTGAAATGAGATGCTGTAATT 360
QY 121 LysSerHisMetThrTrpTrpArgLeuGluAsnLLeAlaLysThrGluProProLysLLe 140
DB 361 AAATCTCATTTGACATCTGAGATTTAGAAACATACCGAAACCTGAACCACTTAAGATT 420
QY 141 PheArgValLysProValLeuGlyLLeLysArgMetLLeGlnLLeGluTrpLLeLysPro 160
DB 421 TTCGGTGTGAACCAAGTTTGGGCATCAACGAATGATTCAAAATTGATGATGAAGCCT 480
QY 161 GluLeuAlaProValSerSerAspLeuLysTrpThrLeuArgPheArgThrValAsnSer 180
DB 481 GAGTTGGCCGCTTTTCATCTGATTTAAATATACACTTCGATTCAGGACAGCAACAGT 540
QY 181 ThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnTrpArgAsn 200
DB 541 AACAGCTGGATGGAAGTCAACTTCGCTAACAGACCGTAAGATAAAAACCAAGTCAAC 600
QY 201 LeuThrGlyLeuGlnProPheThrGluTrpValLLeAlaLeuArgCysAlaValLysGlu 220
DB 601 CTCACGGGGCTGACGCTTTTACAGATATGTCATAGCTCTGGAGTGTGGCTCAAGAG 660
QY 221 SerLysPheTrpSerAspTrpSerGlnGluLysMetGlyWMeThrGluGluAlaPro 240
DB 661 TCAAGTTCTGAGTGACTGGAGCCAAAGAAAAATGGGAATGACTGAGGAAGAGCTCCA 720

QY 241 CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGlyArgArgProVal 260
DB 721 TTGTGCTCGAAGCTGTGAGAGACTCTGAACCAAGCTGAGCGGATGGAAGAGCGCAGTG 780
QY 261 ArgLeuLeuTrpLysValAspGlyValProValLLeGluLysThrLeuGlyTrpAsn 280
DB 781 CGTTGTGTATGGAAGAAGCAAGAGAGAGCCCAAGTCTTAGAAGAAAAACCTTGGCTAAC 840
QY 281 LLeTrpTrpTrpProGlnSerAsnThrAsnLeuTrpGluThrMetAsnThrThrAsnGln 300
DB 841 ATATGTTACTATCCAGAAAGCAACCTAACCTCACAGAAACATATAACACTAACACAG 900
QY 301 GlnLeuGluLeuHisLeuGlyLysGluSerPheTrpValSerMetLLeSerTrpAsnSer 320
DB 901 CAGCTTGAAGTCACTGAGAGCGCAGAGCTTTTGGGTCTCATGATTTCTTAATATCT 960
QY 321 LeuGlyLysSerProValAlaThrLeuArgLLeProAlaLLeGlnGluLysSerPheGln 340
DB 961 CTGGGAAAGTCTCCAGTGGCCACCTGAGAGATTCCAGCTAATCAAGAAAAATCAATTGAG 1020
QY 341 CysLLeGluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSer 360
DB 1021 TGCATTGAGTCAATGAGGCTGCGTGTCTGAGAACCAAGCTAGTGAGTGAAGTGCACAA 1080
QY 361 SerAlaLeuAspValAsnThrTrpMetLLeGlnTrpPheProAspValAspSerGluPro 380
DB 1081 CCTGCTCTAGAGCTGAACCTTGATGATGATGATGATTTCCGAGTGTGACCTCAAGGCC 1140
QY 381 ThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThrLLeGlnGlnAspLys 400
DB 1141 ACCACCCCTTCTGGGAATCTGTCTCAGGCCACAGAACTGAGACATCCAGCAAGATAAA 1200
QY 401 LeuLysProPheTrpCysThrAsnLLeSerValLysProMetLeuHisAspLysValGly 420
DB 1201 TTAAAACTTTGTGGCTATACATCTCTGTATCCATGTGATGATGATGATGATGATGAT 1260
QY 421 GluProTrpSerLLeGlnAlaTrpAlaLysGluGlyValLProSerGlnGlyProGluThr 440
DB 1261 GAGCATATTCATCCAGCTTATGCGAAGAAAGCGTTCCATCGAAGTCTCTGAGACC 1320
QY 441 LysValGluAsnLLeGlyValLysThrValThrLLeThrTrpLysGluLLeProLysSer 460
DB 1321 AAGGTGAGAAATATTGGCGTGAAGACGCTCAAGATCACATGAGAAAGATTCCTCAAGAGT 1380
QY 461 GluArgLysGlyLLeLLeCysAsnTrpThrLLePheTrpGlnAlaGlnGlyLysGly 480
DB 1381 GAGAGAAAGGTATCATCTGCAACTACACCATCTTTACCAAGCTGAGAGTGAAGAAAGGA 1440
QY 481 PheSerLysThrValAsnSerSerLLeLeuGlnTrpGlyLeuGluSerLeuLysArgLys 500
DB 1441 TTCTCCAAACAGTCAATTCAGCATCTTGCAAGTACGCTGAGAGTCCCTGAACGAAG 1500
QY 501 ThrSerTrpLLeValGlnValMetAlaSerThrSerAlaGlyLysThrAsnGlyThrSer 520
DB 1501 ACCCTTACATGTTCAAGTCAAGTCAAGCAAGGCTGGGGGAACCAAGCGGACCAAG 1560
QY 521 LLeAsnPheLysThrLeuSerPheSerValPheGluLLeLLeLeuLLeThrSerLeuLLe 540
DB 1561 ATAAATTTCAACACATTCATTCAGTGTCTTGAGATTATCTCATTAATCTTCTGATT 1620
QY 541 GlyGlyGlyLeuLeuLLeLeuLLeLLeLeuThrValAlaTrpGlyLLeuLysLysProAsn 560
DB 1621 GGTGAGAGCTCTTATTTCTATTATCTGACAGAGTGGCATATAGCTCTCAAAAAACCAAC 1680
QY 561 LysLeuThrHisLeuLysTrpProThrValProAsnProAlaGluSerSerLLeAlaThr 580
DB 1681 AAATTGACATCTGTGTGGCCACCGTTCCAAACCTGCTGAAGATGATAGACCA 1740
QY 581 TrpHisGlyAspAspPheLysAspLysLeuAsnLeuLysGluLysAspAspSerValAsn 600
DB 1741 TGGCATGAGATGATTTCAAGATTAAGCTAAACCTGAAGAGATGTGATGATCTGTGAAC 1800

Qy 601 ThrGluAspArgIleLeuIleuProCySerThrProSerAspIleValIleAspIle 620
Db 1801 ACAGAGCAGGATTTAAACCACTTCCACCCAGTACAACTTGATTTACAG 1860
Qy 621 LeuValIleAspPheGlyAsnValIleuGlnIlePheThrAspGluAlaArgThrGly 640
Db 1861 TTGGTGTGAACTTTGGAAATCTCTCGCAAGAAATTTTACAGATGAAAGCAAGCGGT 1920
Qy 641 GlnGluAsnAsnLeuGlyGlyGlyAsnGlyThrArgIleLeuSerSerCyPro 659
Db 1921 CAGGAAACAAATTTAGAGAGGAGAAAGAAATGCG-----TATGTACCTGCC 1968
RESULT 12
US-09-892-949-1
; Sequence 1, Application US/09892949
; Publication No. US2003009639A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Geo. Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuljper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (171)...(2366)
US-09-892-949-1
Alignment Scores:
Pred. No.: 0 Length: 2402
Score: 3465.50 Matches: 651
Percent Similarity: 99.24% Conservative: 1
Best Local Similarity: 99.09% Mismatches: 2
Query Match: 98.23% Indels: 3
DB: 10 Gaps: 1
US-10-006-265-17 (1-662) x US-09-892-949-1 (1-2402)
Qy 3 LeuSerProGlnProSerCyValIleAsnLeuGlyMetLeuThrProIleLeuThrMet 22
Db 138 CTCCTCTCCCAAGCTTCATGTGTAACTGGGAGATGATGACCTGGGCACTGGATG 197
Qy 23 LeuProSerLeuCyIlePheSerLeuAlaIleuProAlaIleProGluAsnIleSer 42
Db 198 CTCCTCTCTCTCTGCAATTCAGCTGGCACTCTGCAAGCTTAAGCTGAAACATTTCC 257
Qy 43 CyValIleGlyIleGlyIleAsnLeuThrCyThrTrpSerProGlyIleGluThrSer 62
Db 258 TGTGTCTCTACTATAGGAAATTTAACTGCACTTGAAGTCCAGAAAGAAACAGT 317
Qy 63 TyrThrGlnIleThrValIleAlaArgThrTyrAlaPheGlyGlyIleAsnCyThr 82
Db 318 TATACCCAGTACACGTTAAAGAACTTACCTTTTGAAGAAACATGATTAATTGACA 377
Qy 83 ThrAsnSerSerThrSerGluAsnArgIleSerCySerPhePheLeuProArgIleThr 102
Db 378 ACCAATAGTTCTACAGTGAAGAAATGCTGCTGCTCTTTTCTTCTTCAAGAAATACG 437

Qy 103 IleProAspAsnIleThrIleGluValIleGluAsnGlyAspGlyValIleIleSer 122
Db 438 ATCCAGATTAATTAATACATGAGTGAAGCTGAAGTGAAGATGGTAAATTAATCT 497
Qy 123 HisMetThrTyrTrpArgLeuGluAsnIleAlaIleThrGluProProIlePheArg 142
Db 498 CATATGACATCTGAGATTAGAGACATAGCGAAATCGAACACCATTAATTTCCGT 557
Qy 143 ValIleProValIleGlyIleIleAsnGlyMetIleGlnIleGluTrpIleIleProGluLeu 162
Db 558 GTGAACACGATTTGGGATCAAAAGCAATGATTAATGATGAATGAATGAAGCTGAGTTG 617
Qy 163 AlaProValSerSerAspIleuIleuIleuThrIleuArgPheArgThrValAsnSerThrSer 182
Db 618 GCGCTGTTTATGATGATTTAAATACACTTGATTCAGGACAGTCACAGTACAGC 677
Qy 183 TrpMetGluValIleAsnPheAlaIleAsnArgIleAspIleuIleuIleuThr 202
Db 678 TGATGAGAGTCACTTCCTAGAACCTGTAAGATTAAGAAACCAACCTACACTCAG 737
Qy 203 GlyLeuGlnProPheThrGlyIleValIleAlaIleuArgCyAlaValIleGluSerIle 222
Db 738 GGGCTGACGCTTTTACAGATATGATCATAGCTCGGATGTCGCTCAAGAGTCAAG 797
Qy 223 PheTrpSerAspTrpSerGlnIleuIleuMetGlyMetThrGluGluGluValIleProCyGly 242
Db 798 TTCTGGAGTGACTGACCAAGAAATGGAAATGACTGGAGAAAGCTCCATGTGCG 857
Qy 243 LeuGluLeuTrpArgValIleuIleuProAlaGluAlaAspGlyArgProValArgLeu 262
Db 858 CTGAACTGTGAGAGTCTGTAACCAAGCTGAGCGATGGAAGAAGCCAGTCCGTTG 917
Qy 263 LeuTrpIleuIleuValIleArgIleValIleProValIleuIleuIleuIleuIleuTrp 282
Db 918 TTATGAAAG 977
Qy 283 TyrTrpProGlnSerAsnThrAsnLeuThrGluIleuMetAsnThrThrAsnGlnIleu 302
Db 978 TACTATCCAGAAACCAACCACTTACCAAGAAACCAATGAACTTACCAACCACTT 1037
Qy 303 GluLeuHisLeuGlyGlyIleuSerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
Db 1038 GAATGCAATCTGGAG 1097
Qy 323 LysSerProValAlaThrIleuArgIleProAlaIleGlnIleuIleuSerPheGlnCysIle 342
Db 1098 AAGTCTCCAGTGGCCACCTGAGGATTCAGCTATTCAGAAATCAATTCAGTGCATT 1157
Qy 343 GluValMetGlnAlaCyValAlaIleGluAspGlnIleuValIleuIleuIleuIleuIleu 362
Db 1158 GAGGTCAATGACGCTCGTGTGAGAGACCAAGCTAGTGTGAAGTGGCAAAAGCTGCT 1217
Qy 363 LeuAspValAsnThrTrpMetIleGluTrpPheAspValIleAspSerGluProThrThr 382
Db 1218 CTAGACGTGAACCTTGAATGATTAATGATTTCCGATGATGATGATGATGATGATGAT 1277
Qy 383 LeuSerTrpGluSerValIleGlnAlaThrAsnTrpThrIleGlnIleuAspIleuIleu 402
Db 1278 CTTTCTCGGAGATCTGTCTCAGGCCAGCAAGTCCAGCAAGTAAATTAATAA 1337
Qy 403 ProPheTrpCyIleAsnIleSerValIleProMetLeuHisAspIleValIleGluPro 422
Db 1338 CCTTCTCGGAGATCTGTCTCAGGCCAGCAAGTCCAGCAAGTAAATTAATAA 1397
Qy 423 TyrSerIleGlnAlaTyrAlaIleuGluGlyValIleProSerGluGlyProGluThrIleVal 442
Db 1398 TATTCATTCAGGCTTATGCAAGAAAGAGGCTTCAAGAGGCTTGAAGAGAGAGAG 1457
Qy 443 GluAsnIleGlyValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 462
Db 1458 GAGAACTTGGCGGAG 1517


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QY 463 LyeGlyllelCysAntYrThrIlePheTyrglnAlaGluGlyGlySer 482
    |||
Db 1518 AAGGATATCATCTGCAACTACACCATCTTTACCAAGCTGAAGTGAAGAAAGATTCTCC 1577
QY 483 LyeThrValAsnSerSerIleLeuGlnTyrglyLeuGluSerIleuysaaglyThrSer 502
    |||
Db 1578 AACAACGTCATTCAGCATCTTGACAGTACGGCTGAGTCCCTGAAACCAAGACCTCT 1637
QY 503 TyrlleValGlnValMetAlaSerThrSerAlaGlyGlyThraSnglyThrSerIleAsn 522
    |||
Db 1638 TACATGTTGAGTTCATGCGCACACCAAGTCTGGGGGAACCAACGGACCAACATTAAT 1697
QY 523 PheIleThrIleuSerPheSerValPheGlnIleIleuIleThrSerIleuIleGly 542
    |||
Db 1698 TTCACAAACATTCATTCAGTGTCTTGAAGATTATCCTCAATCTCTGATGGTGA 1757
QY 543 GlyLeuLeuIleuIleIleuThrValAlaTyrglyLeuIleuysaaglyThrSer 562
    |||
Db 1758 GGCTCTTATTCATTCATTCATTCAGTACAGTGCATAGTCTCAAAAAACCAACCAATTC 1817
QY 563 ThrIleuCystrProThrValProAsnProAlaGluSerSerIleAlaThrTrpHis 582
    |||
Db 1818 ACTCATCTGTGTGGCCACCTGCTCCACCTGCTGAAGTATAGCCACATGGCAT 1877
QY 583 GlyAspAspPheIleAspIleuAsnLeuIleGluSerAspAspSerValAsnThrGlu 602
    |||
Db 1878 GGAGATGATTTCAAGGATTAAGCTAAACCTGAAGAGCTGATGATCTGTGAACACAGAA 1937
QY 603 AspArgIleuIleuysProCySerThrProSerAspIleuValIleAspIleuVal 622
    |||
Db 1938 GACAGATCTTAAACCATATTCACCCCGACGACAAAGTGTGATGCAAGTGTGTG 1997
QY 623 ValAsnPheGlyAsnValIleuGlnGluIlePheThrAspGluAlaArgThrGlyGln 642
    |||
Db 1998 GTGAACCTTGGGATGTTCTGCAAGAAATTTTCACAGATTAACCCGACGATCAGAA 2057
QY 643 AsnAsnLeuGlyGlyGluysaenglyThraGlyIleuSerSerCyPro 659
    |||
Db 2058 AACAAATTAGAGAGGAAAGAAATGGG-----TATGTGACCTGCCCC 2099

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RESULT 13
US-10-351-157-110
; Sequence 110, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Geo, Zeren
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Dasovych, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (171) ... (2366)
US-10-351-157-110
Alignment Scores:
Pred. No.: 0
Score: 3465.50
Percent Similarity: 99.24%
Best Local Similarity: 99.09%
Query Match: 98.23%
DB: 17
Gaps: 1
Length: 2402
Matches: 651
Conservative: 1
Mismatch: 2
Indels: 3
US-10-006-265-17 (1-662) x US-10-351-157-110 (1-2402)
QY 3 LeuSerProGlnProSerCysValAsnLeuGlyMetThrTrpAlaLeuTrpMet 22
    |||
Db 138 CTCTCTCCCACTTCATGTTTAACTGGGGAGATGTGACCTGGGCACTGGGAGAT 197
QY 23 LeuProSerLeuCyAlaPheSerIleuAlaAlaLeuProAlaLysProGluAsnIleSer 42
    |||
Db 198 CTCCCTCACTCGCAAAATTCAGCTGCGACCTGCGACGCTGACGTAAGCTGAGAACTTCC 257
QY 43 CysValTyrrTyrrTyrrArgIleAsnLeuThrCysThrTrpMetSerProGlyIleGlyThrSer 62
    |||
Db 258 TGTGTTACTACTATAGGAAATTTAACTGCTGAGTGAAGTCCAGGAAAGAAACCACT 317
QY 63 TyrrThrGlnTyrrThrValIleAspArgThrTyrrAlaPheGlyGlyIleuHisAspAsnCystr 82
    |||
Db 318 TATACCACTATACAGATTAAAGAACTTACGCTTTTGAGAAACATATATATGTA 377
QY 83 ThrAsnSerThrSerGluAsnArgAlaSerCysSerPhePheLeuProAlaIleThr 102
    |||
Db 378 ACCAATAGTTCTACAAAGTAAATCGTCTGCTCTTTTCTTCCCAAGAAATTAAG 437
QY 103 IleProAspAspTyrrThrIleGluValGluIleGluAsnGlyAspGlyValIleLysSer 122
    |||
Db 438 ATCCCAATTAATTAACCTTAAAGTGAAGCTGAAAGTGAAGATGTATTAATCT 497
QY 123 HisMetThrTyrrTrpArgLeuGluAsnIleAlaLysThrGluProProLysIlePheArg 142
    |||
Db 498 CATATGACATCTGAGATTAAGAAACATAGGAAACATGAAACCTTAAGATTTCCGT 557
QY 143 ValLysProValLeuGlyIleLysArgMetIleGlnIleGluTrpIleLysProGluLeu 162
    |||
Db 558 GTGAACCACTTTGGGATCAACGAATGATTAATGAATGAATGAATGAATGAATGAGT 617
QY 163 AlaProValSerSerAspLeuysTyrrThrIleuArgPheArgThrValAsnSerThrSer 182
    |||
Db 618 GGCTCTTTCATCTGATTTAAATACACATTCGATTCAGACAGTCAACAGTACACG 677
QY 183 TrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTyrrAsnLeuThr 202
    |||
Db 678 TGGATGGAAGTCAACTCCCTTAAGAACCTTAAGATTAAGAAACCAACGTAACACCTCAG 737
QY 203 GlyLeuGlnProPheThrGluTyrrValIleAlaLeuArgCysAlaValLysGluSerLys 222
    |||
Db 738 GGCTGCAACCTTTTACAAATATGCTAGCTGCGATGCGGTCAAGAGTCAAAAG 797
QY 223 PheTrpSerAspTrpSerGlnGluysMetGlyMetThrGluGluGluAlaProCysGly 242
    |||
Db 798 TTCTGAGAGTCTGAGGCGCAAGAAATGGAATGACTGAGAGAAAGAACTCAGTGTGC 857
QY 243 LeuGluLeuTrpArgValLeuIleuysProAlaGluAlaAspGlyArgArgProValArgLeu 262
    |||
Db 858 CTGGAACCTGAGAGTCTGTAACCAAGTGAAGCGGAGGAGAAAGGCACTGCGGTG 917
QY 263 LeuTrpLysValAlaArgGlyAlaProValLeuGluLysThrLeuGlyTyrrAsnIleTrp 282
    |||
Db 918 TTATGGAAGAGCAAGAGAGAGCCCACTAGAGAAACACTGGCTAACAATATG 977
QY 283 TyrrTyrrProGluSerAsnThrAsnLeuThrGluThrMetAsnThrThrAsnGlnGlnLeu 302
    |||
Db 978 TACTATCAGAAAGCAACTAATCACTCAAGAAACATGAACATTAACCAAGCAGCTT 1037

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Qy 303 GluLeuHisLeuGlyGlySerPheTrpValSerMetIleSerTyrAsnSerLeuGly 322
Db 1038 GAACCTGCACTGGGAGGCGAGAGCTTTGGGGCTATGATTTCTTAATATCTCTTGG 1097
Qy 323 LysSerProValAlaThrLeuArgIleProAlaIleGlnGlyLysSerPheGlnCysIle 342
Db 1098 AAGGCTCCAGTGGCCACCTGAGATTCCAGCTATTCAGAAATAATCTTTCAGTGCATT 1157
Qy 343 GluValMetGlnAlaCysValAlaGluAspGlnLeuValValLysTrpGlnSerSerAla 362
Db 1158 GAGGTCAGCAGGCGCTGCTGCTGATGAGACCGATGCTGAGAGTGGCAAGCTCTCTCT 1217
Qy 363 LeuAspValAsnThrTrpMetIleGluTrpPheProAspValAspSerGluProThrThr 382
Db 1218 CTAGACGTAACACTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1277
Qy 383 LeuSerTrpGluSerValSerGlnAlaThrAsnTrpTrpIleGlnGlnAspLysLeuLys 402
Db 1278 CTTTCTGGGAACTGTGTCTCAGGCCACGAACTGAGATCCAGCAAGATTAATTAATA 1337
Qy 403 ProPheTrpCysTyrAsnIleSerValTyrProMetLeuHisAspLysValGlyGluPro 422
Db 1338 CTTTCTGTGCTATTAACATCTGTGTATCCAAATGTTGACATGACAAAGTTGGCGAGCCA 1397
Qy 423 TyrSerIleGlnAlaTyrAlaLysGluGlyValProSerGluGlyProGluThrIleVal 442
Db 1398 TATTCATCAGGCTTATGCTCAAGAAAGGCGCTTCATAGAAAGCTCGAAGCCAAAGGTG 1457
Qy 443 GluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGluArg 462
Db 1458 GAGAAACATGGCGTGAACCGGTCCAGTCACTGAAAGAGATTTCCCAAGAGTGAAGA 1517
Qy 463 LysGlyIleIleCysAsnTyrThrIlePheTyrGlnAlaGluGlyLysGlyPheSer 482
Db 1518 AAGGATCATCTCACTCACTACCACTTTTACCAAGCTGAAGGTGAAAGATTTCTCC 1577
Qy 483 LysThrValAsnSerSerIleLeuGlnTyrGlyLeuGlnSerLeuLysArgLysThrSer 502
Db 1578 AAGACAGCAATTCAGCATCTTGAGAGAGGCGCTGAGGTCTCTGAAGCGAAAGCCCT 1637
Qy 503 TyrIleValGlnValMetAlaSerThrSerAlaGlyTyrAsnGlyThrSerIleAsn 522
Db 1638 TACATTGTCAGGTCATGCGCAGCAGCGCTGCGGGAACCAACGGAACGACATTAAT 1697
Qy 523 PheLysThrLeuSerPheSerValPheGlnIleIleLeuIleThrSerLeuIleGlyGly 542
Db 1698 TTCAAGACATTTGTCTCAGTGTCTTGAGATTATCTCATTAATCTTCTGATTGTGGA 1757
Qy 543 GlyLeuLeuIleLeuIleIleLeuThrValAlaTyrGlyLeuLysPheAsnLysLeu 562
Db 1758 GGCCTTCTTATTCATTAATCTGACAGTGCATTAATCTCTCATTAATCTTCTGATTGTGGA 1817
Qy 563 ThrHisLeuCysTrpProThrValProAsnProAlaGlnSerSerIleAlaThrTrpHis 582
Db 1818 ACTATCTGTGTGGCCCAACCGTTCACCAACCTGCTGAAGATGATATGCCAATGGCAT 1877
Qy 583 GlyAspAspPheLysAspLysLeuAsnLeuLysGlnSerAspAspSerValAsnThrGlu 602
Db 1878 GGAATGATTTCAAGATTAACCTTAACCTGAAGAGTCTGATGACTCTGTAACACAGAA 1937
Qy 603 AspArgIleLeuLysProCysSerThrProSerAspLysLeuValIleAspLysLeuVal 622
Db 1938 GACAGGATCTTAAACCATGTTCCACCCAGTGCAGAGTTGGTGTGATGACAAATGGTGTG 1997
Qy 623 ValAsnPheGlyAsnValLeuGlnIlePheThrAspGlnAlaArgThrGlyGlnGlu 642
Db 1998 GTGAACCTTGGGATTTCTGCAAGAAATTTTCAAGATGAAGCCAGAACGGGTCAAGAA 2057
Qy 643 AsnAsnLeuGlyGlyLysAsnGlyThrArgIleLeuSerSerCysPro 659
Db 2058 AACCAATTTAGAGGAGGAAAGAAATGG-----TATGTGACCTGCCCC 2099

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RESULT 14
US-10-772-531-1
; Sequence 1, Application US/10772531
; Publication No. US20040142422A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/10/772,531
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (171)...(2366)
US-10-772-531-1

Alignment Scores:
Pred. No.: 0 Length: 2402
Score: 3465.50 Matches: 651
Percent Similarity: 99.24% Conservative: 1
Best Local Similarity: 99.09% Mismatches: 2
Query Match: 98.23% Indels: 3
DB: 18 Gaps: 1

US-10-006-265-17 (1-662) x US-10-772-531-1 (1-2402)
Qy 3 LeuSerProGlnProSerCysValAsnLeuGlyMetTrpThrTrpAlaLeuTrpMet 22
Db 138 CTCTCTCCCAAGCCTTATGATGTTAACTGGGATGATGACCTGGCACTGTGATG 197
Qy 23 LeuProSerLeuCysLysPheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSer 42
Db 198 CTCCCTCAGCTGCAAAATTCAGCTGAGCTGTGCTGACGTAAAGCTGAGAAACATTTCC 257
Qy 43 CysValTyrTyrTyrArgLysAsnLeuThrCysThrTrpSerProGlyLysGluThrSer 62
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; Sequence 3, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: DuBoise, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-708-3

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Best Local Similarity: 98.79% Mismatches: 3
Query Match: 98.23% Indels: 3
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US-10-006-265-17 (1-662) x US-09-972-708-3 (1-2480)
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Search completed: February 23, 2005, 20:18:25
 Job time : 1102.62 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2005, 08:54:07 ; Search time 6085.24 Seconds
(without alignments)
4140.927 Million cell updates/sec

Title: US-10-006-265-17

Perfect score: 3528
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Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Database :

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2: gb_est2:
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4: gb_est3:
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8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	661	18.7	5264	3 BC071555 Homo sapi
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5	473.5	13.4	653	5 BU455838 Mus muscu
6	468.5	13.3	637	7 CF174021 B0932D09-
7	465.5	13.2	2804	3 AK089305 Mus muscu
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21	308.5	8.7	1131	5 BX380515
22	306	8.7	715	7 CF634184
23	305.5	8.7	612	3 AG138991
24	304	8.6	1659	3 CF611411
25	302	8.6	546	6 CA555774
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27	297	8.4	553	6 CA559989
28	294.5	8.3	628	6 CB427282
29	294	8.3	642	6 CB512958
30	294	8.3	697	7 CNE529323
31	291	8.2	459	8 AQ022781
32	289	8.2	1097	5 BX359249
33	286	8.1	751	5 BQ770280
34	286	8.1	1577	3 CB613729
35	282	8.0	761	5 BU460413
36	279	7.9	669	5 BU322304
37	278.5	7.9	1073	5 BX382126
38	278	7.9	721	7 CN454854
39	277	7.9	709	5 BQ185371
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ALIGNMENTS

RESULT 1	AK030512	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS
1	AK030512	2232 bp	mus musculus adult male pituitary gland cDNA, RIKEN full-length full insert sequence.	AK030512	1	GI:26326508	HTC; CAP trapper.	Mus musculus (house mouse)	1	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	Genome Res. 10 (10), 1617-1630 (2000)	11042159	20499374	1	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishii, K., Kikunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,
2	AK030512	2232 bp	mus musculus adult male pituitary gland cDNA, RIKEN full-length full insert sequence.	AK030512	1	GI:26326508	HTC; CAP trapper.	Mus musculus (house mouse)	2	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	Genome Res. 10 (10), 1617-1630 (2000)	11042159	20499374	2	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishii, K., Kikunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,

TITLE
Yonezaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system—384-format
sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
MEDLINE
20030913
11076861
PUBMED

REFERENCE
AUTHORS 4 The RIKEN Genome Exploration Research Group Phase II Team and the

TITLE	FANTOM Consortium.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
DATE	Nature 409, 685-690 (2001)

5
REFERENCE
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research

TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2232)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.

Fukuda, S., Furuno, M., Hanagasaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hizoane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawanaka, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Morita, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiriki, I., Sogaue, Y., Tagami, M., Tagawa, A., Takahashi, F., Takui-Akahira, S., Takeeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M., and Hayashirakzi, Y.

TITLE Direct Submersion
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 220-0045, Japan (E-mail:genome-resgsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,

COMMENT
Fax: 81-43-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>.

FEATURES
source

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(evidence: ProCrest)
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/translation="MASTRAGTNGVRINPKTLSTVPEIYLLTSLVGGGLLLSITK
VTPLGRKRNRLPLCCBPVNPAPASLATAWLDGCKSKMTGSGPTDEVYLRPC
VPALIDKLVVNFENFLEVYLTEBAGKQKQASLGGSEANEYTSBSRPDPGPKSKKE
SVLLEVASDESDSHSTCSRNADEVISELAPQSPSSCSPLGSPREDQANPYLKNSTV
REFLVHENIPEHSGKEV"

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Alignment Scores:	
Pred. No.:	1,3e-67
Score:	735.50
Percent Similarity:	79.25%
Best Local Similarity:	67.74%
Query Match:	20.85%
GB:	3
	Gaps:
	2
	Length: 2232
	Matches: 147
	Conservative: 25
	Mismatches: 42
	Indels: 3

US-10-006-265-17 (1-662) x AK030512 (1-2232)

434 ProSerGluGlyProGluThrLysValGluAsnIleGlyValLysThrValThrIleThr 453

DB 212 CCATTAAGAGTCCCTGAGACCAAGGCTGGAGAACATCCGGCTCGAGGACAGCCACAGATCACA 2/1

OY		454	TTPVSGIUIIEPRLYSSEKGIUARGLYGELYILELLECYAKSNIVIRINILDEPEHYR	4 / 3
D8		272	TGGAGGAGATTCCTAAGAGTGTACGAATCGATTATCAACAATAACTGTATTTTAAC	331

474 GlnIaGlnGlyGlySerLysThrValAsnSerSerIleuGlnTyrGly 493

DB 332 CAAGCTGAGAGGTGMAAAGACTCTCCAGACTGTCTAACTCTCATGCGCCCTGCAGATGTGAC 391

Db 392 CTGAGTCTCTGACACGAGGACCTTTATATCTGTTGGGTGATGGCCAGCACCAGAGCT 451

514 GLYGLYThraSngLYthnSerileasnphelystnleuSerPheSerValphcglutlle 533

DD GGAGGATCCACCGGGTGGAGAATTAACTTCAGAGCAATGGTCTCATCAGTAGGTATGGAAAAT
452
QY ILEAULTERTHSERLEULEGLYGLYLEUULEULEULEILEUTHRALALA 553

Db 512 GTCTTCTACATCTCTAGTGGAGGAGGCTTCTTCTACTTACATCAAAACAGTACT 571

QY	554	TyrGlyLeuLysProAsnLysLeuThnHisLysCysTrpProThrValProAsnPro	573	
DB	572	TTTGCCCTCAAGACCAACCCGGTGACTCCCTGTGTCTCTGATGTTCCCAACCT	631	

574 AlaGluSerSerIleAlaThrTrpHisGlyAspAspPheIysAspLysIleuAsnIleuLys 593

Accession	Sequence	Position
Db	632 GCTGAAGTAGTTAGCCACATGGCTCGGAGATGTTCAAG---AAGTCAATAATGAG 688	632-688

Db

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594 GUSCTGACGAACTCTGGGACACACAGACGCTGCTCTAAACCATGTCCCGTCCCGCG 7488
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oy GUSCTGACGAACTCTGGGACACACAGACGCTGCTCTAAACCATGTCCCGTCCCGCG 7488
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QY 614 AsplysLeuValIleasplysLeuValalaAsnPhcIyAsnValLeuGlnGluIlePhe 6333

DB 749 GAT-----CTCATTTGACACAGCTGGTAGTGAACTTTGAGAAATTTCTCGAAGTAGTATTG 802

Db 803 ACAGAGAGCTCGAAGGCTCAGCGAGCATTTTCGAGAGAGAACCAAT 853

RESULT 2	
BC071555	

DATA LINE	

	14-0000
	TIME 00
	TRAY 000

LOCUS	5264 bp	mRNA	linear	hic	U2-00N-2000
BCU01555					
Homo sapiens	clone IMAGE:4374041,	containing frame-shift			
DEFINITION	errors.				

ACCESSION	GI:4793807
BC071555	
BC071555.1	
KEYWORDS	
HTC.	

SOURCE ORGANISM	
Homo sapiens (human)	
Homo sapiens	
Elkayovota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	

REFERENCE
Mammalia; Eutheria; Primates; Carnathini; Homnidae; Homo.
1 (bases 1 to 5264)

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Stausberg, K.L., Reingold, E.A., Grouse, J.H., Dege, J.G., Aulifors

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,


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Db      1664 CCTGAATCCATAAGCATACCTTAAACAAGCTCCACCTTCCAAAGACCTACTGTTCCG 1723
Qy      442 ValGlaAmIleGlyValIleThrValThIleThrIleThrIleProIleProIleSerGlu 461
Db      1724 AC-AAAAAGATGGAGAAAAAGAAAGCTGCTTCTAGAGGAGCAACTCTCTGTTGATGTT 1782
Qy      462 ArgGlyGlyIleIleCysAsnIleThrIlePheThrGlnIleGluGlyGlyGlyPhe 481
Db      1783 CAGAATGATTTATTCAGAAATTTATCTATTTTATTAAGAACATTCATTTGGAATGAAACT 1842
Qy      482 SerLeuThrValAsnSerSerIleLeuGlnIleGlyLeuGluSerLeuIleValIleThr 501
Db      1843 GCGTGAATGTGATCTTCTCCACACAGATATATCATTTGCTCTTGTGACTGATGACACA 1902
Qy      502 SerTyrIleValGlnIleMetAlaSerThrSerAlaGlyGlyIleThrAsnIleThrSerIle 521
Db      1903 TTGTACATGTGTACGAAATGGCAGATACAGATGAAAGGTGGAAAGATGTTCCAGAAATTC 1962
Qy      522 AsnPheIleThrLeuSerPheSerValPheGluIleIleLeuIleThrSerLeuIleGly 541
Db      1963 ACTTTTACTACACCCCAAGTTGCTTCAAGGAAATTTGAGCCATATGCTGCTGTTTGC 2022
Qy      542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaIleGlyLeuIleValIleProAsnIle 561
Db      2023 TTAGCATTCCTATTGACAACTCTTCTGGAGTCTGTTCTTCTTATTAAGCAGACACTA 2082
Qy      562 LeuThrIleLeuIleValIleProAsnProAlaGluSerSerIleAlaIleThr 581
Db      2083 ATTAAAAACACATCTGGCTTAATGTTCCAGATCTTCAAGAGTCAATATGTTCCAGTGG 2142
Qy      582 -----TTTCCAGAAAGTTCGAAATCAATGAGC----- 2193
Db      2143 TCACCTCACACCTCTCCAAAGCAGACATTTTAATTCAAAAGATCAATG-----TAT 2193
Qy      595 SerAspAspSer-----ValAsnThrGluAspArgIleLeuIlePro 608
Db      2194 TCGATGCGCAATTCTCAGTATGTAAGTGTGTGAAATGAAACAAATGCAAAAAAGCCCT 2253
Qy      609 CysSerThrProSerAspIleValIleAspIleLeuValIleAsnPheGluAsnVal 628
Db      2254 -----TTTCCAGAAAGTTCGAAATCAATGAGC----- 2280
Qy      629 LeuGlnGluIlePheThrAspGluAla-----ArgThrGlyGlnGluAsnLeuGly 646
Db      2281 -----CTGTTCAAAAAGGAAAAAATTAATATCGAAGGACAGACAGCTGATATTGG 2331
Qy      647 GlyGluIleAsnGlyThrArgIleLeuSerSerCysProThrSer 661
Db      2332 GGG-----TCTTCATGATGATCATCT 2352

RESULT 3
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DEFINITION    Rattus norvegicus Acl055 mRNA, complete cds.
ACCESSION     AY310138
VERSION       AY310138.1 GI:32264598
KEYWORDS      HTC.
SOURCE        Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE     1 (bases 1 to 3055)
AUTHORS       Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q.,
              Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
              Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
              Liver regeneration after PH
              Unpublished
              2 (bases 1 to 3055)
              Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q.,
              Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
              Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
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TITLE      Direct Submission
JOURNAL     Submitted (29-MAY-2003) Henan Bioengineering Key Lab, Henan Normal
            University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
            China
FEATURES    source
            Location/Qualifiers
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                SARLWKTLPISEANGKIDIEVTVTQSKSVSGTYTNGTELVNLTNNRYASLAAR
                NVGKSPATVLTIPGSHFRVDKAPKQNLWENTPPSKPVNKTILECVISENSPC
                IPDWQEDGTNVRHLRGLSKCYLITVTFPGGPGSPSMKAYLKQAPSKGPT
                VRTKLVKKEAVLEWDHLPVDVQNFIRNYSISYRTSVGKEMVWVSDSHETVLSL
                SSDLTYVMMAVTEEGKDPPEFTFTLLKFSSSCAASGLMSIANSWPTADASSFD
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                KKPCCDULKSLDFPKKEKISTEGHSSSGIGGSSCSSRPSISSSENBAQSTAYTO
                YSTVHSGTRHVPVQVFSRESSTQPLDSEEREDLDLVDSVDSGDILPRQGFK
                OSCSQGASPDVSHFERSSQVPSGSEDFVRLKQOVSDHISEPYGSEGRLLFQGSV
                ADALGTGIDQIERFESVQETAMVEDLSKSLPQTVVQGYTMPIANIKVHWHQOST
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ORIGIN
Alignment Scores:
Pred. No.:      6,79e-59      Length:      3055
Score:          657.00      Matches:      188
Percent Similarity: 45.26%      Conservative: 108
Beet Local Similarity: 28.75%      Mismatches: 280
Query Match:    18.62%      Indels:      78
DB:             3      Gaps:      23

US-10-006-265-17 (1-662) x AY310138 (1-3055)
Qy      35 ProAlaIysPProGluAsnIleSerCysValIleTyrTyrArgIleAsnLeuThrCysThr 54
Db      362 CCAGATATACCTCAAAATTTGAGTTGCATTGGAATGAGGAGGAAAGACATGCTGTGTGAG 421
Qy      55 TPSPserProGlyIleGluThrSerTyr---ThGlnIleThrValIleAsnArgThrTyrAla 73
Db      422 TGGGACCCGAGAAAGGAGACATACCTTGAAACAACTTGAACCTTGAAGTCAAGATGGGCA 481
Qy      74 PheGlyGluIleHisAspAsnCysThrThrAsnSerSerThrSerGluAsnArgAlaSer 93
Db      482 ---ACAGAGAAGTTTCTGATTTGTCGAACAAGACATGACAGCAGC-----TCC 526
Qy      94 CysSerPhe---PheLeuProArgIleThrIleProAsnIleThrIleGluValGlu 112
Db      527 TGCATGATGGGTATACCCCATCTATTGTC-----AACATGAGAGGTGGGGGAG 580
Qy      113 AlaGluAsnGlyAspGlyValIleIleIleIleIleIleIleIleIleIleIleIleIle 132
Db      581 GCGGAGAAATGCCCTTGGGAATGCTCTCAGAGCCATATCAATTTGACCCCGTGATAA 640
Qy      133 AlaIleThrGluProIleProIlePheArgValIleProValIleGluIleIleIleIle 152
Db      641 GTGAAACCAAGCCACCTCATATTTGTCAGAGACCAACTCAAGAAATATTCACGTATA 700
Qy      153 ILeGlnIleGluThrIleIleIleIleIleIleIleIleIleIleIleIleIleIle 172
Db      701 TTAAACTAGCATGGGTCAATTCAGGTTTGACAGATATTTTAAG---CTGAAGTGGAG 757
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Percent Similarity: 61.11%
 Best Local Similarity: 47.47%
 Query Match: 13.42%
 DB: 5
 Gaps: 1

US-10-006-265-17 (1-662) x BU455838 (1-653)

384 SerTPGJuseValSerGlnAlaThrPheThrIleGlnAlaPheLeuPro 403
 14 TCATGGCATATATTCATAATTCACAAAGTGAAGAACTAACAAAAAACTTTAAATTA 73
 404 PheTPCybTYrAsnIleSerValTYrPheMetLeuHisAspIleValGlyIleProTYr 423
 74 TTTGATGCTCAACAATGCTGATCTATCTATCTATGAAAAATAAGTAGCAGCTCATAT 133
 424 SerIleGlnAlaTYrAlaIleGlyGluValProSerGlyGlyProGluThrIleValGlu 443
 134 TCCATACCAAACTTAATGTTCAAGAAAAAGAGCCATCAGAAAGCCCTGTGCTGATACGGAT 193
 444 AsnIleGlyValIleValThrValThrIleThrIlePheGlyIleProIleSerGluArgIle 463
 194 TTTCCAGCAAAAATGAAAGTTACAAATTAAGAAATGAGATTTCAAAGAGATAAAGAAAT 253
 464 GlyIleIleCybAsnTYrThrIlePheTYrGlnAlaGlyGlyIleGlyPheSerIle 483
 254 GCGTTTATTAGTAATCAATATATTTTAAACCTGAAGGTGGAAGAAAGAGTTGAAATGA 313
 484 ThrValAsnSerSerIleLeuGlnIleTYrGlyLeuIleValArgIleThrSerTYr 503
 314 ACAGGAACCTGATGCTGCTACAGTACACACAGTGAAGTCTTTACAGGCTAATACATATAC 373
 504 IleValGlnValMetAlaSerThrSerAlaGlyIleThrAsnGlyIleThrSerIleAsn 523
 374 ACTGCTATATACATGAGCAAGCAAGACCTGCTGGAACCAAGGAGAGCAAAACATTC 433
 524 TyrThrLeuSerPheSerValPheGluIleLeuIleThrSerIleGlyIleGlyIle 543
 434 AAGACTTTGAAATTCATTAAGAAAGACCTTATTTTCATTCATTCATCCAGTTCGATTAC 493
 544 LeuLeuIleLeuIleIleLeuThrValAlaTYrGlyLeuValPheAsnIleLeuThr 563
 494 ATGTTGTTTCTGTTAGCGCTTGGATACGTCATTATGAAAAA---CACCTGTTTAA 550
 564 HisLeuCybTPPProThrValProAsnProAlaGlyIleSerSerIleAlaThrTYr 581
 551 AAGGTTGCTGCTGATGATGATCCCAATCTCAGAGAGCGTTGCACTGCACTGG 604

RESULT 6
 CFI174021
 LOCUS 637 bp mRNA linear EST 25-JUL-2003
 DEFINITION B0932D09-5 NIA Mouse Unfertilized Egg cDNA Library (long 1) Mus
 musculus cDNA clone NIA:B0932D09 IMAGE:30475340 5', mRNA sequence.
 CFI174021
 CFI174021.1 GI:33283570
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 637)
 Piao Y., Ko N.T., Lim M.K. and Ko M.S.H.
 Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 Genome Res. 11 (9), 1553-1558 (2001)
 MEDLINE 21429098
 PUBMED 11544199
 CONTACT: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@leuun-grc.nia.nih.gov
 Plate: B0932 row: D column: 09

Seq primer: M13 Reverse
 High quality sequence stop: 637
 POLYA=NO.
 Location/Qualifiers
 source

1. 637
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 /clone="NIA:B0932D09 IMAGE:30475340"
 /db_xref="taxon:10090"
 /dev_stage="Unfertilized Egg"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse Unfertilized Egg cDNA Library (long 1)"
 /note="Vector: pCMV-SPORT6 (Invitrogen), Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://leuun-grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library [Ref. Genome Res. 11: 1553-1558 (2001)]. [PMID: 11544199]. Total RNAs were extracted from a pool of 148 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-TGACGAGTCTAGATCGGAGCGGCCCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker Lb-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-5. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."

ORIGIN

Alignment Scores:

Pred. No.: 1,36-39 Length: 637
 Score: 468.50 Matches: 96
 Percent Similarity: 63.59% Conservative: 21
 Best Local Similarity: 52.17% Mismatches: 54
 Query Match: 13.28% Indels: 13
 DB: 7 Gaps: 4

US-10-006-265-17 (1-662) x CFI174021 (1-637)

7 ProSerCybValAsnLeuGlyMetIleThrIleAlaLeuIleProSerIleu 26
 119 CCTCGGAGTGAACGCTGGAAATATGTGACCTTGACATGTGGCATTCCTCTCTC 178
 27 CysIlePheSerLeuAlaIleAlaLeuProAlaIleProGluMetIleSerCybValTYr 46
 179 TGCAAAATTCAGCCCTGGAGTCTCTCCGACCTAAGCAAGAACATTCCTGGCTTTTAC 238
 47 TyrArgIleAsnLeuThrCybThrIleSerProGlyIleGlyIleThrSerTYrGlyTYr 66
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 67 ThrValIleArgIleThrTYrAlaIleGlyIleIleHisAspAsnCybThrIleAsnSer 86
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 87 ThrSerGluAsnArgAlaSerCybSerPhePheLeuProArgIleThrIle-----Pro 104
 335 TATATGACAAATGCTACAGAGCTTCATATTCCTTTCCCGTCCCTGCAATGCCCA 394
 105 AspAsnTYrThrIleGlnValGluAlaGluAsnGlyAspGlyValIleIleSerIleMet 124
 395 GACATCGCAGCTGTGAAAGTACAAAGCTCAAAATGAGATGTGTAAGTTAATCTGACATC 454

QY 125 ThrTTPArgheugluhbnilealaIyethrGluProProlysiIlePhearGVallys 144
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 QY 145 ProvalleuglyIlelysaArgMetIleGlnIleGluTTPriIlelysaProGluIeuaIaPro 164
 DB 515 CCAATT-----TGTATAGAAAGTTCCAGATACAAATG---AAACCGCGTGAAGAAAGACT 565
 QY 165 ValSerSeraspIeuIysrYrThrIleuAArgPhaArgThrValaIenSerThrIserTpmel 184
 DB 566 CGTGGGTTTCCTTACTAGATGATGCTTCGTTGCAAGACTGCAAGTGCACCTGACG 625
 QY 185 GluValaAsnph 188
 DB 626 GAAGTCATTTT 637

RESULT 7
 AK089305
 LOCUS
 DEFINITION
 AK089305 2804 bp mRNA linear HTC 03-APR-2004
 full-length enriched library, +ve dendritic cells cDNA, RIKEN
 stimulating factor 3 receptor (granulocyte), full insert sequence.
 ACCESSION
 VERSION AK089305.1 GI:26105194
 KEYWORDS HTC, CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 JOURNAL sequencing pipeline with 384 multiplex capillary sequencer
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 TITLE FANTOM Consortium.
 JOURNAL Functional annotation of a full-length mouse cDNA collection
 REFERENCE Nature 409, 685-690 (2001)

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research
 JOURNAL Group Phase I & II Team.
 REFERENCE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 AUTHORS Adachi, T., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
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 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M., and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/.
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 putative"

FEATURES
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 DB: US-10-006-265-17 (1-662) x AK089305 (1-2804)

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 Score: 465.50 Matches: 159
 Percent Similarity: 42.11% Conservative: 92
 Best Local Similarity: 26.68% Mismatches: 250
 Query Match: 13.19% Indels: 95
 DB: 3 Gaps: 26

US-10-006-265-17 (1-662) x AK089305 (1-2804)
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 QY 54 ThrTTPSerProGlyIySgluThrSerTyr---ThrGlnTyrThrValIyAsnArgThrYr 72
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 QY 73 AlaPheGlyGluIyShIleAspAnCyThrThrAsnSerSerThr----- 87
 DB 682 AGCTTAGAGAGCGGCCAC--TCTCAGTACCAAGGAGACCACTCCCGATGTGTG 738
 QY 88 ---SerGluAsnArgIaSerCySerPhePheLeuProArgIleThrIleProAsn 106
 DB 739 GCAAAAGAGGAGACCAACTGCTCCATCCCGAAAAAACTGTGCTGTAACGATAT 798
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Db 799 ATGGCCATCTGGGTGCAAGACAGAAATATGTAGGGTCCAGGAGTCCCAAGCTGTGC 858
 Qy 127 TTPARGLEUAGUAENIIeAlaYThrGLUPROpDLYSIIe-----PheArgValLys 144
 Db 859 CTCGACCCCATGAGTGTGTGAAATTGGAGCTCCCATGAGCTGCAGGCCCTGCAGACTTGGC 918
 Qy 145 ProValLeu-----GlyLeuYsaMetIleGlnIleGlyTrrIleLys 159
 Db 919 CCTATGTAAGTCTCTCACACAGCTGGCTGGCTGGCTGAGCTGGAAGCCATGGAAGCCC 978
 Qy 160 ProGluLeuAlaProValSerSerAspLeuYTrpThrLeuArgPheArgThrValAsn 179
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 Qy 180 SerThrSerTrpMetGluValAsnPheAlaYsaMetGlyAspGlyAsnGlnThrTrp 199
 Db 1039 -----TGAGCTCTGGTGTCCAGCTGCCTGCACAGAGAGACAG-----TTT 1080
 Qy 200 AsnLeuThrGlyLeuGlnProPheThrGlyTrpValIIeAlaLeuArgCysAlaValLys 219
 Db 1081 GAGCTCTGGGGGCTCCATCAGAGCCCACTGTAACCTTACAGATGCGATGC-----ATTGCG 1137
 Qy 220 GluSer-----LysPheTrpSerAspTrpSerGlnGlyLysMetGlyMetThrGluGlu 237
 Db 1138 TCATCTGTGCTGGATTCTGGAGCCCTGGAGCCCGGCTGCAGCTGAGGCTACCATG 1197
 Qy 238 GluAlaPro---CysGlyLeuGluLeuTrpArgValLeuLysProAlaGluAlaAspGly 256
 Db 1198 AAGGCCCCCAGCATCAGACTGACAGACGCTGTGTGAGAAAGAACTGAT---CGAGGG 1254
 Qy 257 ArgArgProValArgLeuLeuTrpLysValAlaArgValAlaProValLeuGlu----- 274
 Db 1255 ACAAGTAGTGTGAGCTGTCTGGAAGCCA-----ACGCCCTGCAGAGAGACAGCT 1305
 Qy 275 ---LysThrLeuGlyLysAsnIle---TrpTrpTrpProGluSerAsnThrAsnLeuThr 292
 Db 1306 GGACAGATCCAGGGCTACCTGCTGCTGAGATTCCCAAGATCATCAAGGCGAGACATA 1365
 Qy 293 GluThrMetAsnThrThrAsnGlnGlnLeuGluLeuHisLeuGlyGluSerPheTrp 312
 Db 1366 CACCTTGGCAACACAGCAGCTCAGCTGATCTTCTCTCCCTCCAGGAGCCAGAAC 1425
 Qy 313 ValSerMetIleSerTrpAsnSerLeuGlyLysSerProValAlaThrThrLeuArgIlePro 332
 Db 1426 GTGACCTCTGGCTGCTCAACAAAGAGGAGCTTCTTCACTACTACAGT----- 1476
 Qy 333 AlaIleGlnGluLysSerPheGlnCysIleGluValMetGlnAlaCysValAlaGluAsp 352
 Db 1477 GTTTCTCGAGAGAC-----GAAAGCT 1497
 Qy 353 GlnLeuValValLysTrpGlnSerSerAlaLeuAspValAlaAsnThrTrpMetIleGluTrp 372
 Db 1498 CCAGCTGTGACCGGACTCCATGAGCATGCGCCAGAACCTTACACATCTGGGTGAGCTGG 1557
 Qy 373 ---PheProAspValAspSerGluProThrThrLeuSerTrpGluSerValSerGlnAla 391
 Db 1558 GAAAGCCCCAGAGCTTGTGCTCAGAGGCTATCTCATATGATGGAAATGAGTTCTCCAGC 1617
 Qy 392 ThrAsn-----TrpThrIleGln----- 397
 Db 1618 TACATATAACAGCTATAGCTCTGATGATAGAACCTTAACGGGAACATCATCGAATTCTG 1677
 Qy 398 ---GlnAspLysLeuLysProPheTrpCysTrpAsnIleSerValTrpPrometLeuHis 416
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 Qy 417 AspLysValGlyGluProLysSerIleGlnAlaTrpAlaLysGluGlyValProSerGlu 436
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 Db 1798 GCTCCAGGCGTGCATCTAAAGCATGTTGGCAACCTGGGAGACAGCTGAGTGG----- 1851

Qy 457 IleProLysSerGluArgLysGlyIleIle-----CysAsnTrpThrIlePheTrpGln 474
 Db 1852 GTACCTTAGGGCCCTTAGGCTGGGAGATGATACCTTCAACCCATCAACCATTTCTGGGCC 1911
 Qy 475 AlaGluGlyGlyLysGlyPheSerLysThrValAsnSerSerIleLeuGlnTrpGlyLeu 494
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 Qy 495 GluSerLeuLysArgLysTrpSerTrpIleValGlnValMetAlaSerThrSerAlaGly 514
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 DEFINITION Homo sapiens CSF3R gene, VIRUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY412152
 VERSION AY412152.1 GI:39768117
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2592)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
 Ferritera,S., Wang,G., Zheng,X.H., White,T.J., Smnsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL PUBMED 14671302
 REFERENCE 2 (bases 1 to 2592)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
 Ferritera,S., Wang,G., Zheng,X.H., White,T.J., Smnsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
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 Alignment Scores:
 Pred. No.: 5..8e-38 Length: 2592
 Score: 462.50 Matches: 165

Percent similarity: 39.84% Conservative: 82
 Best Local Similarity: 26.61% Mismatches: 278
 Query Match: 13.11% Indels: 95
 Gaps: 25

US-10-006-265-17 (1-662) x AY12152 (1-2592)

QY CysValAsnLeuGlyMetTrpThrAlaLeuTrpMetLeuProSerLeuCysLys 28
 DB TGGCTGAAC-----TGGGGCAACAGCCTCGACATCTTGAGACCAAGTT---GAG 348
 QY PheSerLeuAlaAlaLeuProAlaLysProGluAsnIleSerCysValTyTyTyArg 48
 DB CTGGCGGCAAGCTTACCTCCAGCATATCCCAACACTCTCCCTGCTC----- 396
 QY LysAsnLeuThr-----CysThrTrpSerProGlyLysGluThrSerTy 63
 DB ATGAACTCTCAACCAAGCAAGCTTCATCTGCAAGTGGAGACAGACCTGAGACCACTA 456
 QY 64 ---ThGlnTyThrValLysArgThrTyArgAlaPheGlyGluLysHisAspAsnCysThr 82
 DB CCACACAGCTCACTCTGAAGAGTTTCAAGAGCGGGGCG-----AACTGTCA 504
 QY ThrAsnSerSerThr-----SerGluAsnArgAlaSerCysSerPhe 96
 DB ACCCAAGGGAGCTCACTCTGAGCTGCGTCCCAAGAGCGGAGAGCACTGCTGCATC 564
 QY PheLeuProArgLethrIleProAspAsnTyThrIleGluValGluAlaGluAngly 116
 DB 565 CCAAGCAACACCTGCTGTGTACCAAGATATGGGCACTGGTGGAGGCAAGAAATGCG 624
 QY 117 AspGlyValIleLysSerHisMetThrTyTrpArgLeuGluAsnIleAlaLysThrGlu 136
 DB 625 CTGGGGACCAAGCATGTCCCAACAATGTGTCTGATCCCATGTGTGTGAACCTGGAG 684
 QY 137 ProProLysIlePheArgValLysProValLeuGlyTleLysArgMetIleGlnIleGlu 156
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 QY 157 TrpIleLysProGluLeuAlaProValSerSer----- 167
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 QY 168 ---AspLeuLysTyThrLeuArgPheArgThrVal---Asn 179
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 QY 180 SerThrSerTrpMetGluValAsnPheAlaLysAsnArgLysAspLysAsnGlnThrTy 199
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 QY 422 ProTySerIleGlnAlaTyArgLysGluGlyValProSerGluGlyProGluThrLys 441
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 QY 442 ValGluAsnIleGlyValLysThrValThrIleThrTrpLysGluIleProLysSerGlu 461
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 QY 542 GlyGlyLeuLeuIleLeuIleIleLeuThrValAlaTyGlyLeuLysLeuProAsnLys 561
 DB 1903 CTCTGCTTTTCTCACTGCTCTGTGTGGAATGCTGTGCTCTGTGGCCCCCAAGG 1962
 QY 562 LeuThrHisLeuCysTrpProThrValProAsnProAlaGluSerSerIleAlaThrTrp 581
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RESULT 9
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 LOCUS BC040954
 DEFINITION Homo sapiens colony stimulating factor 3 receptor (grm1u0cyfe),
 mRNA (cDNA clone IMAGE:558879), containing frame-shift errors.
 ACCESSION BC040954
 VERSION BC040954.1 GI:27155071
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2792)
 Strausberg,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,D., Shenmen,C.M., Schuler,G.D.,

Altechul,S.F., Zeeberg, B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
 Diachenko,L., Marinina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
 Stagleon,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
 Schaefer,T.E., Brownstein,M.J., Uedlin,T.B., Toshiyuki,S.,
 Carinini,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
 McEwan,R.J., Malek,J.A., Gunatane,P.H., Richards,S.,
 Wortley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
 Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmitz,J., Myers,R.M.,
 Buterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalun,D.B.,
 Scherch,A., Schein,J.E., Jones,S.J., and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE
 PUBMED 22388257
 12477932
 2 (bases 1 to 2792)
 Strausberg,R.
 Direct Submission
 Submitted (06-DEC-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadan@systemsbio.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAX Plate: 84 Row: i Column: 2
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 27437046
 This clone has the following problem: frame shifted.

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ORIGIN
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 Pred. No.: 5.16e-34 Length: 2792
 Score: 426.50 Matches: 162
 Percent Similarity: 38.18% Conservative: 85
 Best Local Similarity: 25.04% Mismatches: 234
 Query Match: 12.09% Indels: 166
 DB: 3 Gaps: 25

US-10-006-265-17 (1-662) x BC040954 (1-2792)
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 Oy 29 PheSerLeuAlaIaLeuProAlaLysPrGluIaenLieserCyValTyTrrTyrArg 48

Db 442 CTGGCGGAGGCTACCTCCAGCATACCCAGCAACCTCTGCTC----- 489
 Oy 49 LysaenLeuThr-----CysThrTrpSerProGlyLysGluThSerTyr 63
 Db 490 ATGAACCTCAACAACAGCAGGCTCATCTCCAGTGGAGCCAGACCTGAACCCACCTA 549
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 Oy 83 ThrAnSerSerThr-----SerGluAnAaGAlaSerCysSerPhe 96
 Db 598 ACCCAAGGAGACTCATCTGAGTCTGCTGCCCAAGACGGGAGAGCCACTGCTGCTC 657
 Oy 97 PheLeuProArgIleThrIleProAaPAnTyTrIleGluValGluAlaGluAnGly 116
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 Oy 137 ProProLysIlePheArgValIyAaProValLeuGlyIleLysArgMetIleGlu 156
 Db 778 CCCCCATGCTGGGAGCATGAGACCC----- 804
 Oy 157 TrpIleLysProGluLeuAlaProValSerSer----- 167
 Db 805 ---AGCCTGAAGCGGCCCTCCCAAGCAGCTGCTACAGCTGTGGAGCA 858
 Oy 168 ---AaPLeuLysTyrThrLeuAaGPhaArgThVal---Asn 179
 Db 859 TGGCAGCAGGCTGCACATAATCAGAAAGTGAAGTGCAGCCCAAGCCGACGTGA 918
 Oy 180 SerThrSerTrpMetGluValaIaenPheAlaLysaAnArgLysaBpAsnGluThTyr 199
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 Oy 200 AaenLeuThrGlyLeuGluProPheThrGluTyValIleAlaLeuAaGysAlaVally 219
 Db 970 GAGCTCGGGGCTCTCCCAAGCCAGCCGCTTACACCGTGAATACGCTGATCCGCT-- 1027
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 Db 1078 GCTCAGCTGACCTTCCACTGCTTCAAGAGCCAGAGAGTGGCCCTTGAGCTTAA 1137
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DEFINITION	Mus musculus CSF3R gene, VIRUTUAL TRANSCRIPT, partial sequence,			
ACCESSION	AY412154			
VERSION	AY412154.1	GI:39768119		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 2535) Clark A.G., Gianowski S., Nielson R., Thomas P., Kejarival A., Todd M.A., Tanenbaum D.M., Civeallo D.R., Lu F., Murphy B., Ferriera S., Wang G., Zheng X.H., White T.J., Shinsky J.U., Adams M.D. and Cargill M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment			
AUTHORS	JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302			
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Alignment Scores:				
Pred. No.:	7.77e-31	Length:	2535	
Score:	396.50	Matches:	154	
Percent Similarity:	39.97%	Conservative:	89	
Best Local Similarity:	25.33%	Mismatches:	227	
Query Match:	11.24%	Indels:	140	
DB:	9	Gaps:	24	
US-10-006-265-17 (1-662) x AY412154 (1-2535)				
OY		35	ProAlatypProGLuAsnIIeserCyseValTYTYTYrArglyeAsn---LeuthrCys	53
Db		370	CCTGCAGACCCTCAACCTATCTCTGCTCAAGCACTTCACACACCAAGCCTGCTGTC	429
OY		54	ThrtPsePrroGLyLeGluThrSerTyrr--ThrgInTyThVallyeArghThTyrr	72

Db	430	CAGTGGAGGACAGGCTCTGAGACCCACCTGGCCACAGCTTATCTCTAAAG-----	480
Qy	73	AlApehglYgluYvHiaBrpAnScyThrThraAnSerSerThr-----	87
Db	481	AGCTTACAGAGCCGCGCCCA---TGTCAGTACCAAGGAGAACATCTCCCGATGTGTG	537
Qy	88	---SerGIuAnpAxlAserCySerSerPheRheLeuProAxlIeThrIleProAraAn	106
Db	538	GCMAAGAAAGGACAAACAATCTGCTCTCATCCCGAAAAAACTGCTGTGACAGTAT	597
Qy	107	TyTrThrIleGIuValaIGluValaGluAnngIuAerGIuValaIleLysSerHiaMetThrTy	126
Db	598	ATGGCCATCTGGGTGTCCAAAGCAGAAATATGTCTAAGGTCACAGAGATCCCAAGCTGTGC	657
Qy	127	TrpAerGIuAnpIleAlaLysThrgIuProPolyIle-----PheArgValLys	144
Db	658	CTGCAGCCCATGAGATGTGTGAAATTTGAGGCTCCCATGCTCCAGGCTCCGACATTTGC	717
Qy	145	ProValIleu-----GlyIleLysArgMetIleGlnIleLutPrIleLys	159
Db	718	CCTGATGTAGTCTCTCACACAGCTGGCTGGCTGTGGCTGAGCTGAAAGCCATGAAAGCC	777
Qy	160	ProGIuLeuAlaProValSerSerAerLysTyTrThrLeuAerPheArgThraIaAn	179
Db	778	AGTGAATACATGAAACAGAGATGTGAATCTGCCTACAGCCACAGCTCAAAAGAGCCAA	837
Qy	180	SerThrSerTrpMetGIuValaAsnPheAlaLysAaAaTgLYsAerLYsAaGlnThrTy	199
Db	838	-----TGACCTGTGTGTTCACCTGCTTCACAGAAAGACAG-----TTT	879
Qy	200	AsnLeuThrgIlyLeuGlnProPheThrgIuTrValIleAlaLeuAerGyAlaValLys	219
Db	880	GAGCTCTGGGAGCTCCATCAGAGCCCACTGATACACCTCAAGATGGAGTGC---ATTCCG	936
Qy	220	GIuSer-----LysPheTrpSerAerTrpSerGIuGlnLysMetGlyMetThrgIuGlu	237
Db	937	TCAATCTCTGCTGGATTTGAGGCTCTGGAGCCCC-----	972
Qy	238	GIuAlaProCySGIlyLeuGluLeuThraPrgValLeuLys---ProAlaGluAlaAer	255
Db	973	-----GCGCTGCAGCTAGAGGCTTACCAATGAAGGGTCCCCACCACTAGCTGG	102
Qy	256	-----GlyAerAerProValArgLeuLeuTrp	264
Db	1021	ACAGGTGGTGCAGAAAGCAACTAGATCCAGGAGACAGTG-AGTGTGACGCTGTCTGG	1077
Qy	265	LYsLYsAlaAerGIyAlaProValLeuGluLysThrLeuGlyTyTrAsnIleTrpTyTr	284
Db	1080	AAGCAGAGC-----	108
Qy	285	ProGIuSerAaThraAsnLeuThrgIuThrMetAaThraThraAsnGlnIleuGluLeu	304
Db	1089	-----ATACACCTTTGCCAACACACACAGCTCAGCTGATCTTC	112
Qy	305	HisLeuGlyGIuSerPheTrpValSerMetIleSerTyTrAsnSerLeuGlyLysSer	324
Db	1128	CTTCGTGCCCTCAGAGGCCAGAAAGTGACCTGTGGGCTTACAACAAGACAGGACCTCT	118
Qy	325	ProValAlaThrLeuAerGlyIleProAlaIleGlnGlySerPheGlnCysIleGluVal	344
Db	1188	TCACCTACTAGAGGCT-TTTTCTGGA-----	121
Qy	345	MetGIuAlaCySerValaIaGIuAerGlnLeuValaLysTrpGlnSerSerAlaAaP	364
Db	1214	GAACGAAGGTCTCAGCT-----GTGACCGGACTTCATGCCATGGCCCAAGAC	126
Qy	365	ValaAnThrTrpMetIleGluTrp---PheProAerValaAerSerGIuProThrThraLeu	383
Db	1262	CTTAACACCAATCTGGTGAAGCTGGGAAGCCCCACAGCTTGTGCTCAAGGGATATCATAT	1322
Qy	384	SerTrpGIuSerValSerGlnAlaThraAn-----TrpThrIleGln---	397
Db	1322	GAGTGGAGAAATAGATTTCTCCAGCTACAACTAAAGCACTATAAGTCTCGATGTGATAAACCT	138

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Qy 398 -----GlnAspLysLeuLysProPheTrpCySTyrAsn 408
Db 1382 AACGGGAACATCACTGGATTCTGTTAAAGACACATTAATCCCTTTCAGCTCTACAGA 1441
Qy 409 TlSerValIYrProMetLeuHiSaPlyVaIglYubProTySerIleGlnAlaTyr 428
Db 1442 ATTACAGTGGCTCCCTGTACCCAGCATCGTGGAGCCCTGTAAATGCTTACACCTTC 1501
Qy 429 AlLysGluGlyValProSerGluGlyProGluThrLysValGluMetIleGlyValLys 448
Db 1502 GCTGGAGAGAGAGCTCTCTCATGCTCAGCCGTGATTAAGATGTTGGACAAACC 1561
Qy 449 ThrValThrIleThrTyrLysGluIleProLysSerLysLysGlyIleIle----- 466
Db 1562 TGGGACACAGCTGAGATGG-----GTACCTGAGAGCCCTTACGCTGGAGATACCCCTC 1615
Qy 467 CysAsnTYrThrIlePheTYrGlnAlaGluGlyGlyLysGlyPheSerLysThrValAsn 486
Db 1616 ACCCACTACACATCTTCTGAGCGATGCTGGGACCACTCTTCTCCGACCCCTAAC 1675
Qy 487 SerSerIleLeuGlnTYrGlyLeuGluSerLeuLysArgLysThrSerTYrIleValGln 506
Db 1676 ATCTCCCTCATGACTTGTCTGAAGCACCCTGAGCCCGCAGTTGTATCATGCTTAC 1735
Qy 507 ValMetAlaSerThrSerAlaGlyGlyTYrAsnGlyThrSerIleAsnPhelYsThrLeu 526
Db 1736 CTCATGCGCACACAGTGGGAGGCTGCACCAACAGTACAGGCTTACCTCAGAGACCTTA 1795
Qy 527 SerPheSerValPheGluIleIleLeuIleThrSerLeuIleGlyGlyLeuLeuIle 546
Db 1796 GGTAAAGATATCTCAGAGATCCACTG----- 1822
Qy 547 LeuIleIleLeuThrValAlaTYrGlyLeuLysLysProAsnLysLeuThr-HisLeuCY 566
Db 1823 -----CTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 1876
Qy 566 S-----TyrProThrValProAsnProAl 574
Db 1877 CCTCTGCTCTGCTCTGCTCTGAGAAAGACTTCTTGTGTCAGATGTCAGACCAAGC 1936
Qy 574 agLysSerIleAlaThrTrp 581
Db 1937 CCACAGTACCTGAGCTCTG 1958

RESULT 12
CR610771 1931 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSOD1054YG09 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR610771
VERSION CR610771.1 GI:50491578
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1931)
REFERENCE 1
AUTHORS Li,W.B., Gruber,C., Jeesee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1931)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrete@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a Notti-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

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FEATURES
Source 1. 1931
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1054YG09"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 1.53e-30 Length: 1931
Score: 392.00 Matches: 130
Percent Similarity: 43.95% Conservative: 66
Best Local Similarity: 29.15% Mismatches: 179
Query Match: 11.11% Indels: 71
DB: 3 Gaps: 19

US-10-006-265-17 (1-662) x CR610771 (1-1931)
Qy 199 TYrAsnLeuThrGlyLeuGlnProPheThrGlyTYrValIleAlaLeuArgCys---Ala 217
Db 27 TATGAGCTCTGGGGCTCTCCAGCCAGCGGCTTACACCTCAGATGACATGATCCGC 86
Qy 218 ValLysGluSerLysPheThrSerAspTYrSerGlnGluLysMetGlyMetThrGluGlu 237
Db 87 TGGCCCTTCCCTGGCCACTGAGAGCACTGGAGCCCGACGCTGGAGCTGAGATCCGAA 146
Qy 238 GluAlaPro---CysGlyLeuGluLeuTrp-----ArgValLeuLysProAlaGlu 253
Db 147 CGGGCCCCCAGCTGACAGTGCAGACATGTCGCGGAGAGAGCAGCTGAGACCC----- 200
Qy 254 AlaAspGlyArgArgProValArgLeuLeuTrpLysAlaArgGlyAlaProValLeu 273
Db 201 -----AGGACAGTGCAGCTGTTCTGAAAGCCA-----GTGCCCTGGAG 239
Qy 274 Glu-----LysThrLeuGlyTYrAsnIleTYrTYrProGluSerAsnThrAsn 290
Db 240 GAAAGACAGGAGAGATCCAAAGTTTATGCTTCTTGGAGACCTCAGGCCAGGCTGGG 299
Qy 291 ---LeuThrGluThrMetAsnThrThraGlnGlnLeuGluLeuHiSaLeuGlyGlu 309
Db 300 GCCATCTGCCCTCTGCAACACACAGAGCTCAGCTGACCTTCCACTGCTTCAGAA 359
Qy 310 SerPheTrpValSerMetIleSerTYrAsnSerLeuGlyLysSer-----ProVal 326
Db 360 GCCAGAGAGTGGCCCTTGTGGCTTATTACTAGCCGGAGACCTCTGCTCCACTCCGGTG 419
Qy 327 -----AlaThrLeuArgIleProAlaIleGlnGluLysSerPheGlnCysIleGluVal 344
Db 420 GTCTTTCAGAAAGCAGAGGCCAGCTTGACCAACTCCAT----- 461
Qy 345 MetGlnAlaCysValAlaGluAsp-----GlnLeuValValLysTrpGlnSerSerAla 362
Db 462 -----GCCATGGCCCGAGACCTTCACAGCTCTGGGTAGGTGGAGCCCC----- 509
Qy 363 LeuAspValAsnThrTrp-----MetIleGluTrpPhe-----ProAsp 375
Db 510 -----AATCCAGAGCTCTGAGGCTATGATTTGATGAGTGGGGCTGGCCCCCAGAC 560
Qy 376 ValAspSerGluProThrThrLeuSerTrpGluSerValSerGlnAlaThrAsnTrpThr 395
Db 561 GCGAGCAATAGCAACAAGCTCGAGAGTGAACAGAAATGGAGAGCCAGGGGTTTCTG 620
Qy 396 IleGlnGluAspLysLeuLysAspProPheTrpCySTyrAsnIleSerValTYrProMetLeu 415
Db 621 CTGAAGAGAAC---ATCAGGCTCTTTCAGCTCTATGATCATGATCATGCTGCTCTGTAC 677
Qy 416 HisAspLysValIglYubProTySerIleGlnAlaTYrAlaLysGluGlyValProSer 435
Db 678 CAGGACACATAGGAGCCCTCCAGCATGCTATGCTTCAAGAAATGGCTCCCTCC 737

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OY 436 GUGUGYProGUThrValGluAenileGlyVallyThrValThrleThrTrpLys 455
DB 738 CATGCCCCAGAGCTGCATCTTAAGCATTTGGCAAGAGCTGGCACAGCTGGAGTGGGCTG 797
OY 456 GUUleProLysSerGUArglyGlyleleCyAenTyThrlePheTyGlnAla 475
DB 798 CCGAGAGCCCTGAGCTGGGAAAGAGCCCTTACCACTACACATCTTGGACCAAC 857
OY 476 GUUGlyGlyGlyPhe-----SerLys-ThrValAs 486
DB 858 GCTCAGAACCACTCTTGCCTTATGCTGACCCGTACACCCCTCCAGCGCATCTGTA 917
OY 486 nSerSerleleuGlnTyGlyleuGlnSerleuysArglyThrSerTyrlleValAl 506
DB 918 TGCCTCTCCCTGGCTGCTTGTCTTCATGAGCTGGAGCCCGCCAGCTGTATCACAATCA 977
OY 506 nValMetAlaSerThrSerAlaGlylyThrAnGlyThrSerleleuAsnPhelyThrle 526
DB 978 CCTCATGGCTGCCAGCCAGGCTGGGGCCCAACAGTACAGTCCACCTGATGACCTT 1037
OY 526 userPheSerValPheGUleleleleuThrSerleuileGlyGlyGlyleuLeu1 546
DB 1038 GACCCCAAGAGGGGTGAGAGCTACACATCATCTTGGGCTGTTCGCTCTGCTGCT 1097
OY 546 eleuLeileleuThrValAlAlaTyGlyleuLysProAsnLysleuThrHisleuCy 566
DB 1098 CACCTGCTCTGTGAACTGCTGCTGCTGTTCAGCCCAACAGAGAAATCCCTC-- 1155
OY 566 sTPProThrValProAsnProAlaGlySerSerleleuAlaThrTP----- 581
DB 1156 -TGCCCAAGTGTCCAGACCAGCTCAGACAGCCTGGGCTCTGGTGGCCCAATCAT 1214
OY 582 -HisGUAspAspPheLys-----AspLysleuAsnle 592
DB 1215 GGAGAGAGATGCTCTTCAGCTGCGGCTTGGCAGCCACCATCACCAGCTCAGT 1274
OY 592 uLyglSerAspAsp 597
DB 1275 GCTGAGAGAGATGTA 1290

RESULT 13
BC020454 1512 bp mRNA linear HTC 19-NOV-2003
LOCUS Mus musculus interluekin 6 signal transducer, mRNA (cDNA clone
DEFINITION IMAGE:3598166).
ACCESSION BC020454
VERSION BC020454.1 GI:18045025
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS
1 (bases 1 to 1512)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Scheeter,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Palmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldi,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Umedin,T.B., Tothiyaki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Muhlthay,S.J., Bosak,S.A., McSwan,P.J.,
McGerran,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Wojley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bonfield,G.G., Blakeley,R.W., Touchman,A.J., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalka,J., Smalls,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length

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JOURNAL
MEDLINE
PUBMED
12477932
2 (bases 1 to 1512)
REFERENCE
AUTHORS
Strausberg,R.
TITLE
Direct Submission
JOURNAL
Submitted (03-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
REMARK
COMMENT
Contact: MGC help desk
Email: gcgphs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (ILNL)
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAC Plate: 16 Row: K Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6754337
This clone has the following problem: no poly-a-tail.
FEATURES
location/Qualifiers
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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3598166"
/tissue_type="mammary tumor, C3(1)-Tag model, infiltrating
ductal carcinoma, 5 month old virgin mouse."
/clone_id="NCI CGAP_Mam6"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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Pred. No.: 1,03e-26 Length: 1512
Score: 355.00 Matches: 90
Percent Similarity: 50.33% Conservative: 63
Best Local Similarity: 29.61% Mismatches: 133
Query Match: 10.06% Indels: 18
DB: 3 Gaps: 11
US-10-006-265-17 (1-662) x BC020454 (1-1512)
OY 35 ProAlaLysProGUAnleSerCyValTyTyTyArglyAsnleuThrCyThr 54
DB 613 CCACATTAACCTACAAATTTGACTTGTGATGAGGAGGAATATATGCTGTGCGAG 672
OY 55 TysPserProGUyGlyuThrSerTy---ThrGlnTyThrValLysArgTyThrAla 73
DB 673 TGGGACCCCGAGAGGAGACTTACCTTGAAACAAATPACACTTGAATACAGAGTGGCA 732
OY 74 PheGUyGlyuysHIsAspAsnCysThrThrAsnSerSerThrsSerGUAsnArgAlaSer 93
DB 733 ---ACAGAGAGATTTCCTGATGCTGCACATCAAGATGCACT-----TCA 774
OY 94 CysSerPhe---PheLysProAlaGlyleThrleProAsnTyTyThrleGluValGlu 112
DB 775 TGTATGTGCTACACTACAGCCACCATATATGTC-----AACATGGAAGCTTGAGTGGAA 828
OY 113 AlaGUAnGlyAspGUyValleleLysSerHisMetThrTyTyTPArgLeuGUAnle 132

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Db      829 GCAGAGATGCCCCCTGGGAGGCTCTCCAGAGCTATCAATTGTGACCCCGTGATATAA 888
Qy      133 AlAlvThrcIuPrpPolysIlePheArgValLysProValLeuGlyIleLysArgMet 152
Db      889 GTGAATCCCAACCCCACTAATAATTATATGATGACCACTCAGAGAATATATCCAGTAA 948
Qy      153 IlleGlnIleGluTrpIleLysProGluLeuAlaProValSerSerAspLeuLysTyrThr 172
Db      949 TTAAGATATCATGAGGTCACTTCAAGGCTGGGGCTTT---TTAAGATCTAAAGTCTGAC 1005
Qy      173 LeuArgPheArgThrValAsnSerThrSerTyrMetGluValAsnPheAlaLysAsnArg 192
Db      1006 ATCCAAATATGAGCAACAAAGATGCTCAACTGATCCAGGTCCTCTT---GAAAGATACA 1062
Qy      193 LysAspLysAsnGlnThrTyrAsnLeuThrGlyLeuGlnProPheThrGluTyrValIle 212
Db      1063 ATGTCTCTCGAAGCTTCTTCACTGTGCAGAGACCTCAAGCTTTTACAGAATATGTGTTT 1122
Qy      213 AlAlvArgCysAlaValLysGlnSer-----LysPheTyrSerAspTyrSerGlnGlu 230
Db      1123 AGGATCCGG---TCCATTAAGACAGTGGGAGAGGCTACTGAGTGACTGAGTGAAGAG 1179
Qy      231 LysMetGlyMetThrGluGluAlaProCys---GlyLeuGluLeuTyrPargValLeu 249
Db      1180 GCTAGTGGGACCACTATCGAAGACAGACATCCAAACCAAGTTTCTGTATTAAGACA 1239
Qy      250 LysProAlaGluAlaAspGlyArgArgProValArgLeuLeuTrpLysLysAlaArgGly 269
Db      1240 AATCATCCCATGAGGAGCAAGATATATGATCTGTACGGCTCATATGAGAAAGGACCTCTT 1299
Qy      270 AlaProValLeuGluLysThrLeuGlyTyrAsnIleTrpTyrTrpProGlnSerAsnThr 289
Db      1300 TCTGAAGCCAAATGGGAAATCTTGATATGAAGTG-----ATTCTTACGAGCTCAAG 1353
Qy      290 AsnLeuThrGluThrMetAsnThrThrAsnGlnLeuGluLeuIleLysGlyGlu 309
Db      1354 TCAGTCTCAACAAACGTACACAGTCACTGGCAGAGGTGACCGTGAATCTCACCAATGAC 1413
Qy      310 SerPheTrpValSerMetCysLeuTyrAsnSerLeuGlyLysSerProValAlaThrLeu 329
Db      1414 CGCTATGTAGCGCTCTCTAGCAGCAAGAAACAAAGTGGCAATCAGTCACTGTCTC 1473
Qy      330 ArgIleProAla 333
Db      1474 ACCATCCCCCAGC 1485

RESULT 14
CAS61173      592 bp      mRNA      linear      EST 19-NOV-2002
LOCUS      K0283D09-5N NIA Mouse Unfertilized Egg cDNA Library (Long) Mus
DEFINITION      musculus cDNA clone NIA:K0283D09 IMAGE:30052652 5', mRNA sequence.
ACCESSION      CA561173
VERSION      CA561173.1 GI:25105828
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (base 1 to 592)
Plao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A.,
Martin,K., Aliba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
(Long)
unpublished (2001)
Other_ESTs: K0283D09-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igun.grc.nia.nih.gov
Plate: K0283 row: D column: 09
Seq primer: M13 Reverse

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High quality sequence stop: 592
POLYA=NO.

FEATURES
source Location/Qualifiers

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone="NIA:K0283D09 IMAGE:30052652"
/issue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long)"

/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen]:

5'-pGACTAGTCTAGATCGCAGCGCCGCTTTTCTTTT-3',
treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to

lone-linker lI-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using

Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector.

The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Plao (NIA)."

ORIGIN

Alignment Scores:

Pred. No.: 1,63e-26 Length: 592
Score: 347.00 Matches: 67
Percent Similarity: 65.89% Conservative: 18
Best Local Similarity: 51.94% Mismatches: 34
Query Match: 9.84% Indels: 10
DB: 6 Gaps: 2

US-10-006-265-17 (1-662) x CA561173 (1-592)

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Qy      6 GlnProSerCysValAsnLeuGlyMetMetTrpThrAlaLeuTrpMetLeuProSer 25
Db      229 CAGCGCTCGGGGTGTAAAGCCTGGAATTAATGTGACCTTGCGACTGTGGCATTCCTTTC 288
Qy      26 LeuCysLysPheSerLeuAlaLeuProAlaLysProGlnAsnLysSerCysValTyr 45
Db      289 CTCTGCAAAATTCAGCTCGCAGTCTCTGCGACTTAAGCCAGAAACAATTCCTGCGCTTT 348
Qy      46 TyrTyrArgLysAsnLeuThrCysThrTyrSerProGlyLysGluThrSerTyrThrGln 65
Db      349 TACTTGACAGAAATGTGACTTGACCTTGAGACCAAGAGAAAGAAACATATATACAC 408
Qy      66 TyrThrValLysArgThrTyrAlaPheGlyLysLysAspAsnCysThrThrAsnSer 85
Db      409 TACATGTGACTTGTGACTTACCTCATGAGAAA-----AGC 444
Qy      86 SerThrSerGlnAsnArgAlaSerCysSerPhePheLeuProArgIleThrIle----- 103
Db      445 AATTATATGAGCAATGCTATCAGAGGCTTCATTTCTTTTCCCGTCCGTGCAATGCC 504
Qy      104 ProAspAsnTyrThrIleGluValGluAlaGlnGlyArgGlyValIleLysSerHis 123
Db      505 CCAGACATCTGACGTGTGAAGTACAAAGCTCAAAATGAGATGTAAAGTTAATCTGAC 564

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QY 124 MctHrTYrTPArgLeuGluAnile 132
 Db 565 ATCACTATTGGCATTTAATCTCCATA 591

RESULT 15
 CA560924 479 bp mRNA linear EST 19-NOV-2002
 LOCUS K0279C07-SN NIA Mouse Unfertilized Egg cDNA library (long) Mus
 DEFINITION musculus cDNA clone NIA:K0279C07 IMAGE:30052254 5', mRNA sequence.
 ACCESSION CA560924
 VERSION CA560924.1 GI:25105579
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 479)
 Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A.,
 Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.
 Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
 (Long)
 JOURNAL Unpublished (2001)
 COMMENT Other ESTs: K0279C07-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: K0279 row: C column: 07
 Seq primer: M13 Reverse
 High quality sequence stop: 479
 POLY-A-No.

FEATURES
 source
 1..479
 Location/Qualifiers
 /organism="Mus musculus"
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 /clone="NIA:K0279C07 IMAGE:30052254"
 /tissue_type="Unfertilized Egg"
 /lab_host="DH10B"
 /clone_11b="NIA Mouse Unfertilized Egg cDNA library
 (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI, Site 2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
 extracted from a pool of 1488 unfertilized eggs.
 Double-stranded cDNAs were synthesized with an Oligo (dT)
 primer (Invitrogen):
 5'-GGACTAGTTCTGATCGGAGCGGCCCTTTTTTTTTTTT-3',
 treated with T4 DNA polymerase, and purified by
 ethanol precipitation. The cDNAs were ligated to
 lone-linker L1-SalI, purified by phenol/chloroform, and
 separated from free linkers by Centricon 100. Then, the
 cDNAs were amplified by long-range high fidelity PCR using
 Ex Tag polymerase (Takara) with a primer SalI-S. The
 products were purified by phenol/chloroform and Centricon
 100. The cDNAs were digested with SalI and NotI enzymes
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.
 The DH10B E. coli host was transformed with the ligation
 mixture by the standard chemical method. The average
 insert size is about 2.5 kb. The library was constructed
 by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:
 Pred. No.: 4e-26 Length: 479
 Score: 342.00 Matches: 66
 Percent Similarity: 65.62% Conservative: 18

Best Local Similarity: 51.56%
 Query Match: 9.69%
 Db: 6
 Gaps: 2

US-10-006-265-17 (1-662) x CA560924 (1-479)

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 QY 27 CysIysPheSerLeuAlaAlaLeuProAlaIysProGluAnileSerCyValaTyTr 46
 Db 179 TGCAATTCAGCCTGGCAGTCTCCGACCTAAGCAGAGAACATTCTCGGTCTTAC 238
 QY 47 TyrArgIysAnleUthrCySerThrTrpSerProGluIysGluThrSerTyTrGlnTyr 66
 Db 239 TTCGACAGAAATCTGACTTGCACTTGAGACAGAGAAAGAAACCAATGATACAGCAT 298
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 Db 299 ATGTGACTTGACTTACTCTATGAAAA-----AGCAAT 334
 QY 87 ThrSerGluAsnArgAlaSerCySerPhePheLeuProArgIleThrIle-----Pro 104
 Db 335 TATAGTCATATGCTACAGAGGCTTCAATCTTTCCCTTCTGTCATGCCCA 394
 QY 105 AspAnTyThrIleGluValGluAlaGluAnGlyAspGlyValIleIysSerHisMet 124
 Db 395 GACATCTGCACTGTGAAGTCAAGCTCAAAATGAGATGTGTAAGTAAATCTGCACATC 454
 QY 125 ThrTYrTPArgLeuGluAnile 132
 Db 455 ACATATTGGCATTTAATCTCCATA 478

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Creation date: 03-15-2005

Indexing Officer: NKIDANE - NIGIST M. KIDANE

Team: OIPE Scanning

Dossier: 09757415

Legal Date: 02-14-2005

No.	Doccode	Number of pages
1	SRNT	56

Total number of pages: 56

Remarks:

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